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066205 porcine tra

097517 clostridium

097517 clostridium

09752 saccharomyc

099pk2 drosophila

097784 bacteriopha

097785 bacteriopha

097785 bacteriopha

097785 bacteriopha

09775 rattus sp.

014715 homo sapien

014715 homo sapien

014715 homo sapien

066545 human herpe

06545 human herpe

06545 human herpe

06545 human herpe

06772 litoria rub

07979 drosophila

099410 porcine tra

099410 porcine tra

099410 borcine tra

099413 homo sapien

09135 homo sapien

09443 homo sapien

09443 homo sapien

09443 homo sapien

09443 nomo sapien

09443 nomo sapien

09443 nomo sapien

09443 nomo sapien

09457 gossypium h
           099182 pterolebias
09712 escherichia
09417 canis famil
09477 canis famil
05176 pseudomonas
09777 pseudomonas
09775 streptomyce
P78484 homo sapien
09026 homo sapien
09026 homo sapien
09023 stripa sarce
095723 simian sarce
98573 simian sarce
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
ALPHA-MYOSIN HEAVY CHAIN (FRAGMENT).
01-NOV-1998 cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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P87225
O13591
O9VPK2
O9XNP8
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O11605
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P82440
O61723
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P82072
007354
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09TT78
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09R7H9
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081968
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09R3X0
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Q28742
Q28742;
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Q28742
Q28742 oryctolagus
PR2101 litoria rub
Q15889 homo sapien
Q16468 homo sapien
Q15888 homo sapien
Q9479 mus sp. mep
Q9433 pseudorabie
Q4755 escherichia
Q9417 drosophila
Q9417 drosophila
Q94187 caloglossa
Q91187 caloglossa
Q91187 caloglossa
Q91387 caloglossa
                                             Search time 111.26 Seconds (without alignments)
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EMBL; L32070; AAA73879.1; -.
NON_TER 1 1
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Hum. Mol. Genet. 0:0-0(0).
EMBL; L32069; AAA73878.1; -
NON_TER 1 1
NON_TER 8
SEQUENCE 8 AA; 1068 MW;
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Matches 3; Conservative
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Matches 2; Conservative
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SEQUENCE FROM N.A.
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1 LHPSKLN 7
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1 MHGP 4
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SEQUENCE
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Q16468;
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                                                             "Characterization of genomic clones specifying rabbit alpha- and beta-
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Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
Caskey C.T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-SKIN SECRETION; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.; Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria rubella.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1015889 PRELIMINARY; PRT; 8 AA.
015889 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 07, Last annotation update)
01-NOV-1998 (TrEMBLrel. 07, Last annotation update)
(CLONE XP15H8B) (FRAGMENT).
Homo sapiens (Human).
EUKARYOTE, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Neobatrachia, Bufonoidea, Hylidae,
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SEQUENCE FROM N.A.
MEDLINE; 84221901.
Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.J., Jokovcic S.,
Rabinowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18; DB 13; Length 7; Pred. No. 3e+05;
                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                  Score 20; DB 6; Length 7; Pred. No. 3e+05;
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
BLECTRIN 5.
                                                                                                                        Myosin.
NON_TER 1 1
SEQUENCE 7 AA; 916 MW; 6B1B1AA1E69326B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 7 AMIDATION.
7 AA; 834 MW; 6DD05B076B0B5030 CRC64;
                                                                           ventricular myosin heavy chains.";
Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984)
EMBL; K01698; AAA31415.1;
                                                                                                                                                                                                                                                                                                                                                                     7 AA.
                                                                                                                                                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Litoria rubella (Desert tree frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aust. J. Chem. 52:0-0(1999).
Amphibian skin; Amidation.
MOD. RES 7
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Best Local Similarity 60.0%;
Matches 3; Conservative
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Best Local Similarity 40.0%;
Matches 2; Conservative
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1 IYEPE 5
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EMBL, X88976; CAAG1407.1; -. NON_TER 8 8 8 SEQUENCE 8 AA; 925 MW; FD5411A7376871E6 CRC64:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      James L.A., Ogilvie D.J., Yamakawa K., Nakamura Y., Stirling C.J., Anand R.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                      32.1%; Score 17; DB 4; Length 8; 42.9%; Pred. No. 3e+05;
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01-NOY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DNA FOR COSMID CC13-1134 PCR PRIMER I (FRAGMENT).
Homo sapiens (Human).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
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0474472325A761E7 CRC64;
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Pred. No. 3e+05;
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01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, SXL E1 FORM (FRAGMENT).
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9 AA; 1089 MW;
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Matches 2; Conserv
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EMBL, AJ010303; CAA09075.1; -.

SEQUENCE 8 AA; 875 MW; 262DDAB76AAB05BB CRC64;
                     Gaps
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Kounnas M.Z., Wolz R.L., Gorbea C.M., Bond J.S.;

Meprin-A and -B. Cell surface endopetidases of the mouse kidney.";

J. Biol. Chem. 266:17350-17357(1991).

SEQUENCE 8 AA: 877 MW; 43A5A76AB4069DD4 CRC64;
                                                                                                                                                             Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SUID HERPESYINGS I PUTATIVE UL47 AND UL46 GENES AND PARTIAL GB
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 Length 8;
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Alphaherpesvirinae; Varicellovirus.
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 Score 15;
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ilarity 50.0%;
Conservative 1
 28.3$;
66.7$;
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Best Local Similarity 66,,,
اتم 2; Conservative
                    Conservative
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Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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3 MRDP 6
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MEDLINE; 83195078.
HOOVER T.A., Roof W.D., Foltermann K.F., O'Donovan G.A., Bencini D.A.,
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MEDLINE; 98337843.
Erickson J.W., Cline T.W.;
"Key aspects of the primary sex determination mechanism are conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequence of the structural gene (pyrB) that encodes the catalytic polypeptide of aspartate transcarbamoylase of Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                    Pauza C.D., Karels M.J., Navre M., Schachman H.K.; "Genes encoding Escherichia coli aspartate transcarbamoylase: the
047556 PRELIMINARY; PRT; 9 AA.
0147556 (TEMBLEEL 01, Created)
01-NOV-1996 (TEMBLEEL 01, Last sequence update)
01-NOV-1998 (TEMBLEEL 08, Last annotation update)
ASPARTATE TRANSCARBAMOXLASE REGULATORY CHAIN (FRAGMENT).
PYRI.
Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Bell M., Cline T.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF046045; AAC97605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA; 1085 MW; 99EFD723344AA1F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 80:2462-2466(1983).
EMBL; J01670; AAA24475.1; -.
NON_TER
SEQUENCE 9 AA; 1085 MW; 99FFN733344871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pyrB-pyrI operon.";
Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024(1982)
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Development 125:3259-3268(1998).
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RESULT 078337

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Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai H.; "Reproductive and genetic distinction between broad and narrow entities of Caloglosas continua (Delesserlaceae, Rhodophyta)."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                    Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawiser September and genetic distinction between broad and narrow entities of Caloglossa continua (Delesseriaceae, Rhodophyta)."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AB023381; BAA88912.1;
                                                                                                                                                                                                01-MXY-2000 (TrEMBLrel. 13, Last sequence update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
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Pred. No. 3e+05;
3; Mismatches
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22.2%;
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9 AA; 977 MW;
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Best Local Similarity 22.2
Matches 2; Conservative
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Matches 2; Conservative
                     Conservative
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1 FVETPTANV
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FVETPTANV
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SEQUENCE 9
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SEQUENCE
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Q9TJ85;
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                   Matches
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                                                  Gaps
                                                                                                                                                                                                                                                                                                                                 Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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Eukaryota: Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                               Indels
                   Length 9;
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                                               0;
                Score 14; DB 5;
Pred. No. 3e+05;
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Pred. No. 3e+05;
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Pred. No. 3e+05;
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                                                Mismatches
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                 26.4%;
66.7%;
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22.2%;
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22.2%;
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EMBL; D87813; BAA31279.1;
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Best Local Similarity 22.2
Matches 2; Conservative
                                               Conservative
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Query Match
Best Local Similarity
Lac 2; Conserve
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Best Local Similarity
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DFN 4
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SEQUENCE
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"Evolutionary divergence in the red algae Caloglossa leprieuril and C. apometotica.";
J. Phycol. 34:361-370(1998).
EMBL: DRGAME. TREASTORMENT RESTORMENT OF THE PROPERTY OF TH
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Eukaryota: Rhodophyta: Florideophyceae; Ceramiales; Rhodomelaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zuccarello G.C., West J.A., King R.J.;
"Biogeography of Bostrychia moritziana (Ceramiales).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF126715; AAD55883.1; -.
EMBL; AF126701; AAD55885.1; -.
EMBL; AF126704, AAD58861.1; -.
EMBL; AF126706; AAD58865.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-R.3881.QLD, M3001.MI, R3826.BZ, AND B.R.F.M.BZ;
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Pred. No. 3e+05;
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      Mismatches
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      Conservative
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1 FVETPTANV
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1 FVETPTANV
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SEQUENCE
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NON_TER
SEQUENCE
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STRAIN-JAM1122, AND 962;
Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai I "Reproductive and genetic distinction between broad and narrow entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023883; BAA88916.1; -.
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Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai I "Reproductive and genetic distinction between broad and narrow entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023380; BAA88910.1; --
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Eukaryota: Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
Caloglossa.
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Eukaryota: Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
81BULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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3e+05;
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Pred. No. 3e+05;
                                                                                                                                                                                                                                                            9 AA.
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22.2%;
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Matches 2; Conserv
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1 FVETPTANV
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1 FVETPTANV
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Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
"Evolutionary divergence in the red algae Caloglossa leprieurii and C.
apomeiotica.";
J. Phycol. 34:361-370(1998).
EMBL; D89961; BAA313707.1; -.
NON_TER 1 1
SEQUENCE 9 AA; 977 MW; CAlA4DC1B771AB02 CRC64;
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STRAIN-1048, 902, 490, 932, 880, 1053, 1052;
Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
"Yoolutionary divergence in the red algae Caloglossa leprieurii and C."
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
Caloglossa.
                                                                                                                                                                                                                                                         Caloglossa ogasawaraensis.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
Caloglossa.
                                                                  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1.5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
(FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14; DB 10; Length 9; Pred. No. 3e+05;
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Pred. No. 3e+05;
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apomeiotica.";
J. Phycol. 34:361-370(1998).
EMBL; D89959; BAA31303.1; -.
EMBL; D89949; BAA31283.1; -.
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22.2%;
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EMBL, D89955, BAA31295.1; --
EMBL, D89956, BAA31297.1; --
EMBL, D89957; BAA31299.1; --
EMBL, D89958; BAA31301.1; --
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22.2%;
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Matches 2; Conserv
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Best Local Similarity
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1 FVETPTANV
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Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
"Evolutionary divergence in the red algae Caloglossa leprieurii and C. apomeiotica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.; "Evolutionary divergence in the red algae Caloglossa leprieurii and C. apomelotica."
J. Phycol. 34:361-370(1998).
EMBL: D89950; BAA31285.1; -.
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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Pred. No. 3e+05;
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22.2%;
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EMBL; D89960; BAA31305.1; -.
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Brouillette J.A., Andrew J.R., Venta P.J.;
"Estimate of Nucleotide Diversity in Dogs Using a Pool-and-Sequence Method to Identify Single Nucleotide Polymorphisms.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202073; AAF20918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P., Hermand P., Salmon C., Cartron J.-P., Colin Y.; "Molecular cloning and protein structure of a human blood group Rh polypeptide."; Proc. Natl. Acad. Sci. U.S. A. 97.277.
                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoá; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                        Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.; "Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
THYMIDYLATE SYNTHASE (FRAGMENT).
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Am. J. Hum. Genet. 60:808-817(1997).
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1049 MW;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Atherinomorpha; Cyprinodontiformes; Aplocheiloidei; Aplocheilidae;
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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Murphy W.J., Thomerson J.E., Collier G.E.;
A molecular phylogeny of Neotropical aplocheiloid killifishes
(Cyprinodontiformes, Rivulidae).";
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF002591; AAD01074.1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
HYPOTHETICAL PROTEIN HI0004 (FRAGMENT).
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66.7%;
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1 FVETPTANV
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gene encoding
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Martin K., Morlin G., Smith A., Nordyke A., Eisenstark A., Golomb M.;

"The tryptophanase gene cluster of Haemophilus influenzae type b:
evidence for horizontal gene transfer.";
J. Bacteriol. 180:107-118 (1998).

EMBL; AF003252; AAB96582.1; -.
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EMBL, M28356; AAA99233.1;
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        Score 13; DB 6; Length 8;
Pred. No. 3e+05;
2; Mismatches 0; Indels
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0; Mismatches 0; Indels
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EMBO J. 13:3472-3480(1994).

EMBL: 234523; CAR84282.1; -.

NON_TER 9 9 AA; 1047 MW; 9A8BCB07633B1045 CRC64;
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MEDLINE; 88234523.
Kawakami T., Kawakami Y., Aaronson S.A., Robbins K.C.;
"Acquisition of transforming properties by FYN, a normal SRC-related human gene.";
Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874(1988).
EMBL; M20284; AAA52491.1; -.
NON_TER 1
1 SEQUENCE 9 AA; 1143 MW; 12BA1729D5A6D73B CRC64;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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U-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
FYNC ONCOGENE, 3' END, CLONE PFYN-C-11. (FRAGMENT).
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Cucujiformia; Chrysomelidae; Chrysomelinae; Leptinotarsa
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MEDLINE: 96253074.
Wada C., Ishlgaki M., Toyo-oka Y., Yamabe H., Ohnuki Y., Takada F.,
Yamazaki Y., Ohtani H.;
"[Nucleotide sequences at intron 6 and exon 7 junction of fibroblas'
growth factor receptor 2 and rapid mutational analysis in Apert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
"Copurification of Small heat shock protein with alpha B crystallin
from human stelletal mischle ".
                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
LED-NRY-2000 (TREMBLrel. 13, Last annotation update)
LED-NRY-1-NEUROPEPTIDE F-RELATED PEPTIDE.
LED-NRY-1-NEUROPEPTIDE F-RELATED PEPTIDE.
LEptinotarsa decemilneata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda: Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
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       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
FGFRZ PROFEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
28 KDA HEAT SHOCK PROTEIN HOMOLOG FRAGMENT 1.
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J. Biol. Chem. 267:7718-7725(1992)
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EMBL; S82438; AAD14392.1;
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Best Local Similarity 42.9%;
Matches 3; Conservative
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Best Local Similarity 66.79
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                                                                     Homo sapiens
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MEDLINE: 96245438.

Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,
Van Beaumen J., De Loof A.;

"Insect neuropeptide F (NPF)-related peptides: isolation from Colorado
potato beetle (Leptinotarsa decemlineata) brain.";
Insect Blochem. Mol. Biol. 26:375-382(1996).

SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;
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Devare S.G., Shatzman A.R., Robbins K.C., Rosenberg M., Aaronson S.A.; "Expression of the PDGF-related transforming protein of simian sarcoma virus in E. coll.";
Cell 36:43-49(1984).
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Mindich L., Qiao X., Qiao J., Romantschuk M., Hoogstraten D.;

Mindich L., Qiao X., Qiao J., Romantschuk M., Hoogstraten D.;

Isolation of additional bacteriophages with genomes of segmented double-stranded RNA.";

Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF125675; AAD22555.1;

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SEQUENCE 9 AA; 1048 MW; 9
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Matches 2; Conservative
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Wabhitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
Peptides from the skin glands of the Australian buzzing tree frog Litori electrica. Comparison with the skin peptides from Litoria Aust. J. Chem. 52:0-0(1999).
Amphibian skin; Amidation.
Amphibian skin; Amidation.
BOD_RES
SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Query Match

24.5%; Score 13; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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22.6%; Score 12; DB 13; Length 5;
Best Local Similarity 33.3%; Pred. No. 3e+05;
Matches 1; Conservative 2; Mismatches 0; Indels
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SEQUENCE.
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Search completed: December 16, 2000, 04:22:14 Job time: 4608 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             paramyxoviridae; RNA virus; attenuation; vaccine
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(KITA ) KITASATO KENKYUSHO SH.
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N-PSDB; Q40480.
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10-MAR-1992;
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2.827 Million cell updates/sec
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
                                                                     protein search, using sw model
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Score

Result

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pro pro protein; attenuation; non-segmented; negative sense; vaccine; immunity;

single stranded RNA virus; Mononegavirales

Measles virus. WO9813501-A2

Measles virus Rubeovax vaccine L protein.

(first entry)

13-0CT-1998

W48707 standard; Protein; 2183 AA.

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              The sequence of the entire genome of the attenuated measles virus strain AIK-C has been determined and contains 6 open reading frames. The sequence of the L protein was deduced from the sixth ORF. The virus retains high immunogenicity with reduced pyrogenicity and no neurological complications.
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                     Score 53; DB 14; Length 2183;
Pred. No. 0.16;
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100.0%;
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                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative
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Tatem JM,

Sidhu MS,

Randolph VB,

Murphy BR,

WPI; 1998-230710/20. N-PSDB; V18268.

(AMCY) AMERICAN CYANAMID CO. (USSH) US DEPT HEALTH & HUMAN SERVICES.

96US-0026823.

19-SEP-1997; 27-SEP-1996;

02-APR-1998.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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100.0%; Pred. No. 0.16;
Live 0; Mismatches 0;
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W48708
ID W48708 standard; Protein; 2183 AA.
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Query Match Best Local Similarity Matches 9; Conserv

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L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the L protein from Measles virus Zagreb vaccine
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                                                                                                                       Sidhu MS, Tatem JM,
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Best Local Similarity 100...
9, Conservative
                                                                                                                       Murphy BR, Randolph VB,
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N-PSDB; V18271.
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                                                                                                                                                                                                             N-PSDB; V18270
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W48710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the L protein from Measles virus Moraten vaccine. This sequence is used in a method which involves the isolation of recombinantly generated, attended, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3′ genomic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
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                                                        L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
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Measles virus Moraten vaccine L protein.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Best Local Similarity
Matches 9; Conserv
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522 ylhdpefnl 530
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W48704 standard; Protein; 2183 AA.
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                                                                                                                                                                                                                                                                                                                                                                                             L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
         This sequence represents the L protein from Measles virus AIK-C vaccine. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
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                                                                                                                                                  100.0%; Score 53; DB 19; Length 2183; 100.0%; Pred. No. 0.16; 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                     Measles virus Edmonston isolate wild-type L protein.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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Best Local Similarity
' has 9; Conserv?
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                                                                                                               2183 AA;
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Best Local Similarity
Matches 9; Conserv
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                                                                                                              negative sense; vaccine; immunity;
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100.0%; Pred. No. 0.16;
iive 0; Mismatches 0;
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                                                                                                        L protein; attenuation; non-segmented; negs single stranded RNA virus; Mononegavirales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 116-124; 426pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                  Measles virus 1977 isolate L protein.
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13-OCT-1998 (first entry)
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(NODA ) ZH NODA SANGYO KAGAKU KENKYUSHO.
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Best Local Similarity
'-has 6; Conserve
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                                                                                                                                                                                                                                                                                                                                                           This sequence represents a wild-type L protein from Measles virus isolate 1983. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
         L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                   Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having
                                                                                                                                                                                                                                                                                  single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 53; DB 19; Length 2183; llarity 100.0%; Pred. No. 0.16; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                            Udem SA;
                                                                                                                                                                                                           Randolph VB, Sidhu MS, Tatem JM,
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 134-142; 426pp; English.
                                                                                                                                                                     (AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L-fucose dehydrogenase; L-FDH; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R51284 standard; Protein; 329 AA
                                                                                                                        97WO-US16718.
                                                                                                                                               96US-0026823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92JP-0243372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas sp. No.1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L-fucose dehydrogenase.
                                                                                                                                                                                                                                 WPI; 1998-230710/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                2183 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 522 ylhdpefnl 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YLHDPEFNL 9
                                                                                                                                                                                                                                               N-PSDB; V18266.
                                              Measles virus
                                                                      WO9813501-A2
                                                                                                                       19-SEP-1997;
                                                                                                                                              27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP06090765-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-1994.
                                                                                               02-APR-1998
                                                                                                                                                                                                          BR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                            Murphy
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This sequence represents the wild-type L protein from Human parainfluenza virus (HPIV-3) type 3 isolate JS. This sequence is used in a method which involves the isolation of recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' peononic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L protein; attenuation; non-segmented; negative sense; vaccine; immunity; single stranded RNA virus; Mononegavirales.
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                   The L-FDH gene is new and can be used for the recombinant prodn. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3′ genomer promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus
                                                                                  Novel L-fucose dehydrogenase gene - a new recombinant DNA and the
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                         Length 329;
                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Udem SA;
                                                                                                                                                                                                                                                                       DB 15;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tatem JM,
                                                                                                                                                                                                                                                                     Score 37; DB 1
Pred. No. 21;
0; Mismatches
Otake H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 246-254; 426pp; English.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPIV-3 JS isolate wild-type L protein.
                                                                                                  prepn. of L-FDH using a L-FDH vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidhu MS,
                                                                                                                                                                                                                                                           69.8%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                W48711 standard; Protein; 2233 AA.
                                                                                                                                  Claim 1; Page 5; 6pp; Japanese.
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standard; Protein; 2233 AA.
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                                                                       13-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                           Human parainfluenza virus.
                                                                                                                                                                                                                                                                                                                                                                       Murphy BR, Randolph VB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-230710/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2233 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Canine factor VIII
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530 wlddpefni 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YLHDPEFNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; V18274,
                                                                                                                                                                                                                                                                  19-SEP-1997;
                                                                                                                                                                                                                                                                                                27-SEP-1996;
                                                                                                                                                                                                        WO9813501-A2
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gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-MAY-1999
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W48713
ID W48713
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                                            W48713;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine FRhl cp45 L protein. This sequence is used in a method which involves the isolation of recombinantly generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of the order Mononegavirales which have at least 1 attenuating mutation in the 3' genomic promoter region and at least 1 attenuating mutation in the RNA polymerase gene. This RNA virus can be used as a vaccine to immunise an individual against such a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the Human parainfluenza virus (HPIV-3) type 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Monongavizales - having attenuating mutation in 3′ genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus
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                                                      Length 2233;
                                                      Score 37; DB 19; Length 22
Pred. No. 1.7e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Udem SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.8%; Score 37; DB 19; L ilarity 66.7%; Pred. No. 1.7e+02; Conservative 2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sidhu MS, Tatem JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 265-273; 426pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMCY ) AMERICAN CYANAMID CO.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                            HPIV-3 FRhl cp45 vaccine L protein.
                                                                                                                                                                                                                    W48712 standard; Protein; 2233 AA.
                                                        69.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-US16718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96US-0026823
                                                                                                                                                                                                                                                                              (first entry)
                                          Query Match
Best Local Similarity 66./v
                                                                                                                                                                                                                                                                                                                                                                                  Human parainfluenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy BR, Randolph VB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1998-230710/20.
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Best Local Similarity
Matches 6; Conserv
             2233 AA
                                                                                                                                  :| |||||:
530 wlddpefni 538
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530 wlddpefni 538
                                                                                                                 1 YLHDPEFNL 9
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                                                                                                                                                                                                                                                                                                                                                                                                               WO9813501-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-SEP-1996;
                                                                                                                                                                                                                                                                               13-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          02-APR-1998
                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                  W48712;
                                                                                                                                                                                         RESULT 12
W48712
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protein; attenuation; non-segmented; negative sense; vaccine; immunity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinantly-generated, attenuated, non-segmented, negative-sense, single stranded RNA virus of order Mononegavirales - having attenuating mutation in 3' genomic promoter region and RNA polymerase gene, useful as vaccine to immunise against such virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VIII; canine; dog; diagnosis; animal model; haemophilia A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.8%; Score 37; DB 19; Length 2233; 66.7%; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Udem SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                      single stranded RNA virus; Mononegavirales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 283-291; 426pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sidhu MS,
HPIV-3 Vero cp45 vaccine L protein.
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2343 AA;

Sequence

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This polypeptide comprises canine factor VIII. The canine Factor VIII gene (see v99801) was obtained by concatamerisation of RT-PQR-amplified factor VIII fragments obtained from canine liver total RNA. A cDNA clone, designated pBK-cmv(1-6#3) canine FVIII, is deposited as ATCC 209475. The invention provides canine FVIII, is deposited as ATCC 209475. The invention provides canine factor CIII polypeptides encoded by such isolated nucleic acid molecules, antibodies binding to such polypeptides, penetic constructs comprising the nucleic acid molecules, prokaryotic or enkaryotic comprising canine disorders characterised by factor VIII deficiency, especially haemophilia A. A polynucleotide can be administered via a vector directly into canine cells (gene therapy). The canine can remembhilia in humans. Epitope-bearing portions of canine factor VII cutil polypeptides can be used to generate anti-canine factor VII canine factor VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New canine factor VIII polynucleotide and polypeptide - useful for detection and treatment of haemophilia A using gene therapy
                                                                                        /note= "epitope-bearing region, specifically claimed in Claim 24"
                                                                                                                                  /note= "epitope-bearing region, specifically claimed in Claim 24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lillicrap D, Notley C;
                                                                                                                                                                                                                                                                                              'note= "protein C cleavage site"
                                                                                                                                                                                                                                                                  "protein C cleavage site'
                                                                                                                                                                                                                                       'note= "thrombin cleavage site"
                                                                                                                                                                              "thrombin cleavage site"
                                                                                                                                                                                                          "thrombin cleavage site"
                                           ..2343
ote= "mature protein"
                               'note= "signal peptide"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            1685..1695
/note= "A3 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "sulfation"
1675
                                                                                                                                                                                                                                                                                                                                                       note= "sulfation"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "sulfation"
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97US-0039953.
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                                                                                                                      2278..2351
                                                                                                                                                                                                                      1700..1701
                                                                           1664..177
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753..754
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575..576
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                                                                                                                                                                                                                                                    350..351
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1691
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                                                                                                                                                                Cleavage-site
                                                                                                                                                                                           Cleavage-site
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06-MAR-1997;
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                   Peptide
                                                Protein
                                                                            Region
                                                                                                                      Region
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                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid encoding a canine factor VIII polypeptide for treating a disorder characterized by canine factor VIII deficiency, such as hemophilia A .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents canine factor VIII. The isolated factor VIII nucleic acid molecule and protein can be used for treating a disorder characterised by canine factor VIII deficiency in a canine, especially haemophilia A.
                                                                                                                                                                                                                          factor VIII; haemostatic; diagnosis; haemophilia A; dog.
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Pred. No. 2.7e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                    Horrocks LSH, Hough C, Notley C, Lillicrap D, Cameron C;
  Length 2343;
                        1; Indels
                                                                                                                                                                                                   Canine Factor VIII (DOGLESS1) protein SEQ ID NO:2.
Score 36; DB 20;
Pred. No. 2.7e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: December 16, 2000, 00:51:17
Job time: 18777 sec
                                                                                                                              Y57846 standard; Protein; 2343 AA.
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                                                                                                                                                                                                                                                                                                                                                                            (TOOH ) UNIV QUEENS KINGSTON
 67.9%;
85.7%;
                                                                                                                                                                                                                                                                                                                       99CA-2264431
                                                                                                                                                                                                                                                                                                                                          98US-0035141.
                                                                                                                                                                             (first entry)
Query Match 67.9
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2343 AA;
                                                              617 hdpefql 623
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| 617 hdpefgl 623
                                              3 HDPEFNL 9
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squalus aca
homo sapien
carcinus ma
carcinus ma
carcinus ma
carcinus ma
procambarus
mus musculu
mytilus edu
ascaris suu
ascaris suu
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pichia jadi
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homo sapien
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calliphora
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oryctolagus
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Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCK1_LEUMA STANDARD; PRT; 8 AA.
P21140;
01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
LEUCOKININ I (L-I).
LEUCOKININ I (L-I).
LEUKATYOTA; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neopleca; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.
                            P31890
P939025
P13268
P13268
P13268
P13268
P41982
P41982
P41982
P41805
P81805
P
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CIP2_MYTED
FAR1_ASCSU
FAR2_ASCSU
GFRP_MOUSE
MSCL_SALTY
CAD1_ENTFA
DCM1_FSECF
NEUU_FSECF
NEUU_CAVPO
NEUU_CAVPO
                                                                                                                                                                                                                                           ALL3_CARMA
ALL5_CARMA
FAR2_PROCL
UF03_MOUSE
UN06_PINPS
AL12_CARMA
AL15_CARMA
                                                                                                                                                                                                                                                                                                                                                 ALI7_CARMA
ALI8_CARMA
ALI3_CYDPO
ALL4_CALVO
ALL4_CYDPO
ALL5_CALVO
ALL5_CALVA
ALL7_CARMA
ALL8_CARMA
                                                                                                                                  NEUX_RAT
NSK1_SARBU
OXYA_SCYCA
                                                                                                                                                                               OXYA_SQUAC
UHA2_HUMAN
AL14_CARMA
ALL2_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAR3_HOMAM
AL10_CARMA
AL11_CARMA
FLA2_TREHY
MOSF_CLYJA
OXYT_CYPCA
OXYT_RABIT
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TAL1_PICJA
TAL3_PICJA
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 0
ICKI_LEUMA
ID LCKI_LE
DT 01-MAY
DT 01-MAY
DT 01-MAY
DT 01-MAY
DC LEUCOP
OC EURARY
OC EURARY
OC PLEY
OC
bothrops ja
cydia pomon
leucophaea
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panagrellus
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pseudomonas
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ascaris suu
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scyliorhinu
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helisoma tr
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                                                                                                   Search time 68.03 Seconds (without alignments)
4.227 Million cell updates/sec
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P19989
P20989
P21141
P80975
P62152
P62152
P62152
P62156
P62155
P61875
P641871
P
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P13973
P13736
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                             Compugen Ltd
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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                                                                                                    2000, 04:23:32
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FRA2_PARRE
LCK2_LEUMA
COXE_THUOB
ANG2_BOTJA
ALL1_CYDPO
LCK3_LEUMA
ALL1_LCYDPO
LCK3_LEUMA
UPB_BOVIN
UPB_BOVIN
UPB_BOVIN
TRPI_PSEPU
GLUR_HUMAN
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ALL4_CARNA
FAR1_PANRE
ALL6_CYDPO
ALL6_CYDPO
TMOF_SARBU
TMOF_SARBU
ALL7_CYDPO
AKH_MELMI
ALL5_CYDPO
ULC4_LEDUM
UH09_RAT
FAR5_ASCSU
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FAR3_HIRME
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TRM3_ECOLI
CIP1_MYTED
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Maximum Match 100%
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UPA7_HUMAN
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Gapop 10.0 , Gapext 0.5
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53
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Match Length E
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length: 9
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Gaps

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Indels

Length 8;

RESULT 2 FAR1_PANRE

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Matches

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-!- FUNCTION: MYOACTIVE.
-!- TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED CAUDALLY TO THE BASE OF THE PHARYNX.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE, 93027659.
Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
Garrison R.D., Williams J.F., Friedman A.R.;
"Two FMRFamide-like peptides from the free-living nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Comp. Biochem. Physiol. 84C:205-211(1986).-!- FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=HEAD;
Holman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of two neuropeptides from Leucophaea maderae: members of a new family of Cephalomyotropins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Arthropoda, Trachéata, Hexapoda, Insecta,
Pterygota, Neoptera, Orthopteroidea, Dictyoptera, Blattaria,
Blaberoidea, Blaberidae, Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMIDATION.
DA0B0729C4576AAD CRC64;
                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF2 (SADPNFLRF-AMIDE).
                 AMIDATION.
DC6365A5B9CDC76A CRC64;
                                                                                        Score 19; DB 1; I
Pred. No. 8.8e+04;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 1; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panagrolaimoidea; Panagrolaimidae; Panagrellus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1991 (Rel. 18, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
LECCKININ II (L.II).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                                                                                                                                                                                  9 AA.
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75.0%;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Panagrellus redivivus.";
Peptides 13:209-214(1992).
                                  866 MW;
                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation. MOD_RES 9
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Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 3; Conserv
                                  8 AA;
                                                                                                                                                                  4 DPEFN 8
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P21141;
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P41873;
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SEQUENCE
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides 13:209-214 (1992).
1-1-FUNCTION: MYOACTIVE.
1-1-TISSUE SPECIFICITY: NERVE CORDS AND PAIRED GROUPS OF CELLS LOCATED CAUDALLY TO THE BASE OF THE PHARYNX.
1-1-SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D., Garrison R.D., Williams J.F., Friedman A.R.; "Two FMREmmide-like peptides from the free-living nematode panagrellus redivivus";
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holman G.M., Cook B.J., Nachman R.J.;

"Isolation, primary structure and synthesis of leucokinins VII and
"Isolation, primary structure and synthesis of leucokinins VII and
"Isolation, primary structure and synthesis of leucophace
peptides isolated from head extracts of Leucophace maderae.";
Comp. Biochem. Physiol. 88C:31-34(1987).

-1. FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).

-1. SIMILARITY: TO THE OTHER LEUCOKININS.

PIR; JS0317; JS0317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leucophaea maderae (Madeira cockroach).
¡Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                             Score 24; DB 1; Length 8; Pred. No. 8.8e+04; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35.8%; Score 19; DB 1; Length 8; 75.0%; Pred. No. 8.8e+04; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION.
C6D40729C4576AB5 CRC64;
                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMREMIDE-LIKE NEUROPEPTIDE FF1 (SDFNFLRF-AMIDE).
Panagrellus redivivus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
                                                                                                                                                                                                                                        8 AA.
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                                                                   0; Mismatches
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                                                                                                                                                                                                                                        PRT;
                              45.3%;
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8 AA; 995 MW;
                                                                   Conservative
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MOD_RES 8 8
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                              Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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| DPAFN 5
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                                                                     4;
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                                                                                                                                                                                                                                    FAR1_PANRE P41872;
                                                                                                        4 DPEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LCK7_LEUMA
P19989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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SEQUENCE.
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Gaps

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1; Indels

RESULT 3 LCK7_LEUMA

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Length 9;

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Viperidae; Crotalinae; Bothrops.
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Best Local Similarity
Matches 2; Conserv
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TISSUE=LARVA;
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4 YIH 6
                                                                                                                                                                                                                                                                                                             ALL1_CYDPO
P82152;
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P21142;
                                                                                                                                                                                                                                    1 YLH 3
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2 PHYN
                        SEQUENCE
                                                                                                                                                                                                                                                                                          RESULT 8
ALL1_CYDPO
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0
                                                                                                                                                                                                                                                                   Thunnus obesus (Bigeye tuna).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Scombroidei;
Scombridae; Thunnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   liver.";
Eur. J. Blochem. 248:99-103(1997).
-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASS, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
MITOCHONDRIAL ELECTRON TRANSPORT.
                                                                                                                                                                                                                                                                                                                                                                                           "The subunit structure of cytochrome-c oxidase from tuna heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bothrops jararaca (Jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: 4 FERROCYTOCHROME C + O(2) = 2 H(2)O + 4 FERRICYTOCHROME C.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL INNER MEMBRANE.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
INTERRO: IPRO01349; ...
PROSITE; PS01329; COX6A; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CYTOCHROME C OXIDASE POLYPEPTIDE VIA (EC 1.9.3.1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                              TISSUE=HEART;
MEDIINE; 97454291.
Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
Radenbach B.;
                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                             Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA; 1136 MW; 62E072C9CB0776DB CRC64;
                                  AMIDATION.
DC6365A5B9C8676A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%; Score 18; DB 1; Le
100.0%; Pred. No. 8.8e+04;
ive 0; Mismatches 0;
                                                                            Score 18; DB 1; I
Pred. No. 8.8e+04;
1; Mismatches 1;
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ANGIOTENSIN-LIKE PEPTIDE II (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 AA.
                                                                                                                                                                                                 9 AA.
                                                                                                                                                                                                   PRT;
                                                                            34.0%;
60.0%;
                                           8 AA; 852 MW;
                       Neuropeptide; Amidation.
MOD_RES 8 8
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                  STANDARD;
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Best Local Similarity
Matches 3; Conserv
                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                    || |:
1 DPGFS 5
                                                                                                                       4 DPEFN 8
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Q10582;
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                                                                                                                                                                                                 COXE_THUOB
P80975;
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NON_TER
SEQUENCE
                                  MOD_RES
SEQUENCE
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                                                                                                                                                                            RESULT 6
COXE_THUOB
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Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
TISSUE-PLASMA;
MEDLINE: 96208932.
BOTGAPHETS: R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
BOTGAPHETS: R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
BOTGAPHETS: R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
Plasma of the snake Bothrops jararaca.";
Comp. Biochem. Physiol. 113B:467-473(1996).
INTERPRO: PROJOSS TO THE SERPIN FAMILY.
INTERPRO: PROJO215;
PROSITE; PS00284; SERPIN; PARTIAL.
Vasoconstrictor; Plasma; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1991 (Rel. 18, Last annotation update)
01-MAY-1991 (Rel. 11, Last annotation update)
LEUCOKININ III (L-III).
Leucophaea maderae (Madeira cockroach).
Eukaryota: Merazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Orthopteroidea: Dictyoptera; Blattaria;
Blaberoidea: Blaberidae: Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                              Score 17; DB 1; Length 8;
Pred. No. 8.8e+04;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.2%; Score 16; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                   NON_TER 8 8 8 S SEQUENCE 8 AA; 1046 MW; DDD761E04B42D40A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 8 AMIDATION.
8 AA; 934 MW; C82879C45B51F775 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA.
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66.7%;
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Best Local Similarity 50.0°
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MOD_RES 8 8
SEQUENCE 8 AA; 934 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 DQESNV
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                                                                                                                                                    NON_TER
SEQUENCE
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                    SEQUENCE
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                                                                                                                               NON_TER
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                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 86067985.

Yang H.-Y.T., Fratta W., Majane B.A., Costa E.;
"Isolation, sequencing, synthesis, and pharmacological
characterization of two brain neuropeptides that modulate the action
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TO NEUROPEPTIDE A (AA 5-8) (IDENTICAL). AMIDATION. 87D416C776D9C729 CRC64;
                                                                     Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMYORPODED. PEPTIDE STIMULATES CONTRACTILE
-!- GUNCTION: THIS CECKROACH PROTODEUM (HINGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                              Holman G.M., Cook B.J., Nachman R.J.; ^{\circ} Primary structure and synthesis of two additional neuropeptides
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1-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 2) (FRAGMENT).
                                                                                                                                                              Score 15; DB 1; Length 8; Pred. No. 8.8e+04; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 1; Length 8; Pred. No. 8.8e+04;
                                                  from Leucophaea maderae: members of a new family of
                                                                                                                         AMIDATION.
DC6365B449C866DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of morphine.";
Proc. Natl. Acad. Sci. U.S.A. 82:7757-7761(1985).
-!- FUNCTION: MODULATES THE ACTION OF MORPHINE.
PIR; B24749; B24749.
                                                                                                                                                                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AA.
                                                                                                                                                                                                                                                                           8 AA.
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33.3%;
                                                                                                                                                                28.3%;
60.0%;
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8
1082 MW;
                                                                                                                                 8 AA; 910 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                             Neuropeptide; Amidation.
MOD_RES 8 8
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                           STANDARD;
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           AND SYNTHESIS.
                                                                                                                                                     Query Match
Best Local Similarity
' has 3; Conserve
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2; Conserva
                                                              Cephalomyotropins.
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1 FLFQPQ
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P30087;
                                                                                                                                                                                                                                                                 NPB_BOVIN
ID NPB_BOVIN
AC P15507;
                                                                                                                                                                                                                          1 DOGFN
                                                                                                                                                                                                        4 DPEFN
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MOD_RES
SEQUENCE
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Best Local S.
Matches 2
           SEQUENCE,
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                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               putida.;
Biochimie 71:521-531(1989).
Biochimie 71:521-531(1989).
THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDOLEGIECEROL PHOSPHATE), TRYPI BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
                                                                                                                                                                                                -!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.9, ITS MW IS: 65 KDA.
SWISS-2DPAGE; P30087; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas putida.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of the tryptophan synthase genes of Pseudomonas
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DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 15; DB 1; Length b; Pred. No. 8.8e+04; 2; Indels
                                                                                                                                                "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
TISSUE=PLASMA;
MEDLINE; 93092937.
Hudhes G.J., Frutiger S., Paquet N., Ravier F., Pasq
Sanchaz J.-C., James R., Tissot J.-D., Bjellqvist B.
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                  C01772C455BB06DA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
TRPBA OPERON TRANSCRIPTIONAL ACTIVATOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              683 MW; 77672AA1EDD6F000 CRC64;
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INTERPRO; IPR000847; -.
PROSITE; PS00044; HTH_LYSR_FAMILY; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                     944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eberly L., Crawford I.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=PPG1 C1S;
MEDLINE; 89335826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
6 AA;
                                                                                                                                                                                                                                                                                                                                                                                     8 AA;
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Score 14; DB 1; Length 6;

26.48;

100

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Gaps

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1; Indels

9

Length

3

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MEDLINE; 94286417.
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helisoma trivolvis (Snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptides 15:31-36(1994).
-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
-!- FUNCTION: APPEARS TO BE INVOLVED IN OSMOREGULATION BY AFFECTING
-!- THE KIDNEY, MAINTLE AND THE HEMOLYMPH.
-!- TISSUE SPECIFICITY: KIDNEY, SKIN, MANTLE AND THE HEMOLYMPH.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).
Eukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thorpe A.; \label{eq:substantial} Isolation and identification of multiple neuropeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES 7 7 AMIDATION.
SEQUENCE 7 AA; 851 MW; 69D40729D76AA810 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.5%; Score 13; DB 1; LA 100.0%; Pred. No. 8.8e+04; Live 0; Mismatches 0;
                     Score 13; DB 1; I
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE GDPFLRF-AMIDE.
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                     24.5%;
50.0%;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation.
                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Planorbidae; Helisoma
   Query Match
Best Local Similarity
'Thes 2; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98121193.
                                                                                                                                                                                                                                                                                                   CARCINUSTATIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=KIDNEY;
                                                                                                            : ||
3 YKPE 6
                                                                                       3 HDPE 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FAR1_HELTI
P41871;
                                                                                                                                                                                                            ALL4_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trivolvis.
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                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                              P81807;
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FAR1_HELTI
                                                                                                                                                                        RESULT 15
ALL4_CARMA
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LOTE C.J., Weiss J.B.;

Glycopeptide containing cysteinyl-galactose.";

Biochem. J. 123:25P-25P(1971).

-I- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE

IS DERIVED IS UNKNOWN. NO PHYSIOLGICAL FUNCTION HAS BEEN

ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A

SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIANE: 91271080.
Spittaels K., Schoofs L., Grauwels L., Smet H., van Damme J., Prosost P., Torrekens S., de Loof A.:
BISOLATION, identification and synthesis of novel oviductal motility stimulating head peptide in the Colorado potato beetle, Leptinotarsa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides 12:31-36(1991).
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Chrysomelidae; Chrysomelinae; Leptinotarsa.
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 8;
8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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6B07632B5DD03000 CRC64;
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8 AA; 855 MW; C2D87AA1F5B1EB1E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
 Pred. No. 8.8e+04;
                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) URINE GLYCOPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AA.
                                                                                                                                                                          Ą
                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.4%; Score 14; DB 100.0%; Pred. No. 8.8
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                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
100.08;
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                   Conservative
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                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation.
MOD_RES 6 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE, AND SYNTHESIS.
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Best Local Similarity
Matches 2; Conserv
 Best Local Similarity
Matches 2; Conserv
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CARBOHYD 1
SEQUENCE 8 AA
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                                                                                                                                                                      GLUR_HUMAN
P02729;
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P42985;
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                                                                      HD 4
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OVM_LEPDE
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Length 7;

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                                                                                                                                                                                                                                    SEQUENCE, AND SYNTHESIS.
MEDLINE; 95232026.
MAILA A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P.,
Thim L., Kubiak T.M., Martin R.A., Geary T.G.;
"Isolation and preliminary biological characterization of
KPNFIRFamide, a novel FMRRamide-related peptide from the free-living
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cydia pomonella (Codling moth).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                       nematode, Panagrellus redivivus.";
Peptides 16:87-93(1995).
-!- FUNCTION: MYOACTIVE; INDUCES A RAPID CONCENTRATION-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LARVA;
MEDLINE; 98054539.

MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Dave, W., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 13; DB 1; Length 7; Pred. No. 8.8e+04; 1; Indels 0; Mismatches 1; Indels
 Length 7;
                       Indels
                                                                                                                                                                                                    Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Panagrolaimoidea, Panagrolaimidae, Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation.
MOD_RES R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 8 AMIDATION.
8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION.
69D40059C4576350 CRC64;
24.5%; Score 13; DB 1; Lk
100.0%; Pred. No. 8.8e+04;
tive 0; Mismatches 0;
                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-MAY-2000 (Rel. 39, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF4 (KPNFIRFAMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA.
                                                                                                                          7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                 24.5%;
66.7%;
                                                                                                                                                                                                                                                                                                                                         MUSCLE TENSION INCREASE
                                                                                                                                                                                                                                                                                                                                                                                                7 AA; 921 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                          Neuropeptide; Amidation.
                                                                                                                          STANDARD;
                                                                                                                                                                                            Panagrellus redivivus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 2; Conserv
              Local Similarity
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                                                                                                                        FAR4_PANRE P41875;
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2 PNF 4
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ID ALL6_CYDPO
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                                             DP 5
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   Query Match
               Best Loca
Matches
                                                                                                               FAR4_PANRE
                                                                                                  RESULT
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"Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";

Regul. Pept. 50:61-72(1994).

-!- FUCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS

-!- FUCTION: HAS AN OOSTATIC ACTIVITY. REDUCES THE VITELLOGENIN CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
01-FEB-1996 (Rel. 33, Last annotation update)
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cowden C., Stretton A.O.W.; "Eight novel FMRFamide-like neuropeptides isolated from the nematode Ascaris suum.";
                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascariddida; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 94211930.
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides 16:491-500(1995).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 8;
                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
9CD40059D417687D CRC64;
                      Score 13; DB 1; I
Pred. No. 8.8e+04;
L; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 13; DB 1; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
FMRFANIDE-LIKE NENCOPEPTIDE AF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA.
                                                                                                                                                                                                                                                                     8 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.5%;
                      24.5%;
50.0%;
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                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide; Amidation.
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                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ascarididae; Ascaris.
Query Match
Best Local Similarity
2; Conserve
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nes 2; Conserv
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2 PLYN 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de Loof A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEF 7
                                                                                                                                                                                                                                                                 FAR7_ASCSU P43171;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAMILY
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Best Local S:
Matches 2,
                                                                                                              PEFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 20
TMOF_SARBU
                                                                                                                                                                                                                       RESULT 19
FAR7_ASCSU
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SPECIES-P.MARGINATA; TISSUE-CORPORA CARDIACA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       CYDIASTATIN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=LARVA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :| |
5 DFGL 8
                                                                                                                                                                                                                                                                                                                                                           RESULT 23
ALL5_CYDPO
ID ALL5_CYDPO
AC P82156;
                                                                                                                                                                                                                                                                                                                  : |::
4 YSPDW 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 EFNL 9
                                                                                                                                                                                                                                                                                                     3 HDPEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A unique charged tyrosine-containing member of the adipokinetic hormone/red-bygment-concentrating hormone peptide family isolated and sequenced from two beetle species."; Blochem. J. 275:671-677(1991).
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                            TISSUE-LARVA;
MEDLINE; 98054539.

MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.; Independent peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).

-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

Neuropeptide; Amidation.

AMIDATION.

AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-M.MELOLONTHA, AND G.STERCOROSUS; TISSUE-CORPORA CARDIACA;
MEDLINE; 91248100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melolontha melolontha (Cockchafer),
Geotrupes stercorosus (Dor beetle), and
Pachnoda marginata (Flower beetle).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaelformia; Scarabaeidae; Melolonthinae; Melolontha.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 12; DB 1; Length 7;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
                                                                 0; Indels
                                          Length 6;
          61E72451B7642000 CRC64;
                                        22.6%; Score 12; DB 1; Le
100.0%; Pred. No. 8.8e+04;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-FEB-1994 (Rel. 28, Last annotation update)
ADIPOKINETIC HORMONE (AKH)
                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 7.
                                                                                                                                                                7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA.
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%;
50.0%;
          695 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 22.6
Best Local Similarity 50.0
Matches 2; Conservative
                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                 STANDARD;
                                        Ouery Match
Best Local Similarity
Matches 2; Conserv
         6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :| |
4 DFGL 7
                                                                                                                                          RESULT 21
ALL7_CYDPO
ID ALL7_CYDPO
AC P82158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 EFNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AKH_MELML
P25423;
                                                                                   2 LH 3
                                                                                                          9
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Hormone.
SEQUENCE
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2
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MEDLINE; 92265187.

A Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;

Frimary structures of neuropeptides isolated from the corpora
cardiaca of various cetonid beetle species determined by
pulsed-liquid phase sequencing and tandem fast atom bombardment mass
T spectrometry.

B bol. Chem. Hoppe-Seyler 373:133-142(1992).

- I- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.

- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.

R PIR: S15422: S15422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cydia pomonella (Codling moth).
Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.; "Lepidopteran peptides of the allatostatin superfamily."; Peptides 18:1301-1309(1997).
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                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.6%; Score 12; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 8 AMIDATION.
8 AA; 898 MW; 922879CABB58640D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 12; DB 1; I
Pred. No. 8.8e+04;
3; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LCK4_LEUMA STANDARD; PRT; 8 AA P21143; 01-MAY-1991 (Rel. 18, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.6%;
20.0%;
                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR002047; -. PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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Best Local Similarity
2; Conserve
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Best Local Similarity
Matches 1; Conserv
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ID LCK4_L
AC P21143
DT 01-MAY
DT 01-MAY
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THE FARP (FMRFAMIDE RELATED PEPTIDE)

340B0059D1B76338 CRC64;

AMIDATION

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MEDLINE; 95380362.
Cowden C., Stretton A.O.W.;
"Eight novel FMRFamide-like neuropeptides isolated from the nematode
                                                                                                                                                                               22.6%;
66.7%;
                                                                               Peptides 16:491-500(1995).
                                                                                                                                  9 9
9 AA; 1052 MW;
                                                                                                                                                                                            Best_Local Similarity 66.7
Matches 2; Conservative
                                                                                                                     Neuropeptide; Amidation. MOD_RES 9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                    STANDARD;
 Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=PITUITARY;
MEDLINE; 95062247
                                                                      Ascaris suum.
                                                                                                                                                                                                                                                                                                                                                                            PHASVATOCIN.
                                                                                                                                                                                                                                                                                                                 OXYF_SCYCA P42997;
                                                                                                                                                                                                                                                       4 PTF 6
                                                                                                                                                                                                                                5 PEF 7
                                                                                                           FAMILY
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                                                                                                                                             SEQUENCE
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                         SEQUENCE
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FN
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OXYF_SCYCA
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ID SAP_S'
AC P2404
DT 01-MA
DT 01-MA
DT 01-MA
DT SPERM
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01-NOV-1995 (Rel. 32, Last sequence update)
01-REB-1996 (Rel. 33, Last annotation update)
FWRFAMIDE-LIKE NBUROPEPTIDE AFF.
Ascaris suum (Plg roundworm) (Ascaris lumbricoides).
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=WISTAR; TISSUE=HEART;
Li X.-P., Pleissner K.-P., Scheler C., Regitz-Zagrosek V., Salikov
Jungblut P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 8.9, ITS MW IS: 42 KDA.
                                                                                                                                                      Comp. Biochem. Physiol. 84C:271-276(1986).
-!- FUNCTION: THIS CEPHALOMOTROPIC PEPTIDE STIMULATES CONTRACTILLE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!- SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF HEART TISSUE (SPOT P9) (FRAGMENT).
                                                                                                        Holman G.M., Cook B.J., Nachman R.J.; "Primary structure and synthesis of two additional neuropeptides from Leucophaea maderae: members of a new family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
                                                                                                                                                                                                                                                                                          ;
                  Leucophaea maderae (Madeira cockroach)
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                 Score 12; DB 1; Length 8;
Pred. No. 8.8e+04;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.6%; Score 12; DB 1; Length 8; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA; 1029 MW; 9E0775A6C4140B06 CRC64;
                                                                                                                                                                                                                               8 AA; 906 MW; DC6365B1E9D5BDDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
0
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01-MAY-1991 (Rel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                      8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                    AMIDATION
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                                                                                                                                                                                                                                                                 22.6%;
40.0%;
                                                                                                                                                                                                      Neuropeptide; Amidation.
MOD_RES 8 8
                                                                                                                                                                                                                                                                                          2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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SEQUENCE, AND SYNTHESIS.
          LEUCOKININ IV (L-IV).
                                                                                                                                             Cephalomyotropins."
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Matches 2; Conserv
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                             TISSUE-HEAD;
                                                                                                                                                                                                                                                                                                                  4 DPEFN 8
                                                                                                                                                                                                                                                                                                                                         1 DASFH 5
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SEQUENCE
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P56575;
                                                                                                                                                                                                                                SEQUENCE
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                                  Gaps
                                                                                                                                                                                                                                                                     Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota, Metazoa, Chordata, Cranlata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyllorhinidae; Scyllorhinus.
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                                  ö
                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
Score 12; DB 1; Length 9; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDATION.
17EDD76EB44449DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 12; DB 1; L
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD; PRT; 9 AA. P24047; 01-MAR-1992 (Rel. 21, Created) (01-MAR-1992 (Rel. 21, Last sequence update) (11-MAR-1992 (Rel. 21, Last annotation update) SPERM-ACTIVATING PEPTIDE (SAP).
                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                           9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                0; Mismatches
                                                                                                                                                                            PRT;
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100.0%; Pre
0;
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MEDLINE; 76074708. Starratt A.N., Brown B.E.; "Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                 MEDLINE; 92195954.

Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of RFamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.Shea M., Adams M.E.;
"Pentapeptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of proctolin in the central nervous system of the
                                                                                                                                                                Hirudinida; Hirudinea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Limulus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab) (Green crab).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota: Neoptera; Orthopteroidea: Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
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SPECIES-L. POLYPHEWUS;
MEDLINE: 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.8%; Score 11; DB 1; Length 4; 100.0%; Pred. No. 8.8e+04; Live 0; Mismatches 0; Indels
                                                                                                                                  Hirudo medicinalis (Medicinal leech).
Eukaryota: Metazoa; Annelida: Clitellata; Hirudinida;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOD_RÈS 4 4 AMIDATION.
SEQUENCE 4 AA; 598 MW; 69D4073B3000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
POCTOLIN.
PROCTOLIN.
                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Limulus polyphemus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Life Sci. 17:1253-1256(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eptides 11:205-211(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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MEDLINE; 81225865.
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Matches 2; Conserv
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MEDLINE; 86232789
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Stomopneutes variolaris (Sea urchin).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
                                                                                                                                                                                 MEDLINE; 92097763.
Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.;
"Determination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                          spectrometry.";
FEBS Lett. 294.179-182(1991).
-!- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
--- FUNCTION: CAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
CAMP, CGMP AND CLACTUM LEVELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Plasma protein map: an update by microsequencing."; Electrophoresis 13:707-714(1992).
- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.05, ITS MM IS: 37 KDA.
SWISS-2DPAGE; P30093; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
1-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 18) (FRAGMENT).
Homo saplens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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MEDLINE; 93092937.
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 9;
8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA; 1010 MW; C469B3387B076EB9 CRC64;
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                                                                                                                                  SEQUENCE, AND DISULFIDE BOND.
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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                                                                                   Stomopneustes
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P30093;
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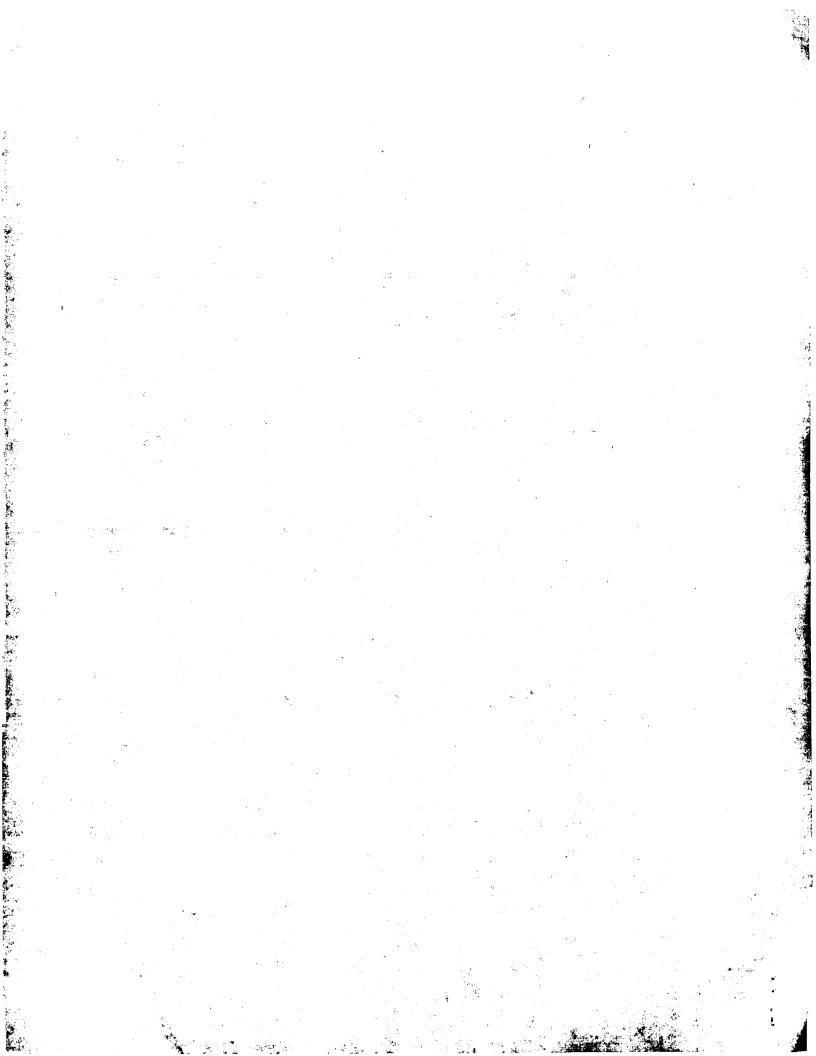
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CIP1_MYTED P13736;
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FAR1_ASCSU
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"Identification and characterization of the products from the trajand tray genes of plasmid R100.";
and tray genes of plasmid R100.";
-1. Bacteriol. 170:2749-2757(1988).
-1. FUNCTION: TRANSFER GENE PROTEIN. IS INVOLVED IN THE CONJUGATION PROCESS OF BACTERIAL CELLS FOR THE EXCHANGE OF PLASMID DNA.
-1. SUBCELLULAR LOCATION: CYTOPLASMIC.
-1. SIMILARITY: TO TRAM PROTEIN OF OTHER PLASMIDS.
Stangier J., Dircksen H., Keller R.; "Identification of proctolin in
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
                      pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-!-FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!-TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND
THE CRAB PERICARDIAL ORGANS.
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                                                                                                                                                                                            Indels
                                                                                                                                                                      20.8%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 AA; 634 MW; 6B1B1AA443500000 CRC64;
                                                                                                                       Neuropeptide.
SEQUENCE 5 AA; 649 MW; 71B7673B44600000 CRC64;
                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M20941; -; NOT_ANNOTATED_CDS.
PIR; A32014; A32014.
Conjugation; Plasmid; DNA-binding.
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                                                                                                                                                                                  llarity 100.0%;
Conservative C
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                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                   TRAM PROTEIN (FRAGMENT).
                                                                                                PIR; A01644; HOROHA.
PIR; A60411; A60411.
                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
Plasmid IncFII R100.
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Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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RESULT 33

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"Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 88240357.
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.,
Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.,
"Structures and actions of Mytilus inhibitory peptides.";
Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
-:- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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-!- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
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Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                              Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
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Pred. No. 8.8e+04;
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6 AA; 621 MW; 72C9C6876DDB1000 CRC64;
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72C9C68775B81000 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE II (MIP II).
                                                01-Jan-1990 (Rel. 13, Created)
01-Jan-1990 (Rel. 13, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
CONȚRACTION-INHIBITING PEPȚIDE I (MIP I).
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6 AA.
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66.7%;
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PIR; A27696; A27696.
Hormone; Amidation.
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STANDARD;
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MEDLINE; 88240357.
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MOD_RES 6
SEQUENCE 6 AA; 62
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Best Local Similarity
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Search completed: December 16, 2000, 04:23:32 Job time: 4567 sec

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rabbit alpha- and beta-ventric
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proctolin - Americ
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ornitho-kinin - c
              membrane protein
180K exoantigen -
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A;Molecule type: DNA
A;Residues: 1-7 <FRL>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha-myosin heavy chain - rabbit (fragment)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 14-Reb-1997 #sequence_revision 14-Reb-1997 #tex
C; Accession: 146668
R; Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044 3048, 1984
A; Title: Characterization of genomic clones specifying in A; Reference number: 146868; MUID:84221901
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S78764
PQ0663
H33098
E48394
B39040
I48293
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A32523
S15422
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S21273
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S65433
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B44510
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60.0%;
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6.409 Million cell updates/sec
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            version 4.5
- 2000 Compugen Ltd.
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                                                                                 December 16, 2000, 03:35:13
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                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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A19780
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Copyright (c) 1993
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Maximum Match 100%
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R;Feeney, A.J.
J. Exp. Med. 114, 115-124, 1991
Jittle: Unctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Pathway: oxidative phosphorylation; respiratory chain
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr
                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytochrome-c oxidase (EC 1.9.3.1) chain VIa - bigeye tuna (fragment)
(S.Species: Thunnus obesus (bigeye tuna)
(S.Species: Thornus obesus (bigeye tuna)
(S.Accession: S77984
S.Y.Bee, J., Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, S.bmitted to the Protein Sequence Database, June 1997
A.Reference number: S77980
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C;Date: 28-Jul-1987 #sequence_revision 28-Jul-1987 #text_change 31-Dec-1993
C;Accession: B24749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell receptor beta chain V-D-J region (161-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0709
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Pred. No. 1.8e+05;
1; Mismatches 0;
                                                                                                    1.8e+05;
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C;Keywords: T-cell receptor
                                                             34.0%; Score 18; DB 100.0%; Pred. No. 1.8
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ilarity 66.7%;
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                                                                                                                                        Conservative
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A; Residues: 1-9 <ARN>
A; Experimental source: heart
C; Genetics:
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Best Local Similarity
Matches 3; Conserv
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| DPE 3
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4 PEF
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R:HOlman, G.M.; Ccok, B.J.; Nachman, R.J.
Comp: Biochem. Physiol. C 88, 31-34, 1987
A;Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin
A;Reference number: JS0317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Mesidues: 1-8 < HOL>
C; Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C; Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ţ
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AFILLE: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase AFILLE: Molecular cloning and quantification of mRNA and protein encoding Ca2+-ATPase AFILLE: Molecular clouds of Ga2+-ATPase AFILLE: Molecular in G4832
AFILLE: MOLECULAR CASE OF AFIL
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C; Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C; Accession: A19780
R; Brock, J.H.; Esparza, I.; Oliver, R.A.; Spooner, R.L.
Biochem Genet. 18, 831-860, 1980
A; Title: Electrophoretic mobility of N- and C-terminal monoferric fragments of bovine A; Reference number: A19780, MUID: 81183891
A; Rocession: A19780
A; Rocelle type: protein
A; Residues: 1-6 <BRO>
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Q2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;AcCession: I64832
R;Wu, K.
                                                                                                                                                                                                                                         C;Species: Leucophaea maderae (Madeira cockroach)
C;Dațe: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 1.8e+05;
1; Mismatches 1; Indels
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1.8e+05;
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Similarity 60.0%;
3; Conservative 1
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Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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C;Genetics:
A;Gene: SERCAlb
C;Keywords: hydrolase
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| DPAFS 5
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MHDEE
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Matches

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C; Species: Bos primigenius taurus (cattle) (C; Species: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1993 (C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 18-Jun-1993 (C; Accession: A.28719 | Bushner, V.; Pecht, M.; Trainin, N. Blochemistry 27, 4066-4071, 1988 | A; Trile: Thymic humoral factor gamma-2: purification and amino acid sequence of an im A; Reference number: A28719; MUID:88326920
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Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)

Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)

C; Species: Homo sapiens (man)

C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C; Accession: Pr0231

B; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991

A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity an A; Reference number: Pr0222; MUID:91108337
                                                                            C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C; Accession: A03188
R; Lote, C.J.; Weiss, J.B.
Biochem J. 123, 25P, 1971
A; Title: Identification in urine of a low-molecular-weight polar glycopeptide contain A; Reference number: A03188; MUID:72062338
                                                                                                                                                                                                                                                                              A;MOlecule type: protein
A;Residues: 1-8 <LOT>
C;Comment: The identity of the glycoprotein from which this peptide is derived is unk
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                                                                                                                                                                                                                                                                                                                                                             re has also been found (see PIR:XGHUE).
C.Superfamily: unassigned animal peptides
C.Keywords: glycoprotein
F:1/Binding site: carbohydrate (Cys) (covalent) #status experimental
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
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Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 1.
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A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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66.7%;
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                                                         urine glycopeptide - human
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Best Local Similarity
Matches 2; Conserva
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Best Local Similarity
Matches 2; Conserv
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5 PKF 7
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5 HD 6
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C; Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 07-Feb-1997
C; Accession: A60108
R; Schlievert, P.M.; Gray, E.D.
Infect. Immun. 57, 1865-1867, 1989
A; Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast
A; Reference number: A60108; MUID:89254013
A; Accession: A60108
A; Molecule type: protein
A; Residues: 1-9 <SCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: unidentified bacterium
C; Species: unidentified bacterium
C; Species: unidentified bacterium
C; Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 28-May-1999
C; Accession: D58503
R; Blnette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
R; Blnette in The Proteins of Kidney and gallbladder stones.
A; Reference number: A58501
A; Reference number: A58501
A; Reference number: A58501
A; Residues: 1-9 < BIN>
A; Residues: 1-9 < BIN>
A; Residues: 1-9 < BIN>
A; Reperfamily: translation elongation factor Tu; translation elongation factor Tu homolc C; Reywords: GTP binding
R;Yang, H.Y.T.; Fratta, W.; Majane, E.A.; Costa, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 7757-7761, 1985
A;Title: Isolation, sequencing, synthesis, and pharmacological characterization of two A;Reference number: A94074; MUID:86067985
A;Accession: B24749
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                            Length 8;
                                                                                                                                                                                                                                                         Score 15; DB 2; Le
Pred. No. 1.8e+05;
2; Mismatches 2;
                                                                                                                                                                                                                                                         28.3%;
33.3%;
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66.7%;
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llarity 66.7%;
Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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                                                                                                                        A Molecule type: protein
A Residues: 1-8 <YAN>
C Keywords: neuropeptide
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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1 FLFQPQ 6
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4 POF
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RESULT 18
B45796
dihydrolipoamide S-succinyltransferase (EC 2.3.1.61) - Pseudomonas fluorescens (fragm
C:Species: Pseudomonas fluorescens
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-May-2000
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 05-May-2000
C;Caccession: B45796
R:Benen, J.A.E.; Van Berkel, W.J.H.; Van Dongen, W.M.A.M.; Mueller, F.; De Kok, A. J. Gen. Microbiol. 135, 1787-1797, 1989
A;Title: Molecular cloning and sequence determination of the lpd gene encoding liboam
                                                                                                                                                                                                                                                                                                        CiSpecies: Ctenopharyngodon idella (grass carp)
CiSpecies: Ctenopharyngodon idella (grass carp)
CiSpecies: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999
CiAccession: S71919
R;Tsui, H.T.; Mock, W.Y.; Lau, K.K.; Fong, W.P.
Biochim: Biophys. Acta 1296, 41-46, 1996
A;Title: Proteolytic activation of grass carp (Ctenopharygodon idellus) liver alcohol A;Reference number: S71919; MUID:96350418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R.M.I.111, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.
Mol. Immunol. 28, 753-761, 1991
A.Title: Barly occurrence of immunoglobulin isotype switching in human fetal liver.
A.Reference number: PT0368; MUID:91312348
A.Recession: PT0368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ig gamma chain C region (gamma-1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31 Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Aug-1996
C;Accession: PT0368
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Pred. No. 1.8e+05;
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                        Score 13; DB 2; I
Pred. No. 1.8e+05;
1; Mismatches 1;
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100.0%; Pred. No. ...
0; Mismatches
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A; Residues: 1-8 <MIL>
A; Experimental source: fetal liver
                          24.5%;
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity 37.5
Matches 3; Conservative
                                                                                Conservative
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A; Status: preliminary A; Molecule type: protein
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C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: ll-Oec-1992 #sequence_revision 11-Dec-1992 #text_change 30-Sep-1993
C;Accession: B60274
R;Nagai, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.
R;Naccession: B60274
R;Napacterial characterization of major protein antigens in the culture A;Naccession: B60274
R;Napacule type: protein
A;Residues: 1-5 <NAG>
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C;Specias: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0665
B;Feeney, A.J.
B;Feeney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT06509; MUID:91277601
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0650
A;Reference number: PT0665
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-7 cFEEA
A;Experimental source: day 4 postnatal thymus, strain BALB/C
C;Keywords: T-cell receptor
                                                                                                                                                                         metallothionein-A - rainbow trout (fragment)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: 151049
R;Olsson, P.E.; Kling, P.; Erkell, L.J.; Kille, P.
Eur., J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) ray. Accession: 151049
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-4 <OLS>
A;Cross-references: EMBL:X80181; NID:g1019799
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C; Species: Rana esculenta (edible frog (fragment)
C; Species: Rana esculenta (edible frog)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C; Accession: P70080
R; Trevesso, S; Zorzato, F; Chiozzi, P; Mandari, P.; Volpe, P.; Pozzan, T.
Biochem. Biophys. Res. Commun. 175, 444-450, 1991
A; Title: Frog brain expresses a 60 kDa Ca2+ binding protein similar to mammalian calr A; Reterence number: P70080; MUID:91207333
A; Accession: P70080
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-9 <TRE>
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A;Molecule type: protein
A;Residues: 1-9 <WUA>
A;Note: the residue designated 'X' is modified lysine in collagen 3(XI) some cross-ll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Collagen alpha 1(II) chain - bovine (fragment)
NiAlternate names: collagen alpha 3(XI) chain
C; Species: Bos prinigenius taurus (cattle)
C; Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 03-Oct-1995
C; Accession: G56978
R; Wu, J.J.; Eyre, DR
F; Wu, J.J.; Eyre, DR
J. Biol. Chem. 270, 18865-18870, 1995
A; Title: Structural analysis of cross-linking domains in cartilage type XI collagen.
A; Reference number: A56978; WUID:95370194
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C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 05-Feb-1999
C; Accession: pD0443
C; Accession: PD0443
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Pred. No. 1.8e+05;
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Best Local Similarity 100.
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A; Residues: 1-9 <KAW>
C; Keywords: CoA-transferase
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Best Local Similarity
Matches 2; Conservat
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|1 DP 2
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R. Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A.FILLE: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac A. Reference number: 536887; MUID: 94009653
A. Accession: S3698
A. Status: preliminary
A. Molecule type: protein
A. Residues: 1-9 < OHA>
C. Keywords: protein blosynthesis; ribosome
                                                                                           A;Molecule type: DNA
A;Residues: 1-9 <BEN>
A;Cross-references: GB:M28356; NID:g151343; PIDN:AAA99233.1; PID:g151344
C;Superfamily: dihydrclippamide acctyltransferase; lippyl/biotin-binding homology
C;Keywords: acyltransferase; coenzyme A; lippamide; tricarboxylic acid cycle
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kidney and bladder stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
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C;Species: Mycobacterium bovis
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
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1; Mismatches 2; Indels
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R. Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A; Description: The proteins of kidney and gallbladder stones.
                                                                                                                                                                                                                                           DB 2; Ler
1.8e+05;
thes 0;
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A Status: preliminary
A: Molecule: type: protein
A: Mosidues: 1-9 - GBIN>
A: Experimental source: human kidney stone, bladder st
A: Experimental source human kidney stone, bladder st
A: Note: a secondary sequence AAKENPXD was also found
                                                                                                                                                                                                                                         Query Match 24.5%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 1.6 Matches 2; Conservative 0; Mismatches
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                          A;Reference number: A45796; MUID:90132584
A;Accession: B45796
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50.0%;
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                                                                       A;Status: preliminary
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2 LPDVKF 7
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fulicin - giant African snail
C;Species: Achatina fulica (giant African snail)
C;Species: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 11-Jul-1997
C;Accession: A44692
R;Ohta, N.; Kubota, I.; Takao, T.; Shimonishi, Y.; Yasuda-Kamatani, Y.; Minakata, H.; Biochen. Biophys. Res. Commun. 178, 486-493, 1991
A;Title: Fullicin, a novel neuropeptide containing a D-amino acid residue isolated fro A;Reference number: A44692; MUID:91315471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito
C;Species: Sarda orientalis (striped bonito)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999
C;Accession: JNO861
R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A;Reference number: JNO859; MUID:94080036
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hydroganulfite reductase (EC 1.8.99.3) chain 2 - Desulfovibrio thermophilus (fragmen
N;Alternate names: bisulfite reductase; desulfofuscidin
C;Species: Desulfovibrio thermophilus
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C; Comment: The carboxyl end is essential for the protein's expression of angiotensin
C; Superfamily: bradykinin-potentiating peptide
C; Keywords: angiotensin-converting enzyme inhibitor
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C; Reyvords: amidated carboxyl end; D-amino acid; neuropeptide
C; Reyvords: amidated carboxyl end; Status experimental
F; 2/Modified site: D-asparagine (Asn) #status experimental
F; 5/Modified site: amidated carboxyl end (Val) #status experimental
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Matches 2; Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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   C; Genetics:
A; Gene: NF2
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                                                                                                         RESULT 24
S39437
D-and-acid oxidase (EC 1.4.3.3) - Trigonopsis variabilis (fragment)
C;Species: Trigonopsis variabilis
C;Species: Trigonopsis variabilis
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1997 #text_change 07-May-1999
C;Accession: S39437
R;Schraeder, T.; Andreesen, J.R.
Eur. <sup>1</sup>J. Blochem. 218, 735-744, 1993
A;Title: Evidence for the functional importance of Cys298 in D-amino acid oxidase from A;Reference number: S39437; MUID:94094869
A;Accession: S39437
A;Molecule type: protein
A;Residues: 1-9 <SCH>
A;Experimental source: CBS 4095
C;Function:
A;Description: oxidoreductase; catalyzes; the oxidation of D-amino acids to their corresp
A;Note: reoxidation of the enzyme by molecular oxygen is accompanied by the release of P;C;Reywords: FAD; oxidoreductase
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Days
C; Accession: 154357
R; Huynh, D.P.; Nechiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A; Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are of A; Reference number: 154357
A; Reference number: 154357
A; Accession: 154357
A; Mulb:95072570
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-4 cRES>
A; Residues: 1-4 cRES>
A; Cross-references: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:g601923
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0; Mismatches 1; Indels
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Calsequestrin, fast skeletal muscle - rabbit (fragment)
Calsequestrin, fast skeletal muscle - rabbit (fragment)
C.Species: Oryctolagus cuniculus (domestic rabbit)
C.Daces: Oryctolagus cuniculus (domestic rabbit)
C.Dacession: B39040
R.Cala, S.E.; Jones, L.R.
J. Biol. Chem. 266, 391-398, 1991
A.Title: Phosphorylation of cardiac and skeletal muscle calsequestrin isoforms by cas A.Reference number: A39040; MUID:91093153
A.Accession: B39040
A.Sacession: B39040
A.Sace
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C; Accession: E48394
R; Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem Mol. Biol. Int. 29, 545-554, 1993
A; Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-II-like sequences.
A; Reference number: A48394; MUID:93250576
A; Scatus: preliminary
A; Molecule type: protein
A; Raperimental source: milk
A; Experimental source: milk
A; Note: sequence extracted from NCBI backbone (NCBIP:131450)
C; Keywords: glycoprotein
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                                                                                                            180K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Sate: 24-uq-1990 #sequence_revision 24-aug-1990 #text_change 09-Jun-2000
C;Sate: 24-uq-1990 #sequence_revision 24-aug-1990 #s.Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A;Reference number: A33098
A;Reference number: A33098
A;Reference protein
A;Rolecule type: protein
A;Rolecule type: protein
A;Residues: 1-7 <NIC>
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C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C;Accession: S11556
R;Fauque, G.: Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I Biochim. Biophys. Acta 1040, 112-118, 1990
A;Title: Purification and characterization of bisulfite reductase (desulfofuscidin) from A;Reference number: S11024; MUID:90335276
A;Accession: S11556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RiBridgen, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A;Title: Sequence determination of the nucleocapsid protein gene of the porcine epidemic issible gastroenteritis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment) C.Specias: porcine epidemic diarrhea virus C.Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999 C.Accession: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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A;Residues: 1-6 <GRA>
C;Keywords: mitochondrion
F;1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ribosomal protein MRP-S23, mitochondrial - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Sate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: S78764
S;Graack, H.R.
Submitted to the Protein Sequence Database, July 1999
A;Reference number: S78760
A;Reference number: S78764
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A,Cross-references: GB:214976; NID:g311650; PIDN:CAA78699.1; PID:g584083 C:Comment: This virus is coronavirus related to human coronavirus 229E. C;Keywords: membrane protein
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Matches 2; Conservative 0; Mismatches 0;
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A; Accession: PQ0663
A; Molecule type: mRNA
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Best Local Similarity 100.0
Matches 2; Conservative
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A; Residues: 1-6 <FAU>
C; Keywords: oxidoreductase
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transforming protein cKi-ras - mouse
C; Species: Mus musculus (house mouse)
C;Date: 02-01-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Ccession: 148293
R; Trusko, S.P.; Hoffman, E.K.; George, D.L.
Nucleic Acids Res. 17, 9259-9265, 1989
A; Title: Transcriptional activation of cKi-ras proto-oncogene resulting from retroviral A; Reference number: 148293
A; Accession: 148293
A; Accession: 148293
A; Accession: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-7 <RBS>
A; Cross-references: EMBL:X15888; NID:950415; PIDN:CAA33898.1; PID:9581942
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2; Indels
1; Mismatches
3; Conservative
                                           4 DPEFNL 9
| | :|
1 DDEEDL 6
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148293
Matches
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Search completed: December 16, 2000, 03:35:13 Job time: 5646 sec

6 EFNL 9 |: | 3 EYKL 6

O.Y Db

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AmEPV spheroidin p
Heat shock protein
Heat shock protein
N-terminal sequenc
Immunogenic peptid
N-terminal sequene
ScFV (dig) variant
Rodent interleutin
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Mimotope peptide #
Pentameric mimotop
Peptide 78 from 88
SEQ ID 104 of US59
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Soybean pepsin dig
Disulphide-circula
Peptide derived fr
N. denitrificans a
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Inhibitor of signa
Penicillium purpur
Protein kinase C-b
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Amino acid copper
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Prostate-specific
Prostate-specific
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Peptide determined
                     Caspase sensitive
Peptide encoded by
IL-1beta protease
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Membrane dipeptida
 Interleukin 1-beta
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Autotaxin peptide
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Polypeptide f
HIV-derived H
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K34850

Y21732

Y21732

K34855

K859594

K869595

K869596

K803313

X203313

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X170014

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W873504

W873504
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R15330
R15336
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R55100
W02239
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R37032
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ID W84423 standard; Peptide; 6 AA.
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Heat shock protein
Synthetic PMELI7 p
Melanoma-specific
Peptide determined
Peptide metermined
Peptide mimetic of
Immunogenic peptid
Fibronectin CSI-de
Fibronectin CSI-de
Fibronectin CSI-de
Aminomethylcoumari
Interleukin-1 beta
                                                                                                                Search time 107.12 Seconds (without alignments)
2.873 Million cell updates/sec
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                  2000, 03:07:20;
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first 75 summaries
                                                                                   protein - protein search, using sw model
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X16929
W38402
R82119
W87248
W87245
W61745
Y77439
Y77440
W52752
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Gapop 10.0 , Gapext 0.5
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53
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Match
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444.7.2
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44.8.4
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25-SEP-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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  δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           w84422-41 represent the peptides obtained from randomised finger 2 sequences of zinc finger nucleotide-binding proteins that bind to HIV-1 target sequences. The peptides were produced in the course of the invention. The specification describes zinc finger nucleotide-binding protein variants with at least two zinc finger modules that bind to a cellular nucleotide sequence and modulate its function. Zinc finger correlations, and compositions containing them, are used to increase or proteins, and compositions containing them, are used to increase or reduce transcription of a gene linked to the cellular nucleotide sequence. The proteins are used specifically for treating or preventing cell proliferative disorders (an humans, animals or plants, including those induced by viruses), particularly where expressed from nucleic acid by gene therapy (including ex vivo methods). Typical diseases that can be created are many forms of cancer, psoriasts, pemphigus vulgaris, Bechet's syndrome and lipid histicoytosis, also treatment of human immune deficiency virus (HIV) and other viral infections, and production of transgenic plants resistant to bacterial and viral diseases. The present oligonucleotide is used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                          zinc finger; nucleotide-binding protein; cell proliferative disorder; gene therapy; cancer; psoriasis; pemphigus vulgaris; Bechet's syndrome; lipid histiocytosis; human immune deficiency virus; HIV; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                            New zinc finger nucleotide-binding protein variant that modulates selected nucleotide sequence - used for treatment of proliferative and viral diseases by gene therapy, and can be made selective for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.2%; Score 25; DB 20; Length 6; 80.0%; Pred. No. 2.1e+05; ive 0; Mismatches 1; Indels
                                   HIV-1 nucleic acid binding protein zinc finger 2 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock protein (hsp) binding peptide.
                                                                                                                                                                                                                                                                             Wright PE;
                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Fig 9; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y16929 standard; peptide; 7 AA.
                                                                                                                                                                                                    98WO-US10801.
                                                                                                                                                                                                                           97US-0863813
                                                                                                                                                                                                                                                                             Barbas CF, Gottesfeld JM,
             22-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                    (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                                                                                                                                    WPI; 1999-059831/05
                                                                                                                                                                                                                                                                                                                                                                  any target sequence
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Best Local Similarity
Matches 4; Conserv
                                                                                                   transgenic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 AA;
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                                                                                                                                                  WO9854311-A1
                                                                                                                                                                                                  27-MAY-1998;
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                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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Y16929
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Conjugate peptide; heat shock protein; hsp; phage display library; virus; surface protein; tethering peptide; chaperone process; cytokine; cancer; neoplastic disease; infectious disease; bacterium; immune system; fungus; acquired immune deficiency; autoimmune disease.
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human leukocyte antigen-Al; HLA-Al; human leukocyte antigen-A3;
HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moroi Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying peptides which bind heat shock proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25; DB 20; I
Pred. No. 2.1e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton A, Mayhew M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SLOK ) SLOAN KETTERING INST CANCER RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Examples; Page 21; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.2%; Scor
100.0%; Pre
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                                                                                                                                                                                                                                                                                                                                           98WO-US22335.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic pMEL17 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-313177/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease of the immurautoimmune diseases.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                WO9922761-A1
                                                                                                                                                                                                                                                                                                                                     22-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                31-OCT-1997;
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                                                                                                                                                                                                                                                                            14-MAY-1999.
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3 1hdp
                                                                                                                                                       Synthetic
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Gaps

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the sequence of unknown peptides or proteins with no sub-sequence identity, to be characterised using mass spectrometry. Sequences W87101 to W87364 represent a library of linear peptides constructed to exemplify the method. The isoleucine residue in these peptides can be replaced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for determination of the amino acid sequence of an unknown peptide. The method comprises (a) determining the molecular mass and an experimental fragmentation spectrum for the peptide; (b) comparing the experimental fragmentation spectrum of the unknown peptide with a theoretical fragmentation spectrum of the unknown peptide library composed of all possible linear sequences of amino acids having a total mass that corresponds to the molecular mass of the unknown peptide; and (c) identifying a peptide in the library with a theoretical fragmentation spectrum that most closely matches the fragmentation spectrum of the unknown peptide. The method is useful in DNA cloning, anti-body production, identification of recombinant products, and the study of post-translational modifications. It allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
         A melanoma-specific immunogen homologous with pWel-17 comprises one or more CTL (cytotoxic T lymphocyte) epitopes from the group R82098-R82194 capable of eliciting a CTL response. The epitopes R82098-R82108 are of particular interest. The immunogen can be used for partial protection in mammals against melanoma peptides which are homologous with pWel-17 are highly potent stimulators of HLA-A2+CTLs in several cell lines and can be used in immunotherapy or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide sequence determination used in e.g. DNA cloning - by comparing mass spectra of the unknown peptide with a library
                                                                                                                                                                                                    Score 25; DB 16; Length 9;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                 Indels
                                                                                                                       incorporated into immunogenic conjugates as vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       determined by the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend RR, Wedd NS;
                                                                                                                                                                                        47.2%; Scor.
100.0%; Pred. No. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear chain known peptide sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 20; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                             W87278 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0011196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97GB-0010582
                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1999 (first entry)
                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parekh RB, Prime SB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-571195/49.
                                                                                                                                                      9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-1998;
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                                                                                                                                                                                                                                                                 2 LHDP 5
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                                                                                                                                                        Sequence
                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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W87278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         The present peptide was used in the preparation of a novel melanoma specific immunogen, comprising at least 1 melanoma specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17 or tyrosinase. The immunogen can be used in vaccines for protection against melanoma in mammals.
                                                                                                                                                                                                    Melanoma-specific immunogens of pMel-17 and tyrosinase - useful in vaccination for producing melanoma-specific cytotoxic T lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Melanoma-specific immunogen comprises epitope(s) homologous with pMel.17 - are highly potent stimulators of HLA-A2+CTL's useful in adoptive immuno-therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Melanoma; immunogen; epitope; homologue; vaccine; immunotherapy; cytotoxic T cell; lymphocyte; HIA-A2.
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                                                                                                                         ä
                                                                                                                         Kittlesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Melanoma-specific mutant immunogen epitope 9mer peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18; Le
2.1e+05;
hes 0;
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                                                                                                                         Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                         Hendrikson RC, Hu
J, Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 25;
Pred. No.
                                                                                                                                                                                                                                                Example 9; Page 65; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 8; Page 51; 148pp; English
                                                                                          (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                            47.2%; Scur
100.0%; Pre
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              97WO-US04958.
                                                          96US-0013972.
                                          96US-0027627
                                                                                                                                       Skipper J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                         Engelhard VH,
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Best Local Similarity
4; Conserve
                                                                                                                                                                      WPI; 1997-479982/44.
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                                                                                                                                       Shabanowitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09522561-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
              17-MAR-1997;
                                            04-0CT-1996;
19-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                          COX AL,
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Pred. No.

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                                                                                                          ;
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leucine to construct another 264 linear peptides to be included in the
                                                                                                                                                                                                                                                                                                                                      Amino acid determination; molecular mass; fragmentation spectrum; DNA cloning; anti-body; recombinant; modification; mass spectrometry.
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide sequence determination used in e.g. DNA cloning - by comparing mass spectra of the unknown peptide with a library of
                                                                                                          ;
                                                                               Length 6;
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                             Peptide determined by the method of the invention.
                                                                               Score 23; DB 19;
Pred. No. 2.1e+05;
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                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear chain known peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
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                                                                                                                                                                                                                               W87245 standard; peptide; 6 AA.
                                                                               43.48;
75.08;
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                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                          Conservative
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                                                                Query Match
Best Local Similarity
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                                        6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                        GB2325465-A.
                                                                                                                                   1 YLHD 4
                                                                                                                                                                                                                                                                                                                                                                                                                                 25-NOV-1998
                                                                                                                                                  1:11
2 yihd
                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                        Seguence
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             library
                                                                                                                                                                                                                                                          W87245;
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                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide mimetic; gamma-chain; cytokine receptor; signal transduction; autoimmune disease; graft vs. host disease; transplant rejection; graft rejection; interleukin; immunosuppressant; T cell; B cell.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) mimicking a loop in the gamma chain of cytokine receptors - inhibit signal transduction through these receptors, useful as immunosuppressants for treating or preventing e.g. leukaemia, autoimmune disease, graft rejection
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                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide mimetic of cytokine receptor gamma chain 12.
2.1e+05;
0;
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 28; 54pp; English.
                                                                                                                                                                                                                                                                 W61745 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYJE-) UNIV JEFFERSON THOMAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0036941.
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                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                            Conservative
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Best Local Similarity
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               Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1998
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                                                                                        1 YLHD 4
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                                                                                                                                         1 yihd 4
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heprf
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                                                                                                                                                                                                                                                                                                                  W61745;
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                                                                                                                                                                                                                  RESULT
W61745
ID W6
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RESULT

Length 6;

DB 19;

43.4%; Score 23;

Query Match

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Fibronectin; FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressing receptor and VLA-4 inhibitors for treating inflammatory and cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New peptidomimetic compounds used as cell surface fibronectin
                                                                                                                         Fibronectin CS1-derived peptide #30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 1; 243pp; English.
      Y77439 standard; peptide; 9 AA.
                                                                                   22-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arrhenius TS, Elices MJ,
                                                                                                                                                                  Fibronectin; FN; CS-1; CD49d/CD29; leukocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                          WO200002903-A1.
                                                                                                                                                                                                                                                                                                                                                                           15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                   20-JAN-2000.
                                                                                                                                                                                                                                                   Mammalia.
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                                            Y77439;
      vassion to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or section con useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
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                                                                                                                                             Immunogenic peptide having a human leukocyte antigen binding motif #2388.
                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .<u>,</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidney J, Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 123; 150pp; English.
                     Y47777 standard; Peptide; 9 AA.
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                                                                                                      01-DEC-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
tes 3; Conserv
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                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         W09945954-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-1998;
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                                                                                                                                                                                                                                                                                                               Synthetic
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                                                              X47777;
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Matches
Y47777
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Chen PG;

Gaeta FCA, He Y, Huyghe BG,

98WO-US26605. 98US-0113689

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The invention relates to peptidomimetic compounds (Y77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking. VLA-4-mediated leukocyte adhesion to the CS-1 FN of endothelial cells is also a critical step in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and acute immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and allograft rejection. They may also be used to treat psortasis and other skin inflammations, demyelinating diseases of the central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (e.g., multiple sclenosis), allergies, atherosclenosis, collis, diabetes, inflammatory bowel disease, kidney inflammation and restenosis, prior art inhibition of VLA-4/CS-1 Interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on repeated administration, or the 25-mer CS-1 peptide, which is large and repetidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and the CS-1 peptide tested for their ability to inhibit VLA-4 Jurkat cells to immobilised CS-1 peptide (Y77410).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.48;
80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 43.4
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
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Y77440
ID Y77440
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RESULT Y77439

1 YLHDP 5

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Mammalia

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The peptide is a specifically claimed example of new aminomethyl-coumarin-labelled tetrapeptides of formula Ac-Xaa-Xaa-Xaa-Xap-AMC. The tetrapeptides are used to generate a fluorescent positional scanning synthetic combinatorial library for the investigation of the substrate specificity of cysteine and serine proteases, e.g. in the analysis of interleukin-1 beta converting enzyme substrate and other caspase substrates, and to identify inhibitors which may mediate inflammations. The library preferably comprises a mixture of at least 200 of the tetrapeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New tetrapeptide coumarin derivatives - useful in combinatorial libraries to identify substrate specificity of cysteine or serine proteases e.g. interleukin-1 converting enzyme
                                                                                                                                                                                                                                                                                                                                                            /note= "the C-terminal is condensed onto 7-amino-4-methyl-coumarin via an amide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human precursor IL-1beta; Graves' disease; Hashimoto's disease.
                                                                                                                                                                                                                                                                                                             /note= "the N-terminal is acetylated"
                                                                                                                                               Aminomethylcoumarin; fluorescent; interleukin; ICE; opositional scanning synthetic combinatorial library.
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Pred. No. 2.1e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thornberry
                                                                                              Aminomethylcoumarin-substituted tetrapeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interleukin-1 beta protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rano T,
                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3; Page 41; 49pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98GB-0003559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0038656
                                            02-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chapman KT, Nicholson D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-523841/45.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                    Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-1997;
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                                                                                                                                                                                                                    Synthetic.
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W52752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to peptidomimetic compounds (Y77415-Y77438) capable of inhibiting the binding of the VLA-4 integrin (alpha-4-beta-1, CD494/CD29) to the CS-1 portion (25 amino acids) of a splice variant of the extracellular matrix protein fibronectin (FN). VLA-4 is expressed on the surface of leukocytes; the CS-1 FN/VLA-4 interaction plays an important role in the maturation and trafficking VLA-4 mediated cleukocyte adhesion to the CS-1 FN of endothelial cells is also a critical enkocyte adhesion to the CS-1 FN of endothelial cells is also a critical cleukocyte adhesion to the CS-1 FN of endothelial cells is also a critical stop in the inflammatory response. The peptidomimetics of the invention may be used to treat both chronic and actte immunoinflammatory conditions, such as asthma, rheumatoid arthritis, osteoarthritis and other conditions, such as asthma, rheumating diseases of the central nervous system of allograft rejection. They may also be used to treat psoriasis and other skin inflammations, demyelinating diseases of the central nervous system (e.g., multiple sclerosis), allergies, atherosclerosis, colitis, clabetes, inflammatory bowel disease, kidney inflammation and restenosis. Prior art inhibition of VLA-4/CS-1 interaction either involves the use of anti-VLA-4 antibodies, which can themselves induce an immune response on corticolysis. Sequences vince smaller in comparison to the CS-1 peptidomimetics of the invention are smaller in comparison to the CS-1 peptide and therefore less expensive to manufacture, and are resistant to proteolysis. Sequences Y77411 and Y77414 and Y774410).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                           Fibronectin, FN; CS-1; endothelial cell; VLA-4 integrin; alpha-4-beta-1; CD49d/CD29; leukocyte; inflammatory cell; inflammation; cell adhesion; inhibitor; peptidomimetic; autoimmune disease; inflammatory disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptidomimetic compounds used as cell surface fibronectin expressing receptor and VLA-4 inhibitors for treating inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen PG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Huyghe BG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 21; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 He Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaeta FCA,
                                                                                                                 Fibronectin CS1-derived peptide #31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 1; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W52752 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US26605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0113689
                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Elices MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-182213/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                        WO200002903-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arrhenius TS,
                                                                  22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                       20-JAN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ||
2 lhgpe (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LHDPE
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Gaps

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Query Match

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11

Length 4; Indels

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Rev-caspase; cysteine protease; zymogen; caspase; cancer; gene therapy; autoimmune disease; caspase-mediated apoptosis; neurodegenerative; tumour cell; myocardial infarction; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid molecules encoding rev-caspases. Rev-caspases are cysteine proteases that specifically cleave proteins after Asp residues and is expressed as a zymogen, in which the small subunit is N-terminal to a large subunit. A gene delivery vehicle comprising a rev-caspase coding sequence is useful for the treatment of cancer, where the gene delivery vehicle is internalised by tumour cells. The gene delivery vehicle can also be used to treat autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule encoding a rev-caspase - used for screening and identifying inhibitors or enhancers for treating
                                                                                                                                                                                                            The sequence is that of pre-interleukin (IL)-lbeta amino acids 112-116 which can be used as part of a method of inhibiting IL-lbeta protease activity in a mammal. It can be used in cpds. for the treatment of inflammation or to treat or prevent autoimmune disease such as inflammatory disorders.
                                                                                    New polypeptide having protease biological activity for interleukin 1-beta - can form inhibitor compsn. and cpds. for treatment of arthritis, auto:immune diseases, inflammation and radiation damage: also for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                               Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                        41.5%; Score 22; DB 14;
75.0%; Pred. No. 2.1e+05;
tive 1; Mismatches 0.
                Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 16; 74pp; English.
                                                                                                                                                                            Claim 10; Page 60; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y21732 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer or autoimmune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US00632.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                Kronheim SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caspase sensitive site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-419353/35.
                                                WPI; 1993-100924/12
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                         5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9935277-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : | |
yvhd
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                RA,
                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X21732;
                Black
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
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Y21732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The 5 amino acids correspond to the sequence of residues 112 to 116 of precursor IL-1 beta (see March et al., Nature, 315: 641-647 (1985)). Inhibitors of the invention comprise from 1 to 5 amino acid residues corresponding to at least a portion of AYVHD. Specific examples of suttable inhibitors are given including Boc-Asp-CH2F, Boc-Phe-Asp-CH2F and Ac-Pro-Asp-CH2F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated Interleukin-1-beta protease - used to improve wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                        /note= "carries electronegative leaving group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   treat arthritis and auto-immune diseases e.g. insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-lbeta; therapeutic; wound healing; treatment; arthritis;
autoimmune disease; radiation; side effects.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 22; DB 12; Length 5; Pred. No. 2.1e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Interleukin 1-beta protease activity inhibiting peptide.
                                                                   "N-terminally protected"
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            Kronheim SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 14; Page 38; 46pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R34850 standard; Protein; 5 AA.
                                                  /label= OTHER
                                                                                                       /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41.5%;
llarity 75.0%;
Conservative
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                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                         Black RA, Sleath PR,
                                                                                                                                                                                                                                                                                                                         (IMMU-) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1991-325220/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       dependent diabetes
                               Modifled-site
                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-SEP-1991;
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                                                                                                                                                                                                                             04-APR-1991;
                                                                                                                                                                                                                                                                                   13-FEB-1991;
                                                                                                                                                                                                                                                                    04-APR-1990;
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                                                                                                                                                                                             17-0CT-1991
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Sequence

R34850;

RESULT 13 R34850

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Gaps

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Cleavage-site
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                            14-JUL-1993
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                                                                                                                                            WO9305071-A
                                                                                                                                                              18-MAR-1993.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YLHD 4
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                                                                                         Synthetic.
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1 yvhd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
            R34855;
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Cells transfected with a rev-caspase expressing vector can be used in identification of inhibitors or enhancers of caspase-mediated apoptosis. In vitro translated rev-caspase can be used to identify an inhibitor or enhancer of caspase processing activity. Caspase inhibitors are useful for treating neurodegenerative diseases as well as for inhibiting apoptosis in the heart following myocardial infarction. Sequences Y21738 represent caspase sensitive sites.
                                                                                                                                                                                                                                                 Peptide encoded by degenerate probe for soybean kunitz trypsin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Toxin protein of Bacillus thuringiensis bacteria - improved in efficacy using a potentiating amt. of a trypsin inhibitor. The sequence contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The peptide is encoded by a degenerate probe and corresponds to amino acids 125-130 of soybean kunitz trypsin inhibitor.
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                Length 5;
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                                                                                                                Indels
                                                                                               Score 22; DB 20; La
Pred. No. 2.1e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                  soybean; kunitz-type trypsin inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                          MacIntosh SC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; page 8; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R34855 standard; Protein; 8 AA.
                                                                                                                                                                                             P93063 standard; peptide; 6 AA.
                                                                                               41.5%;
75.0%;
                                                                                                                                                                                                                                                                                                                                       89EP-0870047
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                                                                                                                                                                                                                                (first entry)
                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                          Kishore GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ambiguity codes.
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-311431/43.
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                                                                                               Query Match
Best Local Similarity
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                                                                      AA;
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                                                                                                                                                                                                                                                                                                                                       10-APR-1989;
                                                                                                                                                                                                                                                                                                                                                       11-APR-1988;
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                                                                                                                                 1 YLHD 4
                                                                                                                                                                                                                                                                                    Glycine max
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1 yvhd
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                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                               P93063;
                                                                                                                                                                                                                                                                  Probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                             using
IUPAC
                                                                                                                                                                            15
                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                             RESULT
                                                                                                                                                                                    P93063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pentapeptide paralogue for use as chromatographic affinity ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide having protease biological activity for interleukin 1-beta - can form inhibitor compsn. and cpds. for treatment of arthritis, auto:immune diseases, inflammation and radiation damage; also for wound healing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                  Interleukin; therapeutic; wound healing; treatment; arthritis; autoimmune disease; radiation; side effects.
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                                                                                                                                                                                                                                                           3.6
/note= "IL-lbeta protease cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                 IL-lbeta protease cleavage site peptide substrate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22; DB 14; I
Pred. No. 2.1e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Page 39; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R12720 standard; Protein; 5 AA.
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75.0%;
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Black RA, Kronheim SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-100924/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA;
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Gaps
                                                                                                    A panel of 88 pentapeptides was designed on the basis of decreasing hydrophobicity and periodic variation of hydrophobic moment. The peptides were labelled with iodine-125 and tested with individual members of a basal antibody repertoire. (Spleen cells were harvested from mice and used to provide a panel of antibody-secreting hybridoma cells as a subset of the complete antibody-secreting hybridoma cells as a subset of the complete actla repertoire. Was observed. The test was than repeated with the addition of a defined amount of analyte to the mixture. A small number of wells showed greatly decreased labelling and these antibodies represented the successful result of an initial screen for those which preferentially bind analyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pentameric mimotope 78 used to obtain highly specific antibodles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing antibodies with high specificity and affinity for an analyte - by immunisation with selected mimotope, also analyte detection kits, useful for immunoassay of materials usually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R69875-969 are pentameric mimotopes designed on the basis of decreasing hydrophobicity and periodic variation of hydrophobic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mimotope; antibody; production; high specificity; detection; immunoassay; high performance liquid chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.6%; Score 21; DB 15; L 100.0%; Pred. No. 2.1e+05; Live 0; Mismatches 0;
mimotype-binding profile of receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                         Example 3; Fig 3; 29pp; English.
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87US-0108130.
93US-0072190.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 AA;
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04-JUN-1993;
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2 hdp 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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R69952
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                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide is one of a panel, each of which have systemicly varied values of at least two parameters. A test protein is matched against the panel, and the paralogues with highest binding affinity are selected. Selected paralogues are bound to a matrix which is incorporated into the HPLC gel and used as affinity ligands. Technique is useful in chromatographic separation, purification and binding assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                        Identifying paralog with specific affinity for analyte - using candidate paralogs with systematically varied values of at least 2 parameters.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mimotope peptide #78 from panel of maximally diverse mimotopes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of candidate drugs for binding to receptor - by inverse image antibody profile of drug with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mimotope panel; rational drug design; candidate drug; screening assay; hydrophobicity; antibody repertoire.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.6%; Score 21; DB 12; L 100.0%; Pred. No. 2.1e+05; Live 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TERR-) TERRAPIN TECHNOLOGIES INC
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                                                                                                                                                                                                                                                                                                                                                                                        Claim 41; Fig 8; 95pp; English
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89US-0447009.
90WO-EP06333
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Best Local Similarity
Matches 3; Conserv
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                                                      31-OCT-1989;
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06-DEC-1989;
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2 hdp 4
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                                                                                                                                                                Kauvar
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moment. All the pentapeptides are acetylated at the N-terminus except E12 (for FTTC) (sic). E12 is not identified in the specification. The mimotopes are used in the method of the invention to obtain antibodies specifically and strongly reactive with a desired analyte. The mimotope is obtd. by reacting a panel of starting antibodies (Abs) representative of the resting B cell reperfoire of a mammal with an analyte (so as to identify analyte-reacting Abs) and then reacting each of a panel of candidate mimotopes representative of a random set of 3D contours with the analyte-reacting Abs) and subject is immunised with one or more mimotopes identified and the product Abs are recovered from the serum of the subject.
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present peptide is a member of a panel of 88 pentapeptide mimotopes designed on the basis of decreasing hydrophobicity, and periodic variation of hydrophobic moment. The panel was synthesised using the method of Geysen, H. M., et al, Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying candidate drugs that bind a specific receptor by competitive reaction with panel of mimetope(s) - useful in rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Panel; mimotope; decreasing hydrophobicity; periodic variation; hydrophobic moment; antibody; repertoire; identification; drug; andidate; receptor; binding; ligand; rational; design; selection; treatment; truncur; production; immunological reagent; analyte; detection; trace contaminant; mimetope.
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                                                                                                                                                                                                                                                   Length 5;
                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide 78 from 88 member diverse mimotope panel.
                                                                                                                                                                                                                                                 39.6%; Score 21; DB 16; I 100.0%; Pred. No. 2.1e+05; iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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87US-0108130.
88US-0255906.
93US-0118133.
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                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                     5 AA;
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08-SEP-1993;
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2 hdp 4
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                                                                                                                                                                                                       Sequence
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Matches
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                           found. The test was then repeated with the addition of a defined amt. of analyte. A small number showed greatly increased labelling, these Ab representing the successful result of an initial screen for those that pref. bind analyte.

The above is an example of a claimed method for identifying members of a panel of candidate drugs, that bind to a receptor having a known ligand. It is useful in rational drug design, e.g. selection of monoclonal Ab for treating individual tumours, and for the prodn. Of immunological reagents for any analyte, including those not normally detectable by immunoassay, e.g trace contaminants in soil,
USA (1984), which uses lots of 96 pins; the remaining 8 polyethylene pins being controls. The mimotopes were then mixed, 125-I labelled and tested with individual members of a basal antibody (Ab) repertoire. Nearly uniform binding to all members was
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                                                                                                                                                                                                                                                                                                  Length 5;
                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                             ore 21; DB 17; 1 red. No. 2.1e+05; Mismatches 0;
                                                                                                                                                                                                                                                                                                Score 21;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Column 151; 131pp; English.
                                                                                                                                                                                                                                                                                     39.6%; Scor.
100.0%; Pre
0;
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92US-0881721.
92US-0996972.
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95US-0450497
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                     5 AA;
                                                                                                                                                                                                                        air or water.
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24-DEC-1992;
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Sequence
                                                                                                                      Query Match
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                                                                                                                                                                                                                                       RESULT
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where at least 1 of the Asp residues at positions 18, 87, 110, 130, 197, or 223 in the wild type sequence (see Y23591) is replaced by a Gln residue. NIFs may be useful for treating shock, stroke, acute and chronic allograft rejection, vasculitis, autoimmune diabetes, rhemmatoid arthritis, inflammatory skin diseases, inflammatory bowel disease, adult respiratory distress syndrome (ARDS), ischemial repertusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis. NIFs or NIF fragments may be used as vaccines against parasitic worm infection.

Chapman and be useful for detection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection of and isolation of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as an inferior and inhibitors may also be used as a compounds. The present sequence is used in the course of
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                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence of synthetic peptide based on clostripain digest fragment of Cathepsin G (CAT. G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New oligopeptide(s) with antimicrobial and antibacterial activity - useful in treatment of bacterial infection, e.g. gingivitis or periodontosis and to kill or control growth of tumour or virus-infected cells
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100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 10; Page 41; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       R20337 standard; Protein; 7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-024198/03.
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              enzyme; protease.
                                                                                                                                                                                                                        5 AA;
                                                                                                                                                                                                  invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUN-1991;
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positive and negative bacteria, fungi and protozoa. They can be used for treatment or prevention of infections and for the treatment and/or prevention of gingivitis. The IIGGR-related (R20331, R20332) can also be used to kill or control the growth of tumour cells or virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of synthetic peptide based on clostripain digest fragment of Cathepsin G (CAT. G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligopeptide(s) with antimicrobial and antibacterial activity - useful in treatment of bacterial infection, e.g. gingivitis or periodontosis and to kill or control growth of tumour or virus-infected cells
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Pred. No. 2.1e+05;
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Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R20345 standard; Protein; 7 AA.
                                                                                                                                                                                                                                                              39.6%;
75.0%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1992-024198/03.
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                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme; protease.
                                                                                                                                                                       7 AA;
                                                                                                                    infected cells.
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acquired immune deficiency; autoimmune disease.
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                         Hoe MH,
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1 hlhsp 5
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                                                                                                                                                                                                                                                                        Ouerfelli O,
                                                                                                                                             22-OCT-1998;
                                                                     WO9922761-A1
                                                                                                           14-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New entomopoxvirus polynucleotide sequences, proteins and vectors - are used for expression of heterologous proteins in both insect
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                                                                                                                                                                                                                                                                                                           gene expression; vector; insect cell culture;
culture; AmEPV; Amsacta moorei; entomopoxvirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 15; Length 7;
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 Indels
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                                                                                                                                                                                                                                                                          AmEPV spheroidin probe RM58 encoded peptide.
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Mismatches
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                                                                                                                                                                 R55584 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moyer RW;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                mammal cell culture; AmEP
DNA probe; hybridization.
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV FLORIDA
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N-PSDB; Q66799.
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Best Local Similarity
Matches 3; Conserv
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3 dpey 6
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                                                                                                                                                                                                                                                                                                               Spheroidin;
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                                      5 PEFN 8
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peyn
                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
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   Matches
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The invention relates to conjugate peptides engineered to noncovalently bind to heat shock proteins (hsp). A method of identifying a hsp binding bind to heat shock proteins (hsp). A method of identifying a hsp binding peptide comprises (a) contacting a phage display library having bacteriophage expressing, in a surface protein, inserted peptides with a hsp target, and bound to a henzoquinone ansamycin antibiotic (BAA), in a prigologic binding buffer; (b) isolating a phage binding to the hsp target; and (c) identifying the inserted peptide expressed. The peptides which bind to a hsp can be used as tethering peptides for a hsp which may serve as an accessory in a chaperone process and/or may comprise a cytokine. They can also be coupled to antigens to induce an immune response. Such compositions can be used for treating neoplastic disease, e.g. cancers, infectious diseases, e.g. diseases caused by a bacterium, virus, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a disease of the immune system, e.g. acquired immune deficiencies or
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying peptides which bind heat shock proteins
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Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                    Houghton A, Mayhew M,
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                                                                                                                                                      (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Examples; Page 24; 155pp; English.
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98WO-US22335
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                                                                                                                                                                                                                                      3 hdp 5
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                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                             vaccine;
                                                                                                                             (R67768)
                                                                                                                                                                                                                                                                                                           Y48130;
                                                                                                                                                                                                                                                                    RESULT 28
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                                                                                                                                                                                                                                                                              X48130
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                                                                                                                                             The invention relates to conjugate peptides engineered to noncovalently beind to heat shock proteins (hsp). A method of identifying a hsp binding peptide comprises (a) contacting a phage display library having bacteriophage expressing, in a surface protein, inserted peptides with a hsp target, and bound to a benzoquinone ansamycin antibicitic (BAA), in a physiologic binding buffer; (b) isolating a phage binding to the hsp target; and (c) identifying the inserted peptide expressed. The peptides which bind to a hsp can be used as tethering peptides for a hsp which may serve as an accessory in a chaperone process and/or may comprise a cytokine. They can also be coupled to antigens to induce an immune response. Such compositions can be used for treating neoplastic disease, e.g. chapers, protozoan, mycoplasma, fungus, yeast, parasite or prion, or a disease of the immune system, e.g. acquired immune deficiencies or
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer; neutrophil inhibitory factor; NIF; inflammation; adhesion; endothelial cells; inflammatory response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal sequence of neutrophil inhibitory factor (AcaNIF9).
                                                                                                                                                                                                                                                                                                                                      Score 21; DB 20; Length 8;
Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                          Identifying peptides which bind heat shock proteins
                                                 Mayhew M,
                            (SLOK ) SLOAN KETTERING INST CANCER RES
                                                                                                                            Disclosure; Fig 1H; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moyle M, Vlasuk GP;
                                                Houghton A,
                                                                                                                                                                                                                                                                                                                                                                                                                                               R67767 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                       39.6%;
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93US-0060433.
93US-0151064.
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         97US-0961707
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                                                MH, Hought
Rothman JE;
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                           WPI; 1999-313177/26.
                                                                                                                                                                                                                                                                                      autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ancylostoma caninum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1994-234706/28
                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                         8 AA;
                                                                                      N-PSDB; X60737
                                               Hartl U, Hoe
Ouerfelli O,
                                                                                                                                                                                                                                                                                                                                                                              1 YLHDP 5
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1 hlhsp !
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foster DL,
                                                                                                                                                                                                                                                                                                           Sednence
                                                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic I lymphocytes (CTLs) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide having a human leukocyte antigen binding motif #2741.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                 Neutrophil inhibitory factors can be used in compositions to inhibit neutrophil activity e.g. adhesion to vascular endothelial cells, and which are useful in the therapy of conditions which involve abnormal or undesired inflammatory responses. The N-terminal end of the proteclytically processed NIF Clone designated AceNIF3 is ambiguous and so for cloning purposes an N-terminal sequence was generated based on sequence homology between this NIF clone and AceNIF3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogenic peptides with HLA binding motif, useful in treatment
Neutrophil inhibitory factor peptide(s) – derived from nematodes, useful for therapy of inflammatory responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 15; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis of cancers and viral diseases
                                                                                                    Example 22(C); Page 125; 239pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 138; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y48130 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A, Kubo RT, Sidney J,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neutrophil inhibitory factor; NIF; mutant, shock; stroke; allograft rejection; vasculitis; autoimmune diabetes; ARDS; rheumatoid arthritis; inflammatory skin disease; myocardial infarction; inflammatory bowel disease; adult respiratory distress syndrome; ischemia-reperfusion injury; acute inflammation; bacterial infection; vaccine; parasitic worm infection; antihelminic.
to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially to treat e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                                                                                                                    39.6%; Score 21; DB 20; Length 9; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                 therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-terminal sequene of a hookworm NIF protein.
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92US-0996972.
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95US-0450497
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                     Seguence
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residue. NIFs may be useful for treating shock, stroke, acute and arthritis, inflammatory skin diseases, inflammancy bowel disease, rheumatory bowel disease, adult respiratory distress syndrome (ARDS), ischemia-reperfusion injury following myocardial infarction, and acute inflammation caused by bacterial infection such as sepsis or bacterial meningitis, NIFs or NIF fragments may be used as vaccines against parasitic worm infection. Anti-NIF antibodies may be useful for detecting infection of a mammalian host by a parasitic worm, as antihelminic agents, and in the detection be useful for the detection of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of NIF from tissue homogenates, cloned cells etc. NIFs may be useful for the detection of MIF mimics or antagonists in other compounds. Other NIF agonists and inhibitors may also be used as antihelminic agents. The present sequence represents a N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enzyme; antibody; catalysing; immune response; digoxin; digitoxin; scFv; assay; cytokine; transcription factor; clotting factor; chelating agent; hormone; receptor; single chain Fv; flourescence activated cell sorting;
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selection of desired polypeptides from candidates - comprises use
host cells containing a library of vectors that encode distinct
candidate polypeptides which are expressed on the surface of the
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                                                                                                                                                                                                                                                                                                                                                                  39.6%; Score 21; DB 20; Length 9; 100.0%; Pred. No. 2.1e+05; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ScFV (dig) variant clone LC2-7 isolated by FACS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 7; Page 81; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W89129 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US08714.
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                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-024054/02.
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                    of hookworm NIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FACS; variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9849286-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 HDP 5
                                                                                                                                                                                                                                                                                                            Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W89129;
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cytokine or chemokine. Sequences W86287 to W86300 represent peptide fragments of a rodent interleukin ($1\mathrm{L}$)-1 delta polypeptide.

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a single-chain antibody that binds immunologically to a digoxin, but does not bind immunologically to digitoxin is also provided. The methods can be used for obtaining desired polypeptides such as an antibody or antibody fragment, an enzyme, a cytokine, a transcription factor, a clotting factor, a chelating agent, a hormone or a receptor. Assays can be conducted with remarkable rapidity as the polypeptides are displayed on the surface of a host cell. The methods allow production of large quantities of these polypeptides, potentially on a kilogram scale, from microorganism cultures. Sequences W89128 to W89131 represent anti-digoxin single chain FV (scFV) antibody variants isolated from a light chain library LCDR3 by flourescence activated cell sorting (FACS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binds polyclonal antibodies (Abs) generated against a 12 consecutive amino acid segment of interleukin (IL)-1 delta or IL-1 epsilon. Agonists or antagonists of these IL polypeptides are used to regulate a cell involved in an inflammatory response. The IL-1 delta or IL-1 epsilon polypeptides and peptides are used to produce Abs and antigen-Ab complexes. The polypeptides, Abs and the corresponding nucleic acids regulate development and/or the immune system, and can be used to diagnose and treat conditions associated with abnormal expression of IL. Agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are used with agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides are used with agonists or antagonists of IL-1 delta or IL-1 epsilon polypeptides may be used as a soluble polypeptide or as a fusion protein with another
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rodent interleukin (IL)-1 delta polypeptide fragment (residues 19-24).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin; IL-1 delta; polyclonal antibody; IL-1 epsilon; cytokine; inflammatory response; immune system; diagnosis; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant polypeptide that specifically
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalian interleukin 1-delta and 1-epsilon - useful for, e.g. regulating the immune system and inflammatory responses
                                                                                                                                                                                                                                                                                                       Length 9;
                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                   Score 21; DB 20; I
Pred. No. 2.1e+05;
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100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 99; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W86288 standard; peptide; 6 AA.
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97US-0837627.
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                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SCHE ) SCHERING CORP
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Best Local Similarity
Matches 3; Conserv
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21-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of an unknown peptide. The method comprises (a) determining actual the molecular mass and an experimental fragmentation spectrum for the peptide; (b) comparing the experimental fragmentation spectrum of the unknown peptide with a theoretical fragmentation spectrum of the unknown peptide with a theoretical fragmentation spectrum of the a peptide library composed of all possible linear sequences of amino acids having a total mass that corresponds to the molecular mass of the unknown peptide; and (c) identifying a peptide in the library with a fragmentation spectrum that most closely matches the fragmentation spectrum of the unknown peptide. The method is useful in DNA cloning, anti-body production, identification of recombinant products, and the study of post-translational modifications. It allows
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                                                                                                                                            Gaps
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                                                                                                        Length 6;
                                                                                                                                            0; Indels
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                                                                                                      37.7%; Score 20; DB 19; 75.0%; Pred. No. 2.1e+05;
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Best Local Similarity
                                                  6 AA;
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|3 ylhn
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Length 6;

37.7%; Score 20; DB 19;

6 AA;

Sequence

Query Match

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7 AA;
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2 dkpfnl
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                                                                    R76987;
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 Pred. No. 2.1e+05;
0; Mismatches 1;
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                                                                                                                                         W87276 standard; peptide; 6 AA.
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Best Local Similarity 75.0%;
Matches 3; Conservative
75.0%;
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 Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 2.1e+05;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W07489 standard; peptide; 7 AA.
R76987 standard; peptide; 7 AA.
                                                                                                               peptide #4.
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66.78;
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                                                                         09-FEB-1996 (first entry)
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                                                                                                               Immune stimulating
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Best Local Similarity
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XX XX XX WPI: 1996-450961/45.
XX WPI: 1996-450961/45.
XX WPI: 1996-450961/45.
XX New peptide(s) isolated from pepsin digest of soybean - have immune activating activity and low toxicity
XX Claim 7: Page 2: 16pp; Japanese.
XX Claim 7: Page 2: 16pp; Japanese.
CC Tive present peptide is a soybean derived peptide, with immune activity and low toxicity.
CC It was prepd. by adding pepsin to a homogenate comprising 1 litre CC It was prepd. by adding pepsin to a homogenate comprising 1 litre CC activating water and 200 g of soybean, and ultrafiltering the resultant hydrolyaste. The filtrate was then conc. in vacuo and contine fraction was then subjected to HPLC to give 8 active fractions, one of which being the present peptide.
CC The peptide may also be prepd. by chemical synthesis using solid
XX Sequence 7 AA;
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Search completed: December 16, 2000, 03:07:21 Job time: 8062 sec

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0; Gaps

37.7%; Score 20; DB 17; Length 7; 66.7%; Pred. No. 2.1e+05; Live 0; Mismatches 2; Indels

Query Match 37.7 Best Local Similarity 66.7 Matches 4; Conservative

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                                                                                                                                      December 16, 2000, 01:51:17; Search time 91.14 Seconds (without alignments) 6.267 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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| 000000000000000 | | African ate kins ver virus (m. 1993 x virus MUID:93 x virus MUID:93 x virus biblosynt binding binding | 9, 6 | 18E12 iana ce_re Kaul, Libra thali b/EMB |
| 155 175 275 275 354 363 375 409 456 456 567 567 571 61100 | | nase (EC 2.7.4.9) - African swine fever ate names: thymidylate kinase as: African swine fever virus, ASFV 28-Aug-1985 #sequence_revision 07-Oct-190n: JQ2161 **R.J.; Rodriguez, J.M.; Rodriguez, J.F. Virol. 74, 1633-1638, 1993 **African swine fever virus thymidylate ance number: JQ2161; MVID:93346971 **It type: DNA **It type: DNA **It type: DNA **It this swine catalyzes the phosphorylate ance or strain BA71V **It this enzyme catalyzes the phosphorylate and source: strain BA71V **It this enzyme catalyzes the phosphorylate and the strain BA71V **Ad.C.** **Ad.C | 100.0%; larity 100.0%; Conservative (NL 9 | YLNVQDLML 214 in-like protein T18E12.14 - Arabidopsis thaliana (mouse -Mar-1999 #sequence_revision n: T02707 to the EMBL Data Library, Se tion: Arabidopsis thaliana ch on umber: 214702 n: T02707 translated from GB/EMBL/DDBJ trype: DNA : 1-170 <rou> itype: DNA :: 1-170 <rou> sitype: ONA :: 1-170 <rou 1-170="" ::="" <rou="" <rou<="" td=""></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou></rou> |
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| | | SULT 1 MP Kinase (EC 2.7.4.9) - African swine fever Alternate names: thymidylate kinase Species: African swine fever systems african swine fever virus, ASFV Date: 28 Aug-1985 #sequence_revision 07-0ct-varies: 28 Aug-1985 #sequence_revision 07-0ct-varies: N.J.; Rodriguez, J.M.; Rodriguez, J.M.; Rodriguez, J.M.; Rodriguez, J.M.; Rodriguez, J.K.; Ritle: African swine fever virus thymidylate Reference number: JQ2161; MUID:93346971 Accession: JQ2161 MOLECULE type: DNA Residues: T-240 <td>atch 3al YLI</td> <td>Db 206 YLNVQDLNL 214 RESULT 2 T02707 SKP1 protein-like protein T18E12.14 - Arabidops1. C;Species: Arabidopsis thaliana (mouse-ear cress C: Date: 24-Mar-1999 #sequence_revision 24-Mar-19C. Accession: T02707 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; submitted to the EMBL Data Library, September 199 A;Description: Arabidopsis thaliana chromosome II A; Accession: T02707 A;Accession: Tannalated from GB/EMBL/DDBJ A;Cession: Tannalated from GB/EMBL/DDBJ A;Coss-references: EMBL:AC005313; NID:g3548797; C;Genetinental source: cultivar Columbia C;Genetics: A;Map position: 2</td> | atch 3al YLI | Db 206 YLNVQDLNL 214 RESULT 2 T02707 SKP1 protein-like protein T18E12.14 - Arabidops1. C;Species: Arabidopsis thaliana (mouse-ear cress C: Date: 24-Mar-1999 #sequence_revision 24-Mar-19C. Accession: T02707 R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; submitted to the EMBL Data Library, September 199 A;Description: Arabidopsis thaliana chromosome II A; Accession: T02707 A;Accession: Tannalated from GB/EMBL/DDBJ A;Cession: Tannalated from GB/EMBL/DDBJ A;Coss-references: EMBL:AC005313; NID:g3548797; C;Genetinental source: cultivar Columbia C;Genetics: A;Map position: 2 |
| 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 | | RESULT JU2161 dTMP kinase (EC 2.7.4.9) N'Alternate names: thymid C'Species: African swine C'Bate: 28-Aug-1985 #seque C'Accession: JQ2161 R'Yanez, R.J.; Rodriguez, J. Gen. Virol. 74, 1633-11 A'Title: African swine fe A'Reference number: JQ216 A'Reference number: JQ216 A'Residues: 1-240 A'AN> A'Cross-references: EMBL: A'Experimental source: std C'Comment: This enzyme ca C'Comment: This enzyme ca C'C'Superfamily: dTWP kinas C'Superfamily: dTWP kinas | Query Ma Best Loc Matches Qy 1 | PD 206 YLNVQDLNL 214 RESULT 2 T02707 SKP1 protein-like protein T18 C; Species: Arabidopsis thalia C; Jacession: T02707 R; Rounsley, S.D.; Lin, X.; Ka submitted to the EMBL Data Li A; Description: Arabidopsis th A; Reference number: Z14702 A; Accession: T02707 A; Status: translated from GB/A; Molecule type: DNA A; Residues: 1-170 <rou>A; Coss-references: EMBL:AC00 A; Experimental source: cultiv C; Genetics: A; Map position: 2</rou> |
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A,Accession: G75041
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-317 < KAM>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50228.1; PID:g545
A;Experimental source: strain Orsay
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C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransfera
F;8-310/Domain: aspartate/ornithine carbamoyltransferase homology <AOC>
                                                                                                                                                                                                     R;anonymous, Genoscope submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
                                                                                                      ornithine carbamoyltransferase (argf) PAB1502 - Pyrococcus abyssi (strain Orsay)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL008970; NID: e1407852; PID: e1332552; PIDN: CAA15601.1
                                                                                                                             C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: G75041
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
C;Accession: T18459
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A;Molecule type: DNA
A;Residues: 1-1236 <LAW>
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Pred. No. 39;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB;
Pred. No. 8.1;
0; Mismatches
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77.88;
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75.0%;
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Best Local Similarity
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695 YLNVQEIN 702
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A; Note: C0515c
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C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: G7119
R;Kawarabayasi, Y:; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamazaki, J.; Yamazaki, Y.; Sawarabayasi, Y.; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Recession: G71119
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Recession: G71119
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-317 < KANA
A;Cross-references: GB:AP000003; NID:93236130; PIDN:BAA29817.1; PID:93257134
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank
C;Genetics:
C;Superfamily: ornithine carbamoyltransferase homology <ACT>
C;Superfamily: ornithine carbamoyltransferase homology <ACT>
                                                                                                                                                                                                                                                                                                                                                                 C; Species: Pyrococcus furiosus
C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
C; Accession: T45077
C; R; Roovers, M.; Hetcke, C.; Thomm, M.; Glansdorff, N.
submitted to the EMBL Data Library, July 1996
A; Description: Enzymatic carbamoylation at high temperatures. Isolation of the gene enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: argF
Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
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                                                                                                                                                                                                                                                                                                                                               ornithine carbamoyltransferase [imported] - Pyrococcus furiosus C;Species: Pyrococcus furiosus
                                                                       78.3%; Score 36; DB 2; Length 170; 100.0%; Pred. No. 4; 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 314;
8;
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A;Reference number: 222907

A;Accession: T45077

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-314 <ROO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A)Cross-references: EMEL:X99225; PIDN:CAA67609.1
C;Genetics:
A;Gene: angr
C;Superfamily: ornithine carbamovltransferase.
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Pred. No. 8.1;
0; Mismatches
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Similarity 77.8%;
7; Conservative
                                                                                                                        7; Conservative
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                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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77 YLNAQDLQL 85
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77 YLNAQDLQL 85
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A; Note: T18E12.14
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Call-division protein (septum formation) ftsA - Bacillus subtilis
Cispeciaes Bacillus subtilis
Cispeciaes Bacillus subtilis
Cispeciaes Bacillus subtilis
Cidate: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
Cidates: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000
R. Beall, B.; Lowe, M.; Lutkenhaus, J.
Dacteriol. 170, 4855-4864, 1988
A.; Title: Cloning and characterization of Bacillus subtilis homologs of Escherichia connected type: 100 # Ascession: 139847
A. Reference number: 139846, MID: 89008108
A. Status: preliminary; translated from CB/EMBL/DDBJ
A. Residues: 1-440 CRES
A. Anolecule type: 10NA
A. Residues: 1-440 CRES
A. Residues: 1-440 CRES
A. Residues: 1-450 CRES
A. Residues: 1-150 CRES
A. Resid
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N;Alternate names: protein L0729; protein YLL043w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24-May-1996 #text_change 06-Feb-1998
C;Accession: $64795; S16712
S;Wedler, H.; Wedler, E.; Scharfe, M.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
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Pred. No. 31;
2; Mismatches 1; Indels
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C;Superfamily: cell division protein ftsA
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-11,'I',13-14 <RE2>
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Similarity 62.5%;
5; Conservative
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Best Local Similarity
Matches 5; Conserv
11111:1:
277 LNVQDINV 284
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83 YINIQDIN 90
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                             A;Molecule type: DNA
A;Residues: 1-373 <PAR>
A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72682.1; PID:g696769
A;Xperimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj0199c
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K;Kutty, R.K.; Kutty, G.; Kambadur, R.; Duncan, T.; Koonin, E.V.; Rodriguez, I.R.; Odenw
J. Biol. Chem. 271, 20641-20649, 1996
A;Title: Molecular characterization and developmental expression of a retinoid- and fatt
A;Reference number: 217776; MUID:96355402
A;Accession: T18812
A;Access
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A; Description: The sequence of C. elegans cosmid F44C8.
A; Reference number: 221086
A; Accession: T31787
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1.421 < DNA>
A; Cross-references: EMBL; AF016438; PIDN: AAB55896.1; GSPDB: GN00023; CESP: F44C8.9
A; Experimental source: strain Bristol N2; clone F44C8
C; Genetics:
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A; Residues: 1-3351 <KUT>
A; Cross-references: EMBL:U62892; NID:g1511645; PID:g1511646; PIDN:AAC47284.1
C; Genetics:
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C.Date: 29-0ct-1999 *sequence_revision 29-0ct-1999 *text_change 29-0ct-1999
C.Accession: T31787
R.Dante, M.: Kramer, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Species: Drosophila melanogaster
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
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100.0%; Pred. No. 2e+02;
iive 0; Mismatches 0; Indels
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Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 2
Pred. No. 16;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lipophorin - fruit fly (Drosophila melanogaster)
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A:Introns: 61/2; 81/1; 173/2; 235/3; 299/2
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75.0%;
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55.6%;
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Best Local Similarity 100...
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 5; Conserv
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121 FLNIKDINE 129
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probable sugar transferase Cj1421c [imported] - Campylobacter jejuni (strain NCTC 1111 C;Species: Campylobacter jejuni
C;Species: Campylobacter jejuni
C;Dates: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Accession: E81287
R;Parkhill, J: Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chil C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Ba Nature 403, 665-668. 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals A;Reference number: A81250; MUID:20150912
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A, Molecule type: DNA
A, Residues: 1-612 < PAR>
A, Residues: 1-612 < PAR>
A, Cross-references: GB:AL139078; GB:AL111168; NID:g6968723; PIDN:CAB73845.1; PID:g696
A; Experimental source: serotype O2, strain NCTC 11168
C, Genetics:
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R; Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, ewes, H.W.; Rudd, S.; Lemcke, R.; Mayer, K.F.X.
submitted to the Protein Sequence Database, April 2000
          Accession: T1807
R.Lawson, D.; Bowman, S.; Barrell, B.
Submitted to the EMBL Data Library, August 1997
A.Reference number: 218935
A.Accession: T18507
A.Scetaus: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-442 < LAW>
A.Residues: 1-442 < LAW>
A.Residues: 1-80251; NID:e1331903; PID:e1331928; PIDN:CAB11146.1
A.Map position: 3
A.Note: C0720w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F9G14.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000
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A;Residues: 1-469 <BEV>
A;Cross-references: EMBL:ALJ62973

A;Experimental source: cultivar Columbia; BAC clone F9G14
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Pred. No. 53;
1; Mismatches
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49;
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Pred. No.
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Best Local Similarity 75.0%;
Matches 6; Conservative
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66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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A; Accession: T48314
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A;Map position: 5
A;Introns: 315/3; 374/3
A;Note: F9G14.240
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C:Species: Actinobacillus pleuropneumoniae
C:Species: Actinobacillus pleuropneumoniae
C:Date: 28-0c1996 #sequence_revision 07-Feb-1997 #text_change 26-Aug-1999
C;Accession: S66574; S55393
R;Dabban, M.; Medrano, A.; Querol, E.
Biochem. J: 315, 257-264, 1996
A;Title: Cloning, sequencing and expression of the transferrin-binding protein 1 gene fr
A;Reference number: S66574; MUID:96207589
A;Accession: S66574
A;Molecule type: DNA
A;Reference number: S66574; MUID:96207589
A;Cross-references: EMBL:Z49708; NID:9853708; PIDN:CAA89810.1; PID:9853709
C;Genetics:
A;Gene: tbpl
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor a
C;Keywords: iron transport; membrane protein; metal binding; receptor
C;Keywords: iron transport; membrane protein; metal binding; receptor
C;Keywords: iron transport: membrane protein; metal binding; receptor
C;Keywords: iron transferrin-binding protein; metal 
                                                                                                                                                         A; Experimental source: strain $2288C
R; van Aelst, L.; Hohmann, S.; Zimmermann, F.K.; Jans, A.W.H.; Thevelein, J.M.
BmBo J. 10, 2095-2104, 1991
A;Title: A yeast homologue of the bovine lens fibre MIP gene family complements the grow mediated cAMP signalling.
A;Reference number: $16712; MUID:91293082
                                                                                                                                    A;Cross-references: EMBL:Z73148; NID:g1360238; PID:e245756; PID:g1360239; MIPS:YLL043w
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C;Species: Plasmodium falciparum
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pred. No. 72;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 2; Length 669;
Pred. No. 49;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A) Cross references: SGD:S0003966; MIPS:YLL043w
A) Map position: 12L
C; Keywords: transmembrane protein
F; 264-280/Domain: transmembrane #status predicted <TM1>
F; 326-342/Domain: transmembrane #status predicted <TM2>
F; 376-390/Domain: transmembrane #status predicted <TM3>
F; 455-471/Domain: transmembrane #status predicted <TM3>
F; 455-471/Domain: transmembrane #status predicted <TM3>
                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-639, 'R', 641-669 <AEL>
A;Cross-references: EMBL:X54157; NID:g3703; PID:g3704
C;Genetics:
A;Gene: SGD:FPS1
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62.5%;
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66.78;
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Best Local Similarity 66.7.
Loc 6; Conservative
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A; Reference number: S64792
                            A; Accession: S64795
A; Molecule type: DNA
A; Residues: 1-669 <WED>
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Matches 5; Conser
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119 YINTQDIN 126
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Oy 1 YLNVQDLN 8 | | | :||| | Db 459 YLNKEDLN 466

Search completed: December 16, 2000, 01:51:19 Job time: 7640 sec

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mus musculu gallus gall drosophila haemophilus caenorhabdi

P14248 Q99715 Q60847 P13944 P33450 P44700 Q09665 P18358 P39905

homo sapien

plasmodium

herpesvirus

staphylococ P48540 mus musculu

homo sapien

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yanez R.J., Rodriguez J.M., Nogal M.L., Yuste L., Enriquez C., Rodriguez J.F., Vinuela E.;
"Analysis of the complete nucleotide sequence of African swine fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yanez R.J., Rodriguez J.M., Rodriguez J.F., Salas M.L., Vinuela E
"African swine fever virus thymidylate kinase gene: sequence and
transcriptional mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 240;
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Transferase; Kinase; Nuclectide biosynthesis; ATP-binding.
NP_BIND
ATP (POTENTIAL):
SEQUENCE 240 AA; 27755 MW; AF899BE6CCE3E44D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 208:249-278(1995).
-!- CATALYTIC ACTIVITY: ATP + THYMIDINE 5'-MONOPHOSPHATE
THYMIDINE 5'-DIPHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- PATHWAY: SYNTHESIS OF DTTP FROM DTMP.
-i- SIMILARITY: BELONGS TO THE THYMIDYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                  African swine fever virus (strain BA71V) (ASFV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 46; DB 1;
100.0%; Pred. No. 0.022;
ive 0; Mismatches (
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NUV-1999 (Rel. 38, Last annotation update)
THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE)
                                                                                                                                                                                                ALIGNMENTS
VP03_HSVSA
ATL_STAAU
RPBI_PLAFU
CA1C_HOWNE
CA1C_CHICK
FAT_DROME
YES7_CAEEL
BINL_STAAU
                                                                                                                                         GDNF_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage;
African swine fever-like viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gen. Virol, 74:1633-1638(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z19544; CAA79604.1; -. EMBL; U18466; AAA65265.1; -. HSSP; P00572; ZTMK.
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Best Local Similarity 100.
دروس 9; Conservative
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                           Compugen Ltd
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Maximum DB seq length: 2000000000
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RESULT 3
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                                                                                                                                                                                                                                                                                                   MEDLINE; 98169451.
Villert, V. Clantin B., Tricot C., Legrain C., Roovers M., Stalon V., Glansdorff N., van Beeumen J.;
The crystal structure of Pyrococcus furiosus ornithine
                                                                                                                                                                                                                                                                                                                                              carbamoyltransferase reveals a key role for oligomerization in enzyme stability at extremely high temperatures.";

Proc. Natl. Acad. Sci. U.S.A. 95.2801-2806(1998).

-! - CATALYTIC ACTIVITY: CARBAMOYL PHOSPHATE + ORNITHINE = CITRULLINE + ORTHOPHOSPHATE.

-! - PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).

-! - SUBCELLULAR LOCATION: CYTOPLASHIC.

-! - SUBCELLULAR LOCATION: OTTOPLASHIC.
                                                                                                                                                                             Roovers M., Hetcke C., Legrain C., Thomm M., Glansdorff N.; "Isolation of the gene encoding Pyrococcus furiosus ornithine carbamoyltransferase and study of its expression profile in vivo and
                                                                                                                         Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roovers M _{\rm J} Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                   01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3) (OTCASE).
                               315 AA
                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
                                                                                                                                                                                                                          Eur. J. Biochem. 247:1038-1045(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X99225; CAA67609.1; -.
EMBL; Y12727; CAA73260.1; -.
EMBL; A115: 17-UN-98.
INTERPRO; IPR002029; -.
INTERPRO; IPR002029; -.
INTERPRO; IPR002029; -.
PFAM; PF00185; OTCace; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 77.00
77. Conservative
                               STANDARD;
                                                                                                                                                        / VC1;
                                                                                                             Pyrococcus furiosus.
                                                                                                                                                       STRAIN=DSM 3638 / MEDLINE; 97433289.
                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                              REVISION TO 207.
                            OTC_PYRFU
Q51742;
                                                                                                                                                                                                               in vitro.
                   OTC_PYRFU
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Pred. No. 3.5;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                       Cunin R., Seumois G., Purcarea C., Van Vliet F., Legrain C "Ornithine carbamoyltransferase from Pyrococcus abyssi."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).
-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F4686B091F76494F CRC64;
                                                                  30-MAY-2000 (Rel. 39, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3) (OTCASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00027; CARBAMOYLTRANSPERASE; 1.

Transferase; Arginine biosynthesis.

CONFLICT 63 63 -> R (IN REF. 1).

CONFLICT 159 159 V -> I (IN REF. 1).

CONFLICT 201 202 EQ -> DE (IN REF. 1).

CONFLICT 264 264 D -> S (IN REF. 1).

CONFLICT 264 264 D -> S (IN REF. 1).
    317 AA.
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EMBL; AJ248287; CAB50228.1; -.
HSSP; Q51742; IALS.
INTERPRO; IPR002039; -.
INTERPRO; IPR002082; -.
INTERPRO; IPR002292; -.
                                              (Rel. 39, Created)
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PRINTS, PR00100, AOTCASE.
PRINTS; PR00101, ATCASE.
PRINTS; PR00102, OTCASE.
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Best Local Similarity
'Local 7; Conserve
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 [2]
SEQUENCE FROM N.A.
                                                                                                                                                                          abyssi
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                                                                                                                                               ARGF OR PAB1502
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ORSAY;
Heilig R.;
                                                                                                                                                                                                                                                                   STRAIN-GE5;
OTC_PYRAB
093656;
                                                                                                                                                                        Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTC_PYRHO
058457;
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Gaps

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Indels

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Pred. No. 3.5; 0; Mismatches

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SEQUENCE FROM N.A. MEDLINE; 91293082.
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P23900;
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FPS1_YEAST
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                                                                                                                                                                                                     MEDLINE: 98344137.

Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,

Kawarabayasi Y., Sawada M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,

Fuuahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,

Masuchi Y., Shizuya H., Kikuchi H.,

"Complete Sequence and gene organization of the genome of a hyper-

thermophilic archaebacterium, Pyrococcus horikoshii OT3.",

DNA Res. 5:55-76(1998).

-I-CATALYIIC ACTIVUTY: CARBAMOYL PHOSPHATE + ORNITHINE = CITRULLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                           Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00100; AOTCASE.
PRINTS; PR00101; ATCASE.
PRINTS; PR00102; OTCASE.
PROSITE; PS00097; CARBMOYLTRANSFERASE; 1.
Transferase; Arginine blosynchesis.
SEQUENCE 317 AA; 35368 MW; D949999E0EBF6BIE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- PATHWAY: ARGININE BIOSYNTHESIS (POTENTIAL).
-:- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ORNITHINE CARBAMOYLTRANSFERASE (EC 2.1.3.3) (OTCASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacillus subtilis.
Bacteria: Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 1;
Pred. No. 3.5;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 24, Last Sequence update) CELL DIVISION PROTEIN FTSA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Staphylococcus group; Bacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AP000003; BAA29817.1; -. INTERPRO; IPR002029; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78.3%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 78.3
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR002292; -.
                                                                                                         Pyrococcus horikoshii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         + ORTHOPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 89008108.
                                                                                                                                                                       SEQUENCE FROM N.A.
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FTSA_BACSU
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"A yeast homologue of the bovine lens fibre MIP gene family complements the growth defect of a Saccharomyces cerevisiae mutant on fermentable sugars but not its defect in glucose-induced RAS-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                        STRAIN=168 / JH642;
MEDLINE; 9235865.
GORDZY-Treboul G., Karmazyn-Campelli C., Stragier P.;
"Developmental regulation of transcription of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                         Gholamhoschian A., Shen Z., Wu J.J., Piggot P.;
Gholamhoschian A., Shen Z., Wu J.J., Piggot P.;
Regulation of transcription of the cell division gene ftsA during sportulation of Bacillus subtilis.";
J. Bacteriol. 174:4647-4656(1992).
-!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT GROWTH (BY SIMILARITY).
MAY INTERACT WITH FTSZ (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FTSA/MREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Pred. No. 13;
2; Mismatches 1; Indels
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6064D55961358C44 CRC64;
Escherichia coli cell division genes fts2 and ftsA.";
J. Bacteriol. 170:4855-4864(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLYCEROL UPTAKE/EFFLUX FACILITATOR PROTEIN.
FPSI OR YLL043W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   669 AA.
                                                                                                                                                                                                                                                                                      J. Mol. Biol. 224:967-979(1992).
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62.5%;
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Cell division; Cell shape.
CONFLICT 12
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EMBO J. 10:2095-2104(1991)
                                                                                              SEQUENCE OF 1-14 FROM N.A.
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Best Local Similarity 62.5°
Local 5; Conservative
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-8 FROM N.A. MEDLINE; 92325056.
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1 YLNVQDLNL
                                                                                                                                                                                                                             Lindquist S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
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                                                                                                                                                              SEQUENCE OF
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P15584;
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                                                                                                                                                                                   MEDLINE;
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NU5M_PARTE
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Eukaryota: Fungi; Ascomycota: Saccharomycetales;
                                                                                     Luyten K., Albertyn J., Skibbe W.F., Prior B.A., Ramos J., Thevelein J.M., Hohmann S., "Fpsl, a yeast member of the MIP family of channel proteins, is a facilitator for glycerol uptake and efflux and is inactive under comptic stress."
                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE TRANSMEMBRANE CHANNEL MIP FAMILY.
                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. CONTAINS 6
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 113.2 KDA PROTEIN IN SSO2-HSC82 INTERGENIC REGION.
WR185W OR YM8010.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -> R (IN REF. 1).
BA9C78056A1251B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00783; MINTRINSICP.
PROSITE; PS00221; MIP; 1.
Glycerol metabolism; Transport; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        981 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.9%; Score 34;
62.5%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                           POTENTIAL TRANSMEMBRANE DOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73877 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X54157; CAA38096.1; -. EMBL; Z73148; CAA97494.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S16712; S16712.
SGD; S0003966; FPS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR000425;
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Matches 5; Conserv
                                                                             MEDLINE; 95246729
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119 YINTQDIN 126
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Q12751;
Q1-NOV-1997 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                            Erkine A.M., Szent-Gyorgyi C., Simmons S.F., Gross D.S.; "The upstream sequences of the HSPB2 and HSCB2 genes of Saccharomyces cerevisiae: regulatory elements and nucleosome positioning motifs."; Yeast 11:579-580(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                                                                                                       "hsp@2 is an essential protein that is required in higher concentrations for growth of cells at higher temperatures."; Mol. Cell. Biol. 9:3919-3930(1989).
                                                                                                                                                                                                                                                                                                       Borkovich K.A., Farrelly F.W., Finkelstein D.B., Taulien J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         981 AA; 113248 MW; 13F29F65C6D4E53B CRC64;
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01-APR-1990 (Rel. 14, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1;
Pred. No. 56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; U20349; AAA87904.1; ALT_INIT.
S0004797; YMR185W.
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650-981 FROM N.A.
                                                                                                                                                                                                                                       976-981 FROM N.A.
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77.88;
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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SEQUENCE FROM N.A.
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DR DR DR SO S

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179 AA.
     PRT;
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83.3%;
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     STANDARD;
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                                                                                                               Haemophilus influenzae
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Best Local Similarity
Matches 5; Conservat
                                                                                                                                                                               SEQUENCE FROM N.A.
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MEDLINE; 95350630.
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                                                                                                HI0459
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67.4%; Score 31; DB 1; Length 155; 75.0%; Pred. No. 16;
                                                                                                                                Length 570;
                                                                                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
                              PFAM; PF00361; oxidored_q1; 1.
PFAM; PF00662; oxidored_q1...1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SEQUENCE 570 AA; 65196 MW; 23636CFDC1B0BC4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
SEQUENCE 155 AA: 17670 MW; DAC9FEEAE69B11C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496'512(1995).
-!- SIMILARITY: STRONG, TO E.COLI YHCH.
-!- SIMILARITY: BELONGS TO THE YHCH/YIAL/YJGK FAMILY.
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                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                              Score 32; DB
Pred. No. 47;
                                                                                                                                                                Mismatches
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75.08;
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                                                                                                                              Query Match 69.6
Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                           STANDARD;
IPR001516; -.
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INTERPRO;
INTERPRO;
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P44583;

YHCH_HAEIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
-!- FUNCTION: COULD BE A TRANSCRIPTIONAL REGULATOR WITH A LOW ACTIVITY AS A URACIL PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.9) (UPRTASE) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                          Fleischman R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soctt J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.K., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: STRONG, TO BACILLUS PYRIMIDINE OPERON REGULATORY
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Haemophilus.
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INTERPRO: IPROBOB36;
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INTERPRO: PROBOB6; PILLOSYLTAN; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
Hypothetical protein; Transferase.
Transferase; Glycosyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 31; DB 1; Length 179;
Pred. No. 19;
1; Mismatches 0; Indels
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
101-NOV-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL PROTEIN HI0459.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HISTIDINOL DEHYDROGENASE (EC 1.1.1.23) (HDH).
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Query Match

Matches

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RESULT 10 Y459_HAEIN

6853C5EA5C67EC34 CRC64;

51973 MW;

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455 AA;
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Best Local Similarity
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01-NOV-1997 (Rel
60 KDA ANTIGEN.
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29 LNLSDLNL 36
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76
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116
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ID EXO1_SCHPO
AC P53695,
DT 01-OCT-1996
                                                                                                                                                                   IPA7_SHIFL
P18014;
      SEQUENCE
                                                                                                                                                                                                                                        IPAH 7.8.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                        Oxidoreductase; NAD.
       "Protein translocation into peroxisomes.";
J. Biol. Chem. 271:32483-32486(1996).
-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                             -!- PATHWAY: TENTH STEP IN HISTIDINE BIOSYNTHETIC PATHWAY.
-!- SIMILARITY: TO OTHER PROKARYOTIC, FUNGAL AND PLANTS HDH.
                                                                                                                                                                                                                                                                                                                                                   67.4%; Score 31; DB 1; Length 398; 62.5%; Pred. No. 50;
                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                      PROSITE; PSO0611; HISOL_DEHYDROGENASE; FALSE_NEG.
Histidine biosynthesis; Multifunctional enzyme; Oxidor.
SEQUENCE 398 AA; 43635 MW; B989B35227ED564B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MATRIX (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PASZ (PEROXIN-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455 AA.
                                                                                                                                                                                                                                                                                                                                                                         2; Mismatches
                                                                                                                                                                                                                                                                   PFAM; PF00815; Histidinol_dh; 1.
PRINTS; PR00083; HOLDHDRGNASE.
                                                                                                                                                                                                                                            EMBL; U82227; AAB63023.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; 272390; CAA96530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomycetaceae; Pichia
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pichia pastoris (Yeast).
                                                                                                                                                                                                                                                         INTERPRO; IPR001692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 97115764.
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363 YANVRDIN 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Subramani S.
                                                                                                      2 NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEX3_PICPA
Q92262;
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PEX3_PICPA
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat; Multigene family,
6 X 14 AA APPROXIMATE TANDEM REPEATS OF
L-X(2)-L-P-X-L-P-X(2)-L-X(2)-L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hartman A.B., Venkatesan M.M., Oaks E.V., Buysse J.M.; "Sequence and molecular characterization of a multicopy invasion plasmid antique gene, ipaH, of Shigella flexneri."; J. Bacteriol, 172:1955-1915(1990).
                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                               ;
0
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    Length 455;
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                                               Indels
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  Score 31; DB 1;
Pred. No. 58;
                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 31; DB 1;
Pred. No. 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       571 AA.
                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                    Shigella flexneri.
Plasmid 210 kb invasion pwR100.
                                                                                                                                                                                                                                                                     Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60955 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigen; Plasmid; Virulence;
67.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M32063; AAA26526.1; -. PIR; A35149; A35149.
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75.0%;
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STRAIN=M90T / SEROTYPE 5;
MEDLINE; 90202708.
                                          6; Conservative
                                                                                                                                                                                                                             STANDARD;
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69
89
109
149
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(Rel. 16, 1
(Rel. 35, 1
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Best Local Similarity
Lac 6; Conserve
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Job time: 8042 sec
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0853; XPGRADSUPER.
PROSITE; PS00841; XPG_1; 1.
PROSITE; PS00842; XPG_2; 1.
DNA repair; Hydrolase; Nuclease; Endonuclease; Nuclear protein.
DNA repair; Hy 1 96; N-DOMAIN.
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0
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85.7%; Pred. No. 76;
1ive 0; Mismatches 1; Indels
                                                                                                                                                                        -i- SUBCELLULAR LOCALLON. ...-
-i- INDUCTION: BY METOSIS.
-i- SIMILARITY: TO OTHER MEMBERS OF THE XPG/RAD2 FAMILY.
                                       Schizosaccharomyces pombe (Fission yeast).
Eukaryota: Fungi: Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                      571 AA; 63867 MW; 7D21B3778104BA9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
 01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EXONUCLEASE I (EXO I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    732 AA.
                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 139-160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostellum discoideum (Slime mold).
Eukaryota; Dictyostelliida; Dictyostellum.
                                                                                                                                                                                                                                                                                                                                                                                               I-DOMAIN
                                                                                                                                                                                                                                                                                                 EMBL; L35174; AAC41648.1; -.
INTERPRO; IPR001532; -.
PFAM: PF00867; XPC_I: 1.
PFAM: PF00752; XPC_M: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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Best Local Similarity
Matches 6; Conserv
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01-0CT-1996
15-JUL-1998
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P90648;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
-i- CATALYTIC ACTIVITY: ATP + [MYOSIN HEAVY-CHAIN] - ADP +
[MYOSIN HEAVY-CHAIN] PHOSPHATE.
-i- DOMAIN: CONSISTS OF AN N-TERMINAL DOMAIN, A CENTRAL NONREPETITIVE
CATALYTIC DOMAIN, AND A C-TERMINAL DOMAIN WITH SEVEN WD REPEATS.
-i- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).
-i- SIMILARITY: BELONGS TO THE MHCK / EF-2 PROTEIN KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          DICTYDB, DD01087; MHKB...
INTERPRO: IPR001080; -
PFAM, PF00400; WDA,7; PR00520; GPROTEINBRPT.
PROSITE; PS00678; WD_REPEATS; 5.
Transferase; Serine/threonine-protein kinase; ATP-binding; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A7233C4BD56D4088 CRC64;
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WD2.
WD4.
WD5.
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381
486
528
568
608
688
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Best Local Similarity
Matches 5; Conserv
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NP_BIND
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Q9svg5 arabidopsis
Q20059 caenorhabdi
Q9xvml caenorhabdi
Q9wll4 drosophila
Q72120 homo sapien
082780 arabidopsis
                                                                               007716 mycobacteri
012150 saccharomyc
09rnb2 microcystis
089031 vesicular s
03084 escherichia
                                                                                                                                                            098yz8 arabidopsis
007544 bacillus su
08011B bacteriopha
067616 aquifex aeo
093458 podarcis si
            c6 arabidopsis
15 arabidopsis
9 caenorhabdi
1 caenorhabdi
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                                                                                                                                   09zgj5 leptospira
007114 mastigoclad
09rp56 escherichia
                                                                                                                                                                                                         09vvy5 drosophila
09y714 schizosacch
P91469 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
TRINETOCHORE (SKPIP)-LIKE PROTEIN.
TH8E12.14.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyte; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=CV. COLUMBIA;

STRAIN=CV. COLUMBIA;

Shounsley S.D., Lin X., Kaul S., Shea T.P., Fujil C.Y., Mason T.M.,

Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;

"Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence.";

"Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AC005313; AAC344483.1;

MENDEL; 31709; Arath,1266;31709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF01466; Skp1; 1.
SEQUENCE 170 AA; 19398 MW; B75BEB9552CF7048 CRC64;
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Last sequence update)
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Pred. No. 9.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                      ALIGNMENTS
009040
Q9SUC6
Q9SVG5
Q20969
Q9XVM1
                                           09W1L4
075120
082780
023496
007716
012150
09RNB2
                                                                                                                QQ3084-
Q9VXH7
Q9ZGJ5
Q9ZGJ5
Q9ZF28
Q9SYZ8
Q9SYZ8
Q07544
Q07546
Q90118
Q6766
Q93458
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100.0%; Pre
0;
 2222
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077346;
01-NOV-1998 (TrEMBLrel. 08,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                   717
7488
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329058
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329058
33903
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3374
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4403
4403
456
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Best Local Similarity
Matches 7; Conserv
114 YLNVQDL 120
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 081055
081055;
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 RESULT
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Q66951 feline infe
Q9vvg0 drosophila
O74224 emericella
Q9yb18 aeropyrum p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              077346 plasmodium
09w125 drosophila
P7141 leptospira
09s4f6 drosophila
09v496 drosophila
01635 caenorhabdi
044125 actinobacil
044126 actinobacil
04416 actinobacil
047390 plasmodium
077390 plasmodium
09xmt9 tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     081055 arabidopsis
                                                          Search time 113.2 Seconds (without alignments)
7.424 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                            297973 seqs, 93374136 residues
                                                             December 16, 2000, 02:01:00;
                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein – protein search, using sw model
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077346
Q9W125
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sp_human:*
sp_invertebrate:*
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sp_mhc:*
sp_organelle:*
sp_phage:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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46
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Match Length DB
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                                                                                                                1 YLNVQDLNL 9
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778.3
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776.1
773.9
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773.9
771.7
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66:
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110:
113:
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Query Match
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RESTOURCE FROM N. A.

RA Addams M. D., Celniker S.E., Holt R.A., Evans C.A., Goayne J.D.,

Addams M. D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.H.C., Blazes R.G., Champe M., Pfeiffer B.D.,

RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abrill J.F., Agbayani A., An H.-J., Andrews Pfannoch C.R., Miklos G.L.G.,

RA Abrill J.F., Baxendle J., Bayraktaroglu L., Beasley E.M.,

RA Besson K.Y., Bernan B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cadaley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cadaley S., Dahlke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C.,

RA Dobin K.J., Evangelista C.C., Ferriers C., Ferriers S., Fleischmann W.,

RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Astannel B.E., Kodira C.D., Kraff C., Kravittz S., Kult D., Lai Z.,

RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Jalai M., Kalush F., Howland T.J., Wei M.-H., Ibegwam C.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Harris N.W. Moy M., Murphy B., Murphy L., Murny D.M., Nelson D.E.,

RA Merkulov G., Milano K.S., Wanders R., Nelson D.K., Palazolo M., Pittman G.S., Pollard J., Murphy B., Shen B.C., Sideeler F., Shen H.,

RA Palazolo M., Pittman G.S., Pollard J., Shen H., Wang X.,

RA Shie B.C., Sideeler K., Senelling A.C., Stapleton M., Strong R., Shen B., Shen B.C., Stapleton M., Strong R., Shen B.C., Shen B., Shen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                        Gaps
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0
                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                    5; Length 1236;
                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                1236 AA; 147954 MW; 011A46685F526E24 CRC64;
                                                                                                                       Hamlin N., Lawson D., Barrell B.; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; ALO08970; CAAl5601.1; -...INTERPRO; IRO01440; -...
 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                     DB
                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                  Score 36; DB
Pred. No. 81;
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                                                                                                                                                                                                                                  78.3%;
75.0%;
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Best Local Similarity 75.00
Local 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                             Plasmodium falciparum.
                                                                                           SEQUENCE FROM N.A.
01-JUN-2000 (Trem
PFC0515C PROTEIN.
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                                                                                                           STRAIN=3D7;
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"The genome sequence of Drosophila melanogaster.";
Science 287.1385-2195(2000).
EMBL: AE003464; AAF47252.1;
FLYBASE; FBGN0035046; CG3683.
SEQUENCE 175 AA; 19845 MW; 508171EEDDF4D9DE CRC64;
                                                                                                                                                                                                                                                                   Gaps
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EMBL, AF144879; AAD52191.1; "
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                                                                                                                                                                                                                            Length 175;
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Pred. No. 28;
                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 35.3 KDA PROTEIN.
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Pred. No. 16;
                                                                                                                                                                                                                                                             1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                    76.18;
87.58;
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77.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=COPENHAGENI (L45);
                                                                                                                                                                                                                                        Local Similarity 87.5
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
7; Conserv?
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15 LNVQELNL 22
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PFAM; PFO
SEQUENCE
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Ry Medans N.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Richards S., Ashbunner M., Henderson S.N.,

Ry George R.A., Lewis S.E., Richards S., Ashbunner M., Henderson S.N.,

Button G.G., Wortman J. R., Yandell N.D., Zhang O., Chen L.X.,

Button G.G., Mortman J. R., Yandell N.D., Zhang O., Chen L.X.,

Ry Bandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Peielffer B.D.,

Ran Bandon R.C., Rogers Y. H. C., Blazel R.G., Champe M., Peielffer B.D.,

Ran Bliew R.M., Basun B.A., Baxendale J., Bayraktracqui L., Bessley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Ry Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Brottier P.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ry Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

Ry Burtis K.C., Busam D.A., Deuck J., Brokstein D., Bolter S.M.,

Burtis K.J., Evangelista C.C., Ferrac C., Ferrac J., Eleischmann W.,

Ry Godek M., Delter A., Deng Z., Mays A.D., Dew I., Diletz S.M.,

Ry Harris N.L., Harvey D., Helman T.J., Hell M.-H., Ibegwan C.,

Ry Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Hostin D., Houston K.A., Howland T.J., Well M.-H., Ibegwan C.,

Ry Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ry Harris N.L., Marvey D., McLood M.P., McPhy B., McLood M.P., McPhy B., Murphy B., Murph
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Perygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidea; Drosophila.
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                     2; Length 303;
                                                                                    35284 MW; 1D27E8DF517FB52D CRC64;
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Last annotation update)
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                                                                                                                                                                     DB
28;
                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                     Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
INTERPRO; IPR001173; -
PFAM; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                  76.1%;
77.8%;
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                                                                                                                                                                  Query Match 76.1
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                     Hypothetical protein. SEQUENCE 303 AA; 3
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09V496;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                          Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                               76.1%; Score 35; DB 5; Length 2307; 100.0%; Pred. No. 2.5e+02; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.1%; Score 35; DB 5; Length 3351; 100.0%; Pred. No. 3.7e+02; live 0; Mismatches 0; Indels
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PFAM: PF001347; Vitellogenin_N; 1.
SEOUENCE 3351 AA; 372640 MW; DAABFA99D02A17C8 CRC64;
PF01347; Vitellogenin_N; 2.
NCE 2307 AA; 255889 MW; 61A5F749A300B2E3 CRC64;
                                                                                                                                                                                                                                                                                                                                            01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAX-2000 (TrEMBLrel. 13, Last annotation update)
RETINOID- AND FATTY ACID-BINDING GLYCOPROTEIN.
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Last annotation update)
                                                                                                                                                                                                                                                                                                         3351 AA.
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EMBL; U62892; AAC47284.1; --
FLYBASE; FBGN0016724; RfaBp.
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05,
13,
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Best Local Similarity 100.v
                                                            Query Match
Best Local Similarity 100.
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01-MAY-2000 (TrEMBLrel.
F44C8.9 PROTEIN.
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01-JAN-1998 (TrEMBLrel.
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INTERPRO; IPR001846;
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MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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MEDLINE; 96355402.
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Last sequence update)
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Created)

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Actinobacillus pleuropneumoniae (Haemophilus pleuropneumoniae).
Plasmid pTF205/023.
                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                               898 AA; 102217 MW; AD627D5BC0B7E6E2 CRC64;
                                                                                                                                                                                                                                  Thesis (1995), Institut fuer Mikrobiologie, Tieraerztliche Hochschule Hannover, Germany EMBL, 254191; CAAP0896-1; INTERRO, IPRO0531; TONE_BOXC; I. PFAM; PF00593; TONE_BOXC; I. PROSITE; PS01156; TONE_DEPENDENT_REC_2; I.
                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-MAY-2000 (TrEMBLrel. 13, TRANSFERRIN RECEPTOR.
                                      PRELIMINARY;
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Matches 6; Conserv
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 6; Conserv
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709 YENVQDIKL 717
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742 YFNVQDIKL 750
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                                                                                                                                                                      Actinobacillus.
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                                                 044158;
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Q44127;
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Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jonss M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mcmurray A., Mortinore B., O'Callaghan M., Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Shownkeen I. Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaudin M., Vaudin M., Watson A., Watschon P., Matson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.:
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Bacteria: Proteobacteria: gamma subdivision; Pasteurellaceae;
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MEDLINE; 96036198.
GONZAIEZ G.C., Yu R.H., Rosteck P.R. Jr., Schryvers A.B.;
Sequence, genetic analysis, and expression of Actinobacillus pleuropneumoniae transferrin receptor genes.";
Microbiology 141:2405-2416(1995).
EMBL; U16017; AAC43485.1;
                                                                                                                                                                                                                                                                                                                                                                            73.9%; Score 34; DB 5; Length 421; 75.0%; Pred. No. 63; 1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 2; Length 898;
Pred. No. 1.4e+02;
1; Mismatches 2; Indels
                                                                                                                                                                          Dante M., Kramer J.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                          Waterston R.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AR016438; ARB65896.1; ..
HSSP; P20393; 1A6Y.
INTERPRO; IPR001628; ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR000531; -. PFAM; PF00593; TonB_boxC; 1. PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1. SEQUENCE 898 AA; 102187 MW; 4E49988810A3752A CRC64;
                                                                                                                                                                                                                                                                                                         PFAM; PF00105; Zf-C4; Z. PRINTS; PR00047; STROIDFINGER. SEQUENCE 421 AA; 48563 MW; EE29AFA49DFF6A85 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
TRANSFERRIN BINDING PROTEIN 1.
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66.7%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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                                                                                                                       Nature 368:32-38(1994).
                                                                                                                                  SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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709 YENVQDIKL 717
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
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Gonzalez G.C., Yu R.H., Rosteck P.R. Jr., Schryvers A.B.;
Gonzalez G.C., Yu R.H., Rosteck P.R. Jr., Schryvers A.B.;
Sequence, genetic analysis, and expression of Actinobacillus
pleuropneumoniae transferrin receptor genes.";
Microblology 141:2465-2416(1995).
EMBL: U16019; AAC43487.1; -.
INTERPRO; IPROMO531; -.
PFAM: PF00593; Tonb_boxc; 1.
PROSITE; PS01156; TONB_DEPENDENT_REC_2; 1.
SEQUENCE 931 AA; 106369 WW; CE88D077D03C54F9 CRC64;
                          Length 898
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Score 34; DB 2; Length 690
Pred. No. 1.46+02;
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66.7%; Pred. No. 1.5e+02;
Live 1; Mismatches 2; Indels
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last ann
TRANSFERRIN BINDING PROTEIN 1.
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STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y. Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adms M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Salzberg S.L., Fraser C.M., Venter J.C.;
Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                 "Complete sequence, gene content and organization of the mitochondrial genome of Tetrahymena pyriformis. Comparison with Paramecium aurelia mitochondrial DNA.";
                                                                                Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
Tetrahymenina; Tetrahymena.
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Burassicates;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Burger G., Zhu Y., Littlejohn T.G., Greenwood S.J., Schnare M.N.,
Lang B.F., Gray M.W.;
                                                                                                                                             Edgvist J., Burger G., Gray M.W.; "Expression of mitochondrial protein-coding genes in Tetrahymena pyriformis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF160864; AAD41924.1; -.
INTERPRO; IPR001135; -.
                                                                                                                                                                                                   Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
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SEQUENCE 997 AA; 111134 MW; DA93A1446C422F31 CRC64;
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PROSITE; PS00535; COMPLEX1 49K; 1.
Oxidoreductase; Mitochondrion.
SEQUENCE 442 AA; 51109 MW; BDBCF2AB2E4D24DF CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update) NADH DEHYDROGENASE SUBUNIT 7 (EC 1.6.5.3).
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Pred. No. 1.1e+02;
1; Mismatches 2;
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66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                Tetrahymena pyriformis.
                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                            SEQUENCE FROM N.A.
SETAINA-ATCC 27088;
MEDLINE; 96207588.
BABAI M., Medrano A., Querol E.;
Daban M., Medrano A., Querol E.;
I gene from Actinobacillus pleuropneumoniae.";
Biochem. J. 315:257-264(1996).
EMBL: 249708: CAA89810.1;
EMBL: 249708: TOA89810.1;
FINTERPRO; IPRO0531;
PRO0531; TONB_DOXC;
PROM: PRO0593; TONB_DOXC;
PROSITE: PS01156; TONB_DEPENDENT_REC_2; 1.
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Actinobacillus.
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1; Mismatches 2; Indels
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; 298551; CAB11146.1;
SEQUENCE 442 As. 52477 MW: 465780FA491DCC52 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      22 POTENTIAL.
931 TBP1 GENE.
106326 MW; D777366E2FDA54F9 CRC64;
                                                                Last sequence update)
Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
               931 AA
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Fra 6; Conservative
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01-NOV-1998 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
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CHAIN 23
SEQUENCE 931 AA;
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PFC0720W.
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Search completed: December 16, 2000, 02:01:01 Job time: 5935 sec

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Human prostate tum
Feline infectious
Tetrahydrocannabin
Mutant YLRO87c pro
Saccharomyces cere
Canine ICAM-R poly
Canine ICAM-R prot
Barley alpha-gluco
Arabidopsis thalia
Black widow spider
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Transferrin bindin
                                                                                                                                                         December 16, 2000, 00:51:15 ; Search time 108.84 Seconds (without alignments) 2.827 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  268485 segs, 34193795 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
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W04867
Y73970
R88469
Y88391
W36093
W22050
W81457
Y50760
W13408
R80096
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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46
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Match Length DB
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Perfect score:
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| Black widow spider RPP1-WSB antho aci Plasmodium falcipa Human phosphatase Human cdc25b vacci RSPBV strain RSP15 S. pneumoniae form Human PRO1411 (UNQ H. pylori GHPO 155 Helicobacter polyp Sequence of bovine Human neuron-deriv Apoptopic cerebral Amino acid sequenc H. fells ORF1 prot Water soluble beta Fragment of gial- w09914235 Seq ID N (Gly33-11e134) tru (Arg32-11e134) tru | rotein; 240 AA. t entry) 1. Tmpk; AIDS; prodrug; AZT; 3'-azido-3-deoxythymidine; DNA chain termination; AZT activation pathway; sophate; AZT-DP; AZT-diphosphate; anticancer; therapeutic analog. D-EP00945. P-0102546. GES FOERDERUNG WISSENSCHAFTEN. 4, Lavie A, Reinstein J, Schlichting I; 2. Atth increased activity on nucleoside and inseed to improve conversion of prodrugs, e.g. |
|---|--|
| R80097 Y78972 Y31949 W35380 W35536 W38554 W386554 W16539 W16539 W16539 W1651 W1651 W1651 W1658 W1665 W18052 W18052 W18052 W18053 W18052 W18053 W18053 W18053 W18053 W18053 W18053 W18053 W18053 W18058 W18058 W18058 W18058 W18058 W18058 | ALIGNMENTS LLY) K; AIDS; prodrug; chain termination; ate; AZT-DP; AZT-diare; AZT-DP; AZT-diarej analog. 72546. FOERDERUNG WISSENS Lavie A, Reinstein increased activity ed to improve conve |
| 00088888888888888888888888888888888888 | ; 240 y) AIDS hain the sin t |
| 1221 1420 185 185 185 185 185 185 185 185 185 185 | dard; protein; (first entry) kinase-1. kinase; Tmpk; cation; DNA charmophosphate; ctivity; therappd. 2. 99WO-EP0094 ; 98EP-010254 PLANCK GES FOE: Konrad M, Lavi 08654/42. inases with incanalogs, used to |
| | idard; pr. (first; kinase; cation; -monopho; 99WO; 98EP; PLANCK; 98EP; planck inases wanalogs, irefirst |
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| 00000000000000000000000000000000000000 | 4 sta 4 / 4/ 4 / 199 4 / 199 6 / 199 6 - 199 8 - 199 9 / MB |
| 84444444444444444444444444444444444444 | RESULT 1 Y28784 XX X2878 AC Y2878 AC Y2878 AC Y2878 XX YX DDE THYMLI KW YITAL KW AZT-M KW AZT-M XX Unide XX Unide XX Unide XX XX Unide XX XX Unide XX XX (PLAC XX YX (PLAC XX YX (PLAC XX YX (PLAC XX XX XX (PLAC XX XX XX (PLAC XX XX (PL |
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prepare antibodies (useful for serotherapy) and to prepare
to prepare autoridiagnostic reagents.
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                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                   04-NOV-1999.
                                                                                                                                                                                                                                                                                                                treatment
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                                   Sequence
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R88469
ID R8
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                     The present sequence is a thymidylate kinase. TmpK is involved in the activation of the AIDS prodrug; AZT. AZT-TP inhibits viral replication by DNA chain termination. TmpK which catalyses the second phosphorylation step, from the monophosphate (AZT-MP) to the diphosphate (AZT-MP), is the rate limiting enzyme in the AZT activation pathway. Increasing the kinase activity of TmpK results in higher concentrations of the active form of the therapeutic analog especially AZT-triphosphate (AZT = 3, -azido-3 deoxythymidine) and thus a greater therapeutic effect, while reducing the concentration of the toxic monophosphate intermediate. This has anticancer and antiviral activities.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                   Transferrin binding protein 1; Tbp1; vaccine; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferrin binding protein 1 (Tbp1) (W04867) of Actinobacillus pleuropneumoniae (App) strain 1370, derived from strain Hpn-1 (ArCC 27088) of serotype 1, is probably a transmembrane protein that serves as a channel for transport of iron across the outer membrane. Its amino acid sequence was deduced from a gene (T$3071) obtd. From App genomic DNA. Recombinant Tbp1, or its antigenic fragments, can be produced in transformed host cells. It is used to formulate vaccines against porcine pleuropneumonia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Actinobacillus pleuropneumoniae transferrin binding protein 1 - production of antibodies useful diagnostically and in universal
                                                                                                                                                                                                                 0;
                                                                                                                                                                                         DB 20; Length 240;
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                                                                                                                                                                                           Score 46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1..22
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
Claim 7; Page 68-69; 84pp; English.
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                                                                                                                                                                                        100.0%;
100.0%;
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                                                                                                                                                                                                     Best Local Similarity
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206 ylnvgdln1 214
                                                                                                                                                       240 AA;
                                                                                                                                                                                                                                       1 YLNVQDLNL 9
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                                                                                                                                                                                                                                                                                                                                                                       19-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-1996;
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                                                                                                                                                        Seguence
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W04867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ü
                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human nucleic acid sequences from pancreatic tumors, and related
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pancreas; tumor; EST; expressed sequence tag; human; cytostatic;
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                                                           Length 931;
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                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Human prostate tumor EST fragment derived protein #157.
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                                                       Score 34; DB 17;
Pred. No. 1.1e+02;
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Pred. No. 5.4;
2; Mismatches
                                                                                                  1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R88469 standard; Protein; 1464 AA.
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                                                                                                                                                                                                                                                                             Y73970 standard; Protein; 43 AA.
                                                       73.98;
66.78;
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66.78;
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                                                                                                6; Conservative
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                                                         Query Match
Best Local Similarity
                                                                                                                                                              | ||||: |
742 yfnvgdikl 750
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931 AA;
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ylnfqdvs1 15
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Gaps

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This sequence represents the Cannabis sativa tetrahydrocannabinolic acid (THCA) synthase amino acid sequence. The THCA gene sequence can be used to produce an expression vector containing the gene. Cells can be transformed using the vector, so that they produce a protein with THCA synthase activity. THCA can be used for anaesthesia, pain-killing, intraocular pressure lowering and anti-inflammatory treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New strains of bread-making yeast with low fermentative activity at low temperature - allows production of doughs that can be stored cold for many hours before final baking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mutant; cold sensitive; yeast; complementation; breadmaking; dough; sugar; leavening agent; brewing; winemaking; truncation.
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                                                                                                                                                                                                                                                                                                               Length 545;
                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mutant YLR087c protein from cold sensitive yeast strain.
                                                                                                                                                                                                                                                                                                           Score 32; DB 21;
Pred. No. 1.4e+02;
2; Mismatches 1;
                                                                    New tetrahydrocannabinolic acid synthase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "encoded by AGR"
Misc-difference 1582
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                                                                                                    Claim 2; Page 8-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W36093 standard; Protein; 2496 AA.
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Best Local Similarity 66./م
المالية و: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
                                  N-PSDB; A13340, A13341.
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                WPI; 2000-285930/25
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                                                                                                                                                                                                                                                             545 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the feline infectious peritonitis 1 virus (FIPV-I) spike protein. The FIPV-I spike protein may be used in the production of a vaccine for the prevention and treatment of FIPV-I infection. The spike protein may be produced by transforming a host cell with the spike protein DNA and expressing the sequence such that the spike protein can be isolated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding feline infectious peritonitis I virus spike protein used in a vaccine for prevention and treatment of {\tt FIPV-I} infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                  Feline infectious peritonitis 1 virus; FIPV-I; spike protein; vaccine; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 17; Length 1464; Pred. No. 2.8e+02; 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetrahydrocannabinolic acid synthase amino acid sequence.
                                                                                  Feline infectious peritonitis 1 virus spike protein.
                                                                                                                                                                       Feline infectious peritonitis 1 virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 14-17; 23pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y88391 standard; Protein; 545 AA.
                                                                                                                                                                                                                                                                                                                                              (KITA ) KITASATO KENKYUSHO SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.78;
55.68;
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                                                14-AUG-1996 (first entry)
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-072341/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1464 AA;
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86 yintqnlni 94
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                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; T10166
                                                                                                                                                                                                                                                                           10-JUN-1994;
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                                                                                                                                                                                                     JP07327683-A
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Sequence

Query Match

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x88391

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2942 AA;
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26-JAN-1993;
05-AUG-1993;
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26 - MAY - 1992;
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    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                 W81457;
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                                   This is the amino acid sequence of a mutant protein (designated YLR087c) isolated from a cold sensitive strain of Saccharomyces cerevisiae. The gene sequence was isolated from the clone YCp50-10.39 which was able to complement the cold sensitive strain HL13.2.30. This protein is a truncated mutation as compared to the wild type sequence. The wild type apen contains a open reading frame of 884 bases encoding a protein of 2958 amino acids. The mutant gene has an open reading frame of 7488 bases encoding a protein of 2496 amino acids. Yeast strains containing processes, i.e. in processes where the delay between mixing the dough and baking exceeds 6 hr. Particularly they are used to make French-style bread (no added sugar) or breads with sugar content below 58. The strains can also be used in brewing and winemaking as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is a protein capable of complementing a mutation showing low temperature sensitivity in fermentation. This is encoded by a novel genomic DNA CSF-1 (cold sensitivity of fermentability). The Saccharomyces cerevisiae YHK 1243 has an inactivated gene encoding this new protein or has the novel DNA sequence contained in its chromosome. This protein can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae; cold sensitivity of fermentability; CSF-1; low temperature sensitivity; yeast; bread; ethanol; fermentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein for complementing low temperature sensitivity in fermentation - can be inactivated in yeast and used for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae protein encoded by novel CSF-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.6%; Score 32; DB 18; Length 2496; 66.7%; Pred. No. 7.9e+02; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in dough to produce bread, and to produce ethanol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tokai M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Pages 21-40; 48pp; Japanese.
Example 4; Page 59-64; 76pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W22050 standard; Protein; 2942 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kawasaki H, Kikuchi Y, Ouchi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KYOW ) KYOWA HAKKO KOGYO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-JP03862.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                   cold-sensitive phenotype.
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N-PSDB; T74989.
                                                                                                                                                                                                                                                                                                                                                                                                           2496 AA;
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Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| | |:
| 642 ylnvndhni 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fermentation - ca
bread and ethanol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLNVQDLNL 9
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W22050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Intercellular adhesion molecule polypeptide; ICAM-R; humanised; ICR 1.1; monoclonal antibody; therapeutic; inflammatory; asthma; tumour; graft-versus-host disease; viral infection; toxin; radionuclide; neovascularisation site; canine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ICAM-R) polypeptide. Antibodies specific for ICAM's are potentially useful as therapeutic compounds, for treating e.g. immune-mediated inflammatory conditions (e.g. graft-versus-host disease), asthmatumours or viral infections. Monoclonal antibodies specific for ICAM-R, or their conjugates formed with e.g. toxins or radionoclides are useful for therapeutically targeting or detecting neovascularisation sites. This represents the amino acid sequence of the longest canine ICAM-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Humanised antibodies specific for intercellular adhesion molecule polypeptide - useful for therapeutic or diagnostic purposes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to humanised ICR 1.1 and ICR 8.1 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 targeted to the human intercellular adhesion molecule polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                        0;
  Length 2942;
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75.0%; Pred. No. 2.2e+02;
.ive 1; Mismatches 1; Indels
Score 32; DB 18; Length 29
Pred. No. 9.5e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone, isolated using human ICAM-R sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 31; Columns 157-160; 116pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Canine ICAM-R polypeptide sequence
                                                                                                                                                                                                                                                                                                                   W81457 standard; Protein; 528 AA.
69.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0827689.
92US-0889724.
92US-0894061.
93US-0009266.
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93US-0102852
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                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ξ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-023535/02.
Query Match
Best Local Similarity
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                                                                                                                                                                        642 ylnvndhni 650
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X50760;

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RESULT Y50760

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This sequence represents a novel barley alpha-glucosidase protein. Recombinant alpha-glucosidase can be used to increase the rate of starch grain hydrolysis when used together with alpha-amylase or can supplement glucoamylase in industrial starch hydrolysis systems. Useful DNA sequence characteristics from this enzyme can be identified which can be used as hybridisation probes for identifying germplasm with high levels of efficient hydrolytic enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding barley alpha-glucosidase protein – useful for producing recombinant protein to increase rate of starch grain hydrolysis when used with alpha amylase
                                                                                                                                                                 Alpha-glucosidase; barley; starch grain hydrolysis; alpha-amylase; glucoamylase; industry; germplasm; hydrolytic enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana plant morphogenesis regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant, morphogenesis; regulation; short; stem; alteration; inflorescence; extraneous; gene; expression; transformation; increase; control; form; length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 31; DB 19; Length 87
Pred. No. 3.9e+02;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          (WISC ) WISCONSIN ALUMNI RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Col 21-26; 19pp; English.
                                                                                                                             Barley alpha-glucosidase protein.
                    W59040 standard; Protein; 877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W13408 standard; Protein; 976 AA
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ilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                 95US-0430925.
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                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Thes 6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-347329/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               877 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               296 ylnvsdl 302
                                                                                                                                                                                                                     Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; V11736.
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                                                                                                                                                                                                                                                                                                                                                                  28-APR-1995;
                                                                                           37-AUG-1998
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                                                                                                                                                                                                                                                                                             .8661-NUC-60
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   W59040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes a novel method for identifying a compound that modulates phosphorylation of human intercellular adhesion molecule polypeptide (ICAM-R) by protein kinase C isoform. The method comprises: (a) exposing a purified peptide consisting of the cytoplasmic domain of ICAM-R to protein kinase C isoform and labeled adenosine triphosphate in the presence and absence of a test compound; (b) measuring labeled in phosphate transferred to the peptide; and (c) identifying a test compound that affects transfer of the labeled phosphate as a modulator compound. The method is useful for identifying compounds that modulate the phosphorylation of human intercellular adhesion molecule polypeptide which might form the basis for the development of therapeutic and diagnostic agents. This sequence represents a canine ICAM-R protein which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying modulators of protein kinase C phosphorylation of human intercellular adhesion molecule polypeptide .
                                                                                                                                                                                                                                                                      ICAM-R; canine; intercellular adhesion molecule; phosphorylation; protein kinase C; modulator.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 34; Column 163-166; 122pp; English.
                                                                                                                         Y50760 standard; Protein; 528 AA
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92US-0894061.
93US-0009266.
93WO-US00787.
93US-0102852.
95US-0487113.
                                                                                                                                                                                                                                                                                                                                                                                                                                          96US-0720420
                                                                                                                                                                                                  16-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0.
                                                                                                                                                                                                                                    Canine ICAM-R protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vazeux R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-022778/02.
N-PSDB; 224362.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ICOS-) ICOS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          528 AA;
                   :4111 11
461 mnvqdrnl 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :1111 11
461 mnvqdrn1 468
                                                                                                                                                                                                                                                                                                                              Canis familiaris.
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LNVQDLNL 9
LNVQDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallatin WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                          27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-1992;
05-JUN-1992;
22-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                              US5989843-A.
                                                                                                                                                                                                                                                                                                                                                                                                    23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-1993
05-AUG-1993
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Gaps

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JP09056382-A

Sequence

RESULT

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Length 877;

Gaps

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Length 991; Indels

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Polypeptide(s) expressed by truncated genes, esp. spider delta-latroinsectotoxin - also related non toxic precursor polypeptide. isolated from Black Widow spider, useful as insecticide
                                                                                                                          This protein may be expressed recombinantly in E. coli BL21 (DB3) cells transformed with pT7-7 vectors comprising the truncated form of the sequence. The encoded protein is an insect-specific neurotoxin, delta-lactroinsectotoxin, which is useful as an oral or topical insecticide. Expressing the truncated gene allows large-scale production of active toxin in bacteria, eliminating the need mammals and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            widow spider; insecticide; pesticide; delta-latroinsectotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This protein is an insect-specific neurotoxin, delta-
lactroinsectotoxin, which is useful as an oral or topical
insecticide. This neurotoxin is harmless to mammals and plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Black widow spider delta-latroinsectotoxin precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 16; Length 1214;
Pred. No. 5.6e+02;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31; DB 16; L
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galkina TG, Grishin E,
ikov KA, Shamotienko OG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Khovotchev MV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Latrodectus mactans tredecimguttatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRTE-) BRITISH TECHNOLOGY GROUP LTD.
                                          Claim 10; Page 35-38; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 61; Page 43-47; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R80097 standard; Protein; 1214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spider venom; neurotoxin; toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krasnoperov V, Pluzhnikov KA,
Volkova T, Galkina T, Khovotc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94GB-0008466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95GB-0008298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 71.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bell DR, Dulubova I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity
'.^< 5; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-360758/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1214 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                991 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||:|
636 lniqdvn 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; T04688.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LNVQDLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB2288807-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R80097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Black
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
\mathbf{x} \times 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide(s) expressed by truncated genes, esp. spider delta-latroinsectotoxin - also related non toxic precursor polypeptide. isolated from Black Widow spider, useful as insecticide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Black widow spider; insecticide; pesticide; delta-latroinsectotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               morphogenesis regulatory protein (MRP), which can be used to yield a plant with, e.g. short stems or altered inflorescence. The MRP acts on a plant at a specific site for a specific period, and can therefore be used to regulate extraneous gene expression in a plant. The MRP's cDNA or genomic DNA can be used to transform a plant to increase its MRP expression, and therefore control the form (particularly stem length) of the plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - useful to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khvotchev MV;
Usherwood PNR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding plant morphogenesis regulatory protein - yield plants with short stems or altered inflorescence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is an Arabidopsis thaliana plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 31; DB 18;
Pred. No. 4.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bell DR, Dulubova I, Galkina TG, Grishin E,
Krasnoperov V, Pluzhnikov KA, Shamotienko OG,
Volkova T, Galkina T, Khovotchev MV;
                                                                                                                                                                                                                                                              (MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.
(CHIK-) ZH CHIKYU KANKYO SANGYO GIJITSU KENKYU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Black widow spider delta-latroinsectotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Latrodectus mactans tredecimquttatus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BRTE-) BRITISH TECHNOLOGY GROUP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Pages 6-10; 17pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R80096 standard; Protein; 991 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                spider venom; neurotoxin; toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.4%;
75.0%;
                                                                                95JP-0216187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95GB-0008298
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                                                                                                                                                                         95JP-0216187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-360758/47.
N-PSDB; T04687.
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-206629/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          976 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 LNVQDLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T62124
                                                                                                                                                                         24-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1995;
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                                                                                    24-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB2288807-A.
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RESULT 12

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Gaps

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Usherwood PNR;

Khvotchev MV;

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New proteins useful for treatment of Plasmodium infections in humans, especially malaria
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                                                                                                                                                                                                                         CLAG2; cytoadherence linked asexual gene; CLAG; erythrocyte; red blood cell; malaria; infection; therapy; vaccine.
                                                                                                                                                                             Plasmodium falciparum cytoadherence gene protein CLAG2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 136-145; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MENZ-) MENZIES SCHOOL HEALTH RES.
                                           Y31949 standard; Protein; 1430 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kemp DJ, Trenholme KR,
                                                                                                                                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-591099/50.
                                                                                                                                                                                                                                                                                                                                     W09949048-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-1999;
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                                                                                                                                 21-DEC-1999
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Matches
RESULT
Y31949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein class. Each gene recognises different pathogen aviralence geness or alleles. Together the RPP1 genes comprise a complex resistance locus containing a functionally variable family of resistance genes found on the bottom arm of chromosome 3. The RPP1 nucleotide sequences can be used for identifying, cloning or amplifying RPP1 sequences. Transgenic plants containing the RPP1 sequences have increased resistance to the fungus P. parasitica. The methods are useful for influencing or affecting the degree of resistance of a plant to such a fungus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peronospora parasitica resistance genes from Arabidopsis thaliana useful in transgenic plants having increased resistance to the fungus
                                                                                                                                                                                                                                                                                                                                   Recognition of Peronospora parasitica 1; RPP1-WSB; downy mildew; blotrophic oomycete; chromosome 3; nucleotide binding-LRR protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botella-Mesa MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beynon JL, Parker JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 3G-3H; 80pp; English.
                                                                                                                                                   Y78972 standard; Protein; 1220 AA.
                                                                                                                                                                                                                                                                                       RPP1-WsB amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                             fungicide; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-0017278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB02609
                                                                                                                                                                                                                                           05-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-205727/18.
N-PSDB; 298619, 298620.
                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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Best Local Similarity
5; Conserv?
                         WO200008189-A2.
2 LNVQDLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-AUG-1999;
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                                                                                                                                                                                               Y78972;
                                                                                                            RESULT 14
                                                                                                                                      178972
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Cowman AF;

Holt DC,

Gardiner DL,

99WO-AU00213. 98AU-0002580.

(first entry)

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Gaps
linked asexual gene 2 (CLAG2) protein that facilitates cytoadherence of erythrocytes parasitised with plasmodium spp. to other cells. It is encoded by a gene located on chromosome 2 of a falciparum. It is a member of a family of CLAG proteins (see also Y31945-48). The identification of clag genetic species, and the products encoded by them, enables a range of therapeutic agents to be rationally designed and/or identified that are useful for the prophylaxis and treatment of disease conditions caused or exacerbated by infection with Plasmodium spp., e.g. malaria,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1430;
                                                                                                                                                                                                                                                                                                                                                                                                                                               67.4%; Score 31; DB 20; Length 14
83.3%; Pred. No. 6.7e+02;
ive 1; Mismatches 0; Indels
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Job time: 18776 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                     in humans.
                                                                                                                                                                                                                                                                                                                                                1430 AA;
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| 645 ylnigd 650
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Gaps

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Length 1220;

Score 31; DB 21; Length 12 Pred. No. 5.6e+02; 3; Mismatches 1; Indels

3;

Conservative

6

1 YLNVQDLNL

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67.48; 55.68;

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099410 portine uring 099410 portine traing 051594 escherichia 05259 buchnera ap 094024 homo sapien 031409 locusta mig 094240 saccharomyc 037854 bacteriopha 089312 murine hepa P8.2082 limnodynast 097799 haemophilus p7.8484 homo sapien 0916386 homo sapien 091638 homo sapien 091638 aretus norv 054248 streptomyce 0008433 simian viru 008433 simian viru 099499 drosophila
                                                                                                                                                                                                                                                                                                                 Q921e9 neisseria m
Q05403 saccharomyc
Q94414 homo sapien
Q94413 homo sapien
Q94695 physarum po
Q9ubil albinaria h
Q9524 nicotiana t
Q6227 mus spretus
P82083 limnodynast
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016276 homo sapien
030v82 drosophila
031653 anser caeru
07837 caloglossa
09t187 caloglossa
09t188 caloglossa
09t188 caloglossa
09t389 caloglossa
09t387 caloglossa
09t387 caloglossa
09t387 caloglossa
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081964 caloglossa
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  aeromonas s
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Q44468 aeromonas c
Q9uqw0 homo saplen
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homo sapien
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Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Bombycoidea, Bombycidea, Bombyxidae,
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Last annotation update)
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                                                                                                                                                                                                           Q9R7H9
P78484
Q163886
Q9TRW2
Q84333
Q84333
Q64248
Q907354
Q907354
Q97459
Q97453
Q97453
Q97453
Q97857
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Q97857
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071837
097180
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041452
081964
081968
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Q51594
Q9ZEZ9
  Q57328
Q44001
Q44377
Q44468
Q43928
Q9UQWO
Q9UQA3
Q90417
Q88612
Q89491
                                                                                                                                                                                      Q83332
P82082
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Q34909
Q9T2W0
Q37854
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oryza sativ
                                                                                  (without alignments)
7.553 Million cell updates/sec
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                                                                       Search time 111.26 Seconds
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                                                                                                                                                                                                            436
           4.5
Compugen Ltd
                                                                                                                                                                                                           Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                      297973 segs, 93374136 residues
                                                                         ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
          GenCore version
Copyright (c) 1993 - 2000
                                                                       December 16, 2000, 04:22:13
                                                                                                                                                                                                                                                                                    summaries
                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P82003
Q9UCN5
P77556
Q9XNP8
Q50832
Q508866
Q35792
Q40659
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Gapop 10.0 , Gapext 0.5
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095953
Q9XJN0
Q9RQ57
Q9RQ49
P87225
Q15889
Q9UMH9
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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Maximum Match 100%
Listing first 75 su
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sp_phage:*
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sp_bacteria:*
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Match Length
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length: 9
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Perfect score:
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08
                                                    OM protein
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STRAIN=N; MEDLINES, 99297341.

MEDLINES, 99297341.

Campbell N.J.H., Barker S.C.;

"The novel mitochondrial gene arrangement of the cattle tick,

"The novel mitochondrial gene arrangement of the cattle tick,

Boophilus microplus: fivefold tandem repetition of a coding region.";

MOI. Biol. Evol. 16:732-74(1999).

EMBL; AF110616; AAD28386.1;
"Mosaic structure of plasmids from natural populations of Escherichia
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Parasitiformes, Ixodida, Ixodidae, Boophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.6%; Score 15; DB 8; Length 8; 66.7%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ATP SYNTHASE 6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          D335A5B0544735A1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 17; DB 2;
Pred. No. 3e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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               coli.";
Genetics 143:1091-1100(1996).
EMBL, U50650; AAC44245.1;
EMBL, U50650; AAC44235.1;
EMBL, U50652; AAC44235.1;
EMBL, U50653; AAC44236.1;
EMBL, U50654; AAC44239.1;
EMBL, U50655; AAC44239.1;
EMBL, U50655; AAC44240.1;
EMBL, U50659; AAC44241.1;
EMBL, U50659; AAC44241.1;
EMBL, U50660; AAC44242.1;
EMBL, U50660; AAC44242.1;
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50.0%;
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Best Local Similarity
Matches 3; Conserv
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Matches 2; Conserv
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P72279;
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                                   STRAIN=C145 X N140; TISSUE-BRAIN;
Hua Y.-J., Tanaka Y., Nakamura K.;
"Identification of a prothoracicostatic peptide (PTSP) from the larval brain of the silkworm, Sombyx mori.";
J. Blol. Chem. 0:0-0(1999)
-i- FUNCTION: INHIBITS ECDYSTEROIDOGENESIS BY PROTHORACIC GLAND IN THE
                                                                                                                                                                                                                                                                                                                                                          Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Raboudi N., Julian J., Rohde L.H., Carson D.D.;
"Identification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95).";
J. Biol. Chem. 267:11930-11939(1992).
SEQUENCE 9 AA; 1008 MW; CB56D0544732C732 CRC64;
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01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                          0; Indels
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                                                                                                                                                                                                                                                                                                              Length 9;
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3878C5B4472AB6C3 CRC64;
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Last annotation update)
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Pred. No. 3e+05;
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MEDLINE; 96400908.
Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
                                                                                                                                                             SILKWORM.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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100.0%; Pre
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9 AA; 1090 MW;
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Best Local Similarity
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3 QDLN 6
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Q9UCN5;
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SEQUENCE FROM N.A.
MEDIANE: 86120353.
Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
Sijbach plastid genes coding for initiation factor IF-1, ribosomal protein S11 and RNA polymerase alpha-subunit.";
Nucleic Acids Res. 14:1029-1044(1986).
Chloroplast.
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Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.
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Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
Rodriquez R.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE: 81069885.

MEDLINE: 8.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino Menitz S.G., Coruzzi G., Thalenfeld B.E., Tzagoloff A., Macino Massembly of the mitochondrial membrane system. Structure and nucleotide sequence of the gene coding for subunit 1 of yeast
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01-NOV-1996 (TrEMBLrel. Ol, Last sequence update)
01-NOV-1998 (TrEMBLrel. OB, Last annotation update)
OXI3 LOCUS IN YEAST MITOCHONDRION (STRAIN D273-10B)
(CODES FOR CYTOCHROME OXIDASE SUBUNIT 1).
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Last annotation update)
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                                                                                                                                                   644729D77409C420 CRC64;
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Pred. No. 3e+05;
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Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  8 AA.
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Best Local Similarity 66.7%;
Matches 2; Conservative
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EMBL; V00694; CAA24063.1; -.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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7 AA; 907 MW;
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Best Local Similarity 40.0
Matches 2; Conservative
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SEQUENCE 8 A.
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1 LKDYN 5
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Q35792;
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                                                                                                                Asturias J.A., Diaz E., Timmis K.N.; "The evolutionary relationship of biphenyl dioxygenase from gram-positive Rhodococcus globerulus P6 to multicomponent dioxygenases from gram-negative bacteria.";
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"Non-repetitive AT-rich sequences are found in intergenic regions of
Methanococcus voltae DNA.";
EBBO J. 4:805-809(1985).
EMBL; X02518; CAA26355.1; -.
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; Caryophyllidae; Caryophyllales;
Chenopodlaceae; Spinacia
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                                                      Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
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Pred. No. 3e+05;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CYTOCHROME B/F SUBUNIT IV (FRAGMENT).
Spinacia oleracea (Spinach).
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Pred. No. 3e+05;
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 40.0
Matches 2; Conservative
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8 AA;
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MEDLINE; 88105390.
WINDLINE; 88105390.
Van der Vossen J.M., der Lelie D., Venema G.;
"Isolation and characterization of Streptococcus cremoris Wg2-specific promoters.";
Appl. Environ. Microbiol. 53:2452-2457(1987).
EMBL; M24763; AAA74720.1; -.
NON_TER 9
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MEDLINE; 92005680.
Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;
Point mutations in human keratin 14 genes of epidermolysis bullosa simplex patients: genetic and functional analyses.";
Cell 66:1301-1311(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

PROMOTER 23 DNA FRAGMENT (FREGMENT).

Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaee;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5AF3A44AA4469443 CRC64;
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Last annotation update)
cerevisiae.";
Gene 94:209-216(1990).
EMBL; M62916; AAA33892.1; -.
NON TER
SEQUENCE 8 AA; 948 MW; EBC694444732D6D6 CRC64;
                                                                                                                                                                                                               28.3%; Score 13; DB 10;
60.0%; Pred. No. 3e+05;
iive 1; Mismatches 1
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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1 MQVLN 5
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3 NMND 6
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SEQUENCE
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Q14715;
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Q48686;
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048686
AC 048686
DT 048686
DT 01-NOV-
DT 01-NOV-
DE PROMOTI
OS Lactocc
CC Bacter
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Mindich L., Qiao X., Qiao J., Romantschuk M., Hoogstraten D.;
Mindich L., Qiao X., Qiao J., Romantschuk M., Hoogstraten D.;
"Isolation of additional bacteriophages with genomes of segmented
double-stranded RNA.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF125675; AAD22555.1;
NON_TER
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U77631; AAD15626.1; -.
                                                                                                                                                                                            Length
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
GALACTOCEREBROSIDASE (EC 3.2.1.46) (FRAGMENT).
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Last annotation update)
                                                                                                                           BE300AA449C456D6 CRC64;
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bacteriophage phi-10.
Viruses; dsRNA viruses; Cystoviridae; Cystovirus.
                                                                                                                                                                                          Score 13; DB 4;
Pred. No. 3e+05;
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Pred. No. 3e+05;
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Pred. No. 3e+05;
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bullosa simplex.";
Hum. Mol. Genet. 3:1171-1172(1994).
EMBL; D28807; BAA05967.1; -.
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40.0%;
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75.0%;
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50.0%;
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                                                                                                                         1138 MW;
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NON_TER 9 9
SEQUENCE 9 AA; 1069
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 3; Conserv
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Hum. Mol. Genet. 0:0-0(0).

EMBL; L32070; AAA73879.1; -.

NON_TER 8

SEQUENCE 8 AA; 865 MW; 0474472325A761E7 CRC64:
                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota: Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 273169; CAA97518.2; -.
NON_TER
                                                                                                                                                                     SEQUENCE FROM N.A. Wedler E., Scharfe M., Wambutt R.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, La
01-NOV-1999 (TrEMBLrel. 12, La
GIN11 PROTEIN (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, 1
01-MAY-2000 (TrEMBLrel. 13, 1
RHCE PROTEIN (FRAGMENT).
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hes 3; Conserv
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AC Q9UMH9;
DT 01-MAY-
DT 01-MAY-
DT 01-MAY-
DT RICE PR
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Q15889
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NIFS PROTEIN HOMOLOG (FRAGMENT).
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Mol. Biol. Evol. 16:1586-1598(1999).
EMBL; AF130812; AAF13797.1; -.
NON_TER
SEQUENCE 8 AA; 980 MW; F3A73B504771A336 CRC64;
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66.7%; Pred. No. 3e+05;
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EMBL: AF130814; AAF13805.1; -.
NON_TER
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE; 20022990.
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6 YLD 8
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Q9RQ57;
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Q9RQ49;
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Q9RQ49
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P87225
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 9179-79) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rarlyshev A.V., Macintyre S.;
Study of the intergenic exeF-exeG region and its application as a
simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL: X89461; CAA61637.1; -.
                                                                                                                                                                                                                               Karlyshev A.V., Macintyre S.;
"Study of the intergenic exeF-exeG region and its application as simple preliminary test for Aeromonas Spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89466; CAA61647.1;
NON_TER
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                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=132, FROM DR M. ALTWEGG UNIV. ZURICH CULTRE COLLECTION;
MEDLINE; 97089747.
                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Aeromonas group,
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN 132) (FRAGMENT).
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Pred. No. 3e+05;
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Pred. No. 3e+05;
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66.7%;
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Best Local Similarity 66,,,,
2; Conservative
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PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=CDC 9179-79;
MEDLINE; 97089747.
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Best Local Similarity
Matches 2; Conserv
                                                                                                                     Aeromonas sobria.
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"Two novel mutations in Thai patients with hereditary
methemoglobinemia types I and II: a subtle amino acid change causes
instability of NADH-cytochrome b5 reductase.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF061830; AAF06818.1; -.
                                                                                              TISSUE=BLOOD;
Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
"Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
                                                                                                                                                                                                                               TISSUE-BLOOD;
BIDLINE; 90349591.
Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
Cherif-Zahar B., Bloy C., Cartron J.-P., Colin Y.;
Hermand P., Salmon C., Cartron J.-P., Colin Y.;
"Molecular cloning and protein structure of a human blood group Rh
          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT).
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Pred. No. 3e+05;
1; Mismatches 0; Indels
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Pred. No. 3e+05;
1; Mismatches 0; Indels
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888 MW; 76C5B73B5051F6D8 CRC64;
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EMBL; E87030; CAB09726.1; -.
NON TE
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                                                                                                                                                                phenotype.";
Am. J. Hum. Genet. 60:808-817(1997).
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llarity 66.7%;
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Martial J.A.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                      Karlyshev A.V., Macintyre S.;
"Study of the intergenic exef-exeG region and its application as simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89464; CAA61643.1;
EMBL; X89460; CAA61639.1;
EMBL; X89460; CAA61655.1;
EMBL; X89460; CAA61639.1;
EMBL; X89460; CAA61641.1;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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Pred. No. 3e+05;
3; Mismatches
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Pred. No. 3e+05;
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66.7%;
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llarity 25.0%;
Conservative
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Q9UQA3;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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9
1060 MW;
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Best Local Similarity 66.7
Matches 2; Conservative
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                              SEQUENCE FROM N.A.
STRAIN=VARIOUS STRAINS;
MEDLINE; 97089747.
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Best Local Similarity
Local 1; Conserve
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SEQUENCE FROM N.A.
MEDLINE; 84182507.
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9 AA;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 1306-83) (FRAGMENT).
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN ATCC 49659) (FRACMENT).
EXEF'.
                                                                                                                                             Karlyshev A.V., Macintyre S.; Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas Spp."; FEMS Microbiol. Lett. 137:37-44(1996).
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STRAIN-CDC 1306-83;
MEDLINE; 9708747.
Karlyshev A.V., Macintyre S.;
"Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
                                                             Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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043928; Q43918; Q43920; Q43921;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1998 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
EXEF.
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Pred. No. 3e+05;
1; Mismatches
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Pred. No. 3e+05;
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ilarity 66.7%;
Conservative
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llarity 66.7%;
Conservative
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
                                                                                                     SEQUENCE FROM N.A. STRAIN-ATCC 49659; MEDLINE; 97089747.
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                                              Aeromonas trota
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ELN 4
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044468;
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SEQUENCE FROM N.A.
STRAIN=LYMPHOTROPIC VARIANT;
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J. Virol. 570:656-669(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prototype strain.";
J. Virol. 57:656-669(1986).
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Best Local Similarity 40.0
Matches 2; Conservative
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NON_TER
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3 YIPTQ 7
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                                                                                                  "Two short sequences have positive effects on the human p27(Kip1) gene
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Erickson J.W., Cline T.W.;
"Key aspects of the primary sex determination mechanism are conserved
                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Brāchycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                         Gaps
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                                        Euteleostomi;
                                                                               ., Iwahashi Y., Yanagisawa Y., Suzuki Y., Sugano S., Yuasa
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                                                                                                                                                                                                                                                                                                                                                                     Drosophila virilis (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                             Homo sapiens (Human).
'Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
|Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26.1%; Score 12; DB 5; Length 9; llarity 66.7%; Pred. No. 38+05; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                   Score 12; DB 4; Length 9; Pred. No. 3e+05;
                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bell M., Cline T.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AR046045; AAC97605.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                088612;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
STRUCTURAL POLYPROTEIN (FRAGMENT).
01-MAY-2000 (TrEMBLrel. 13, Last annotation update) P27KIP1 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9A8BD1AAA9C449CA CRC64;
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Development 125:3259-3268(1998).
                                                                                                          transcription.";
Gene 228:93-100(1999).
EMBL; AB005590; BAA76715.1; -.
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50.0%;
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9 AA; 1089 MW;
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Best Local Similarity 50.0.
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Best Local Similarity
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3 NVRVSN 8
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                                                                                          Maruyama K.;
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MEDLINE: 87061199.
MICHAEL WILLIAM WARD D.C.;
MOTHER PROBLES BATCHERS ARE USED to excise the small intron common to all minute virus of mice RNAS.";
J. Virol. 60:1170-1174(1986).
EMBL: M12032; AAA67112.1;
EMBL: V01115; CAA24311.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                   SEQUENCE FROM N.A.

MEDLINE, 83039424.

Ou J.H., Rice C.M., Dalgarno L., Strauss E.G., Strauss J.H.;

Sequence studies of several alphavirus genomic RNAs in the region containing the start of the subgenomic RNA.";

Proc. Natl. Acad. Sci. U.S.A. 79:5235-5239(1982).

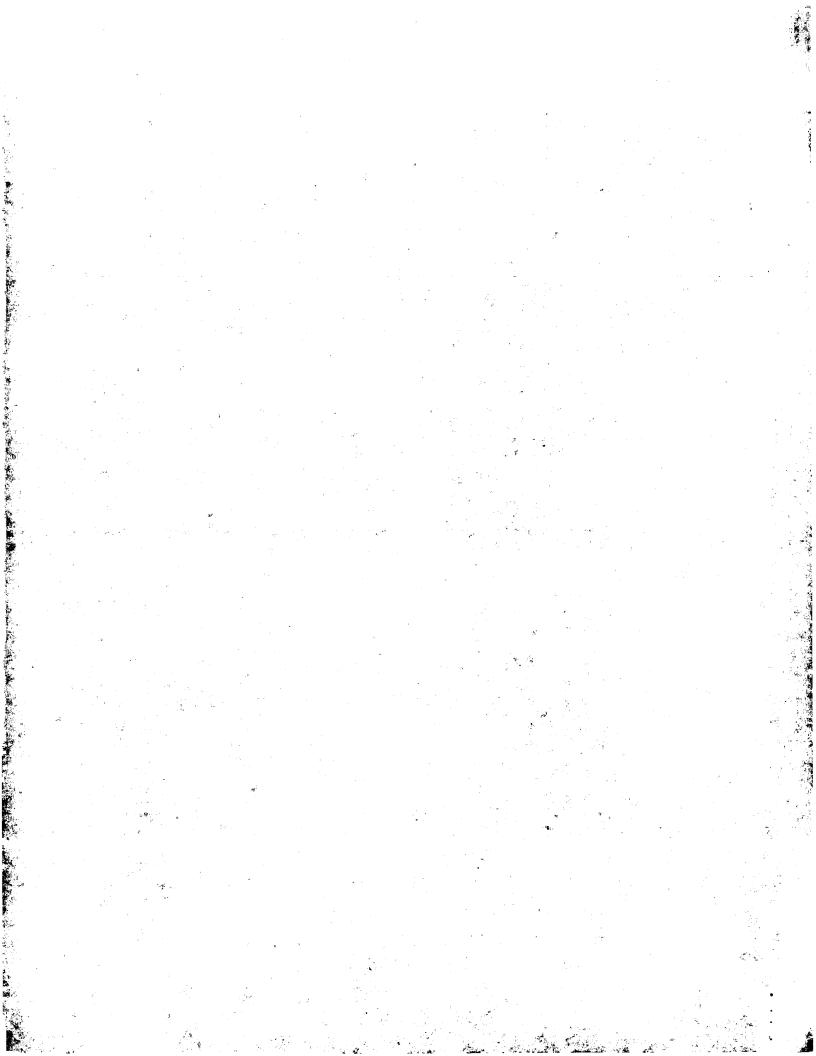
EMBL; J02246; AAA96655.1; -.
Middelburg virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
Alphavirus.
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Askell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 86115415.
Satell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice,
MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Astell C.R., Thomson M., Merchlinsky M., Ward D.C.; "The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 1.1 KDA PROTEIN.
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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Pred. No. 3e+05;
1; Mismatches 2
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8 AA;. 998 MW;
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Matches 2; Conserv
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01-MAY-2000 (
01-MAY-2000 (
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1 MNSQ 4
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1 LQRLDI
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Enjuanes L.;
                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                         porcine transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                    "Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes."; J. Virol. 73:1535-1545(1999).
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                           Length 9;
                                           Indels
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL FUSION PROTEIN.
C3FD405863637862 CRC64;
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Last annotation update)
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                         DB 12;
3e+05;
                         Score 12; DB 1
Pred. No. 3e+05
1; Mismatches
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                         Query Match 26.1%;
Best Local Similarity 66.7%;
Matches 2; Conservative
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ΜW,
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1061
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Best Local Similarity
Matches 2; Conserv
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AA;
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Q51594;
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Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
"Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Weber P.C., Palchaudhuri S.; "Incompatibility repressor in a RepA-like replicon of the IncFI plasmid Colv2-F94."; J. Bacteriol. 166:1106-1112(1986).

EMBL: M13472; AAA23194.1; ...
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01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
2-ISOPROPYLMALATE SYNTHASE (EC 4.1.3.12) (FRAGMENT).
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Last annotation update)
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Pred. No. 3e+05;
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Pred. No. 3e+05;
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EMBL; AJ006874; CAA07290.1; -.
Lyase; Plasmid.
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SEQUENCE. MEDLINE; 92035078
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Cartron J.P., Colin Y.;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CBS1 PRECURSOR=PROTEOLYTIC PROCESSING SITE.
Saccharomyces cerevisiae (Baker's yeast).
Mitochondrion.
Fukaryota: Fungi: Ascomycota: Saccharomycetes; Saccharomycetales;
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034909, 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TREMBLR).
01-NO
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J. Hum. Genet. 60:808-817(1997).
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alpha-dextrin endo-1,6-alpha-glucosidase (EC 3.2.1.41) - Bacillus sp. (strain S-1) (f C;Species: Bacillus sp. (cjate: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999 C;Accession: PN0649 R;Kim, C.H.; Choi, H.I.; Lee, D.S. Biosci. Biotechnol. Biochem. 57, 1632-1637, 1993 A;Title: Purification and biochemical properties of an alkaline pullulanase from alka A;Reference number: PN0649; MUID:94080025
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A; Residues: 1-7 <KIM>
C; Comment: This enzymes used togther with glucoamylase to improve the efficiency of
ntent in high maltose syrups.
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Rosidues: 1-9 <RRA>
A;Note: 2-Met is also found
C;Comment: Cardon-monoxide dehydrogenase consists of three polypeptide chains: large, C;Keywords: oxidoreductase
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A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal
                                                                                                                                                                                                                                                                                                                                              PL0139 carbon-monoxide dehydrogenase (EC 1.2.99.2) large chain - Pseudomonas carboxydoflava
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Apr-1993
C;Accession: PL0139
C;Accession: PL0139
R;Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A;Title: Homology and distribution of Co dehydrogenase structural genes in characterice number: PL0139;MUID:90055678
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C;Species: Mus musculus (house mouse)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 24-Jun-1993
C;Accession: B35640
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C. Species: Gryllus binaculatus (two-spotted cricket)
C. Species: Gryllus binaculatus (two-spotted cricket)
C. Species: 26-Jan-1996 #sequence_revision 26-Jan-1996
C. Accession: A5/44
R. Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21103, 1995
A; Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the can reference number: A5/444
A; Reference number: A5/444
A; Reference number: A5/444
A; MulD:95403341
A; Residues: L9 <LOR>
A; Residues: 1-9 <LOR>
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C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: B57444
B;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Titlerence number: A57444
A;Titlerence number: A57444; MUID:95403341
A;Accession: B57444
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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Pred. No. 1.8e+05;
L: Mismatches 0; Indels
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1.8e+05;
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Pred. No. 1.86
0; Mismatches
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B57444
neuropeptide Grb-AST B2 - two-spotted cricket
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100.0%; Pre-
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75.0%;
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Best Local Similarity 100.0
Matches 4; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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Cycochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C; Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C; Accession: T13818
R; Delarbre, C; Barriel, V; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Bvol. 14, 807-813, 1997
A; Title: The main features of the craniate mitochondrial DNA between the NDI and the A; Reference number: 217775; MulD:97398704
A; Accession: T13818
A; Molecule type: DNA
A; Residues: 1-8 cDEL>
A; Residues: 1-8 cDEL>
A; Cross-references: EMBL:Y09527; NID:e1011465; PID:e329906; PIDN:CAA70718.1
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C; Species: Macropus eugenii (tammar wallaby)
C; Date: 30-0ct-1992 #sequence_revision 30-0ct-1992 #text_change 13-Sep-1996
C; Date: 30-0ct-1992 #sequence_revision 30-0ct-1992 #text_change 13-Sep-1996
C; Accession: A43001; P00012
R; Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A; Title: Cholecystokinin octapeptide purified from brains of Australian marsuplals.
A; Reference number: P00012; MUID:88234141
       N; Alternate names: CCK
C; Species: Dasyurus viverrinus (southeastern quoll)
C; Species: Dasyurus viverrinus (southeastern quoll)
C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 13-Sep-1996
C; Accession: P00012
R; Fan, Z.W.; Eng, J.; Shaw, G.; Yalow, R.S.
Peptides 9, 429-431, 1988
A; Title: Cholecystokinin octapeptide purified from brains of Australian marsupials.
A; Reference number: P00012; MUID:88234141
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A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;2/Binding site: sulfate (Tyr) (covalent) #status predicted
F;8/Modified site: amidated carboxyl end (Phe) #status predicted
                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-8 <FAN>
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; hormone; neuropeptide; sulfoprotein
F;Z/Binding site: sulfate (Tyr) (covalent) #status predicted
F;B/Modified site: amidated carboxyl end (Phe) #status predicted
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Pred. No. 1.8e+05;
1; Mismatches 3; Indels
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Best Local Similarity 33.3%;
Matches 2; Conservative
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cholecystokinin - tammar wallaby
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A: Note: COI
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2 YMGWMD 7
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 23-Feb-1997
C;Accession: S58797
R;Nagao, Y.
Biochim: Biophys. Acta 1245, 130-143, 1995
A;Title: Expression of c-mos protein in cultured rat spermatogenic cells and evidence the A;Reference number: S58797; MUID:95383384
A;Accession: S58797
A;Accession: S587
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Pred. No. 1.8e+05;
2; Mismatches 0;
A;Reference number: A35640; MUID:9022173
A;Accession: B35640
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-6 <CHE>
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PQ0012
cholecystokinin - southeastern quoll
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50.0%;
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Best Local Similarity 50.v.
Laga 2; Conservative
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Matches 2; Conservative
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3 EDLD 6
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4 EDL 6
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R;Gaede, G.; Lopata, A.; Kellner, R.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 373, 133-142, 1992
A;Title: Primary structures of neuropeptides isolated from the corpora cardiaca of va
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Argase RI subunit - wood tobacco (fragment)
C;Species: Nicotiana sylvestris (wood tobacco)
C;Species: 16-Feb-1994 #sequence_revision 18 Nov-1994 #text_change 23-Feb-1997
C;Accession: D48186
R;De Paepe, R.; Forchioni, A.; Chetrit, P.; Vedel, F.
Proc. Natl. Acad. Sci. U.S.A. 90, 5934-5938, 1993
A;Title: Specific mitochondrial proteins in pollen: presence of an additional ATP syn A;Accession: D48186
A;Accession: D48186
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C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C5744
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Reference number: A57444; MUID:95403341
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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Tratches 0; Indels
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Pred. No. 1.8e+05;
2; Mismatches 0; Indels
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A;Residues: 1-9 <DE1>
A;Experimental source: pollen
A;Note: sequence extracted from NCBI backbone (NCBIP:134871)
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Pred. No. 1.8e+05;
); Mismatches 1;
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                                                                                                                    ectrometry. A:Reference number: S21663; MUID:92265187
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llarity 50.0%;
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Best Local Similarity 66.7.
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-8 <GAE>
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Matches 2; Conserv
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C;Species: Solanum tuberosum (potato)
C;Species: Solanum tuberosum (potato)
C;Accession: 522428
C;Accession: 52428
C;Acc
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R.Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Arai, R.; J. 1995
A.Title: Sequencing and characterization of the downstream region of the genes encoding y for biosynthesis of heme dl.
A. Reference number: JC4552; MUID:96144254
A. Accession: Pc4131
A. Status: preliminary
A. Accession: Pc4131
A. Status: Draiminary
A. Residues: 1-8 «KAWA
A. Residues: 1-8 «KAWA
A. Residues: DNA
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C;Species: Pseudomonas aeruginosa
C;Date: 20-Apr.2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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C;Species: Pachnoda marginata
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
C;Accession: $21663
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llarity 66.7%; Pred. No. 1.8e+05;
Conservative 1; Mismatches 0;
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C; Keywords: mitochondrion
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1 MDDLS 5
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C;Keywords: neuropeptide

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181836
20k protein - Rickettsia rickettsii (fragment)
20k protein - Rickettsia rickettsii
(c;Species: Rickettsia rickettsii
(c;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 28-May-1999
(c;Accession: B31836
(c;Accession: B31836
(d;Accession: Bact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proctolin - Atlantic horseshoe crab
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Species: Limulus polyphemus (Atlantic horseshoe crab)
C;Bate: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt R;Groome, J.R.; Tillication of proctolin in the central nervous system of the horseshoe c A;Reference number: A60411; MuID:90287800
A;Accession: A60411
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: protein
A;Molecule type: Totolin and hindgut motility in the hoc;Keywords: neuropeptide
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C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0278
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 113, 395-407, 1991
A;Tile: Preferential utilization of specific immunoglobulin heavy chain diversity an A;Reference number: PT0222; MUID:91108337
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iive 0; Mismatches 0;
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A.Residues: 1-5 <STA>
A.Residues: 1-5 <STA>
A.Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmad R:O'Shea, M.: Adams, M.E.
Science 213, 567-569, 1981
A.Title: Pentapeptide (proctolin) associated with an identified neuron.
A.Reference number: A94260; MUID:81225865
A:Contents: annotation; biological source
C;Comment: This peptide is found in the lateral white neurons, which occur (in the cockr innervate the striated hindgut muscles in insects and stimulate contraction of these mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWilliams, C.B.; Gutman, G.A.
J. Immunol. 142, 1027-1035, 1989
A.Title: T cell receptor beta-chain genes in the rat. Availability and pattern of utiliz
A.Reference number: A30563; MUID:89110038
A.Accesslon: B30572
A.Status: preliminary; not compared with conceptual translation
A.Molecule type: mRNA
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R;Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A;Title: Cucture of the pentapeptide proctolin, a proposed neurotransmitter in insects
A;Reference number: A93048; MUID:76074708
A;Accession: A01644
                                                                                                                                    C;Accession: A37027
R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
R;Yoshizuka, N.; Xoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
R;Yoshizuka, N.; Yoshimura, M.; Tsuchiya, S.; Okamoto, K.; Kobayashi, Y.; Osawa, T.
A;Title: Macrophage chemotactic factor (MCF) produced by a human T cell hybridoma clone.
A;Reference number: A37027; MUID:89376581
A;Accession: A37027
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macrophage chemotactic factor - human (fragment)
N;Alternate names: T-cell hybridoma D6-18 protein
C;Species: Homo sapiens (man)
C;Species: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Apr-1989 #sequence_revision 03-Apr-1989 #text_change 30-May-1997
C;Accession: B30572
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C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
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Pred. No. 1.8e+05;
2; Mismatches 2; Indels
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Llarity 66.7%; Pred. No. 1.8e+05;
Conservative 1; Mismatches 0;
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33.3%;
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Best Local Similarity 33.39
Matches 2; Conservative
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C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                           A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-9 <YOS>
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Best Local Similarity
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1 WLGRZD 6
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C; Accession: S78024
R;Kitakawa, M.; Graack, H.R.; Grohmann, L.; Goldschmidt-Reisin, S.; Herfurth, E.; Wit Eur. J. Biochem. 245, 449-456, 1997
A;Title: Identification and characterization of the genes for mitochondrial ribosomal A;Title: Identification and characterization of the genes for mitochondrial ribosomal A;Title: S78024
A;Molecule type: S78024
A;Molecule type: protein
A;Residues: 1-7 <KIT>
C;Genetics:
A;Genetics:
A;Geneme: nuclear
C;Keywords: mitochondrion; protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aspartate transaminase (EC 2.6.1.1), mitochondrial - sheep (fragment)
N;Alternate names: aspartate aminotransferase, mitochondrial
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: O5-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 20-Aug-1999
C;Accession: Al1483
R;Campos-Cavieres, M.; Milstein, C.P.
Biochem. J. 147, 275-281, 1975
A;Title: The sequences of the coenzyme-binding peptide in the cytoplasmic and the mit A;Reference number: Al1483; MUID:76039441
A;Mclecule type: proclein
A;Residues: 1-7 <CAM>
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R;Komatsu, S.; Kajiwara, H.; Hirano, H.
R;Komatsu, Poologion and Poologion and Poologion and Poologion Poologion Poologion R;Komologion Poologion R;Komologion R;
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C;Keywords: aminotransferase; mitochondrion; phosphoprotein; pyridoxal phosphate
F;2/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
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C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
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R. Renault, P.; Gaillardin, C.; Heslot, H.

B. Bacteriol. 171, 3108-3114, 1989

A. Title: Product of the Lactococous lactis gene required for malolactic fermentation is A. Reference number: A44510; MUID:89255069

A. Steference number: A44510; MUID:89255069

A. Steference number: A4510; MUID:89255069

A. Steference number: A4510; MUID:89255069

A. Steference: EMBL: M90762
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C;Species: Ascaris suum (pig roundworm)
C;Species: DoJun-1993 #sequence_revision 10-Jun-1993 #text_change 28-Apr-1995
C;Accession: JH0784
R;Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan, K Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992
A;Title: The primary structure of TE-6: a novel neuropeptide from the nematode Ascaris A;Reference number: JH0784; WUID:93038603
A;Reference number: protein
A;Residues: 1-6 <SMA>
A;Residues: 1-6 <SMA>
A;Residues: lockein
A;Residues: neuropeptide
C;Keywords: neuropeptide
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C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 30-Sep-1993
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Pred. No. 1.8e+05;
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Pred. No. 1.8e+05;
0; Mismatches 2; Indels
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                                 A Molecule type: DNA
A;Residues: 1-5 cYRM>
A:Experimental source: B lymphocyte
C;Reywords: heterottetramer; immunoglobulin
                                                                                                                                                                                                                                  23.9%;
llarity 50.0%;
Conservative
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us-09-529-121-9.lim9.rpr

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RESULT 32
A61230
calsequestrin, cardiac and slow skeletal muscle - northern leopard frog (fragment)
N;Alternate names: 58K dihydropyridine-binding protein; aspartactin; calmitine; lamin
C;Species: Rana pipiens (northern leopard frog)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 16-Jul-1999
C;Accession: A61230
R;McLeod, A.G.: Shen, A.C.Y.; Campbell, K.P.; Michalak, M.; Jorgensen, A.O.
Circ. Res. 69, 344-359, 1991
A;Fitle: Frog cardiac calsequestrin. Identification, characterization, and subcellula rdium.
A;Reference number: A61230; MUD:91316784
A;Accession: A61230
A;Molecule type: protein
A;Residuas: 1-9 cMCL.
C;Comment: Calsequestrin is a high-capacity and moderate-affinity calcium binding pro
C;Comment: Calsequestrin acts as a calcium buffer, and the release of calcium bound t
C;Comment: The fast skeletal muscle isoform of calsequestrin can be phosphorylated in
C;Superfamily: calsequestrin
C;Keywords: calcium binding; cardiac muscle; glycoprotein; heart; phosphoprotein; ske
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 calliFMRFamide 1 - bluebottle fly (Calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Species: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: A41978
R;Duve, H; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tho Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)
N;Alternate names: blastogen A; scarlet fever toxin
C;Species: Streptococcus pyogenes
C;Date: 10.Nov-1992 #sequence_revision 10-Nov-1992 #text_change 07-Feb-1997
C;Accession: A60108
R;Schlievert, P.M.; Gray, E.D.
Infect. Immun. 57, 1865-1867, 1885
Infect. Immun. 57, 1865-1867, 1888
A;Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and BA;Reference number: A60108; MuID:89254013
A;Reference number: A60108
A;Molecule type: protein
A;Residues: 1-9 <SCH>
C;Keywords: exotoxin
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                           Indels
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100.0%; Pred. No. 1.8e+05;
tive 0; Mismatches 0;
    Pred. No. 1.8e+05; 3; Mismatches 1
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  20.0%;
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Best Local Similarity 50.۰۰
نسم 2; Conservative
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Best Local Similarity
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Best Local Similarity
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2 EGLN 5
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                                                                                                                                                                                R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A;Reference number: PT0222; MUID:91108337
A;Accession: PT0311
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                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major postsynaptic density protein - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 26-May-1994
C;Accession: A42689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
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Proc. Natl. Acad. Sci. U.S.A. 89, 3015-3019, 1992
A/Title: On the identity of the major postsynaptic density protein.
A/Reference number: A42689; MUID:92212958
A/Status: preliminary
A/Robecule type: protein
A/Residues: 1-8 <WUA>
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                                                                    Ig heavy chain CRD3 region (clone 6-100) - human (fragment) C;Species: Homo saplens (man)
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A;Note: sequence extracted from NCBI backbone (NCBIP:63199)
C;Superfamily: caldesmon
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100.0%; Pred. No. 1.8e+05;
iive 0; Mismatches 0;
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R; Ikebe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A:Title: Determination of the phosphorylation sites
A; Reference number: A44873; MUID:91378498
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A Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
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28.6%;
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Best Local Similarity 28.۰۰
احد 2; Conservative
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Matches 2; Conserv
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2 LKVPNIS 8
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7 YL 8
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A; Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi A; Reference number: A41978; MUID:92196111
A; Accession: A41978
A; Status: preliminary
A; Molecule type: protein '
A; Molecule type: protein '
A; Residues: 1-9 < DUV>
C; Keywords: amidated carboxyl end; neuropeptide
F; 9/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Callipheramide 13 - bluebottle fly (calliphora vomitoria)
C;Species: Calliphora vomitoria
C;Species: Calliphora vomitoria
C;Species: Calliphora vomitoria
C;Species: Oscap-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C;Accession: D44787
R;Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A;Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi A;Reference number: A41978; MUID:92196111
A;Reference number: protein
A;Ression: preliminary
A;Accession: protein
A;Residues: 1-9 <DUVA
C;Keywords: amidated carboxyl end; neuropeptide
F;9/Modified site: amidated carboxyl end (Phe) #status experimental
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Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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23.9%; Score 11; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels
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panagrellus
papio anubi
papio hamad
theropithec
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pandalus bo
macaca fusc
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raja clavat
hirudo medi
artioposthi
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panagrellus
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staphylococ
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aplysia cal
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MEDLINE; 92179466.
MEDLINE; 92179466.
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
Isolation, identification and synthesis of locustamyoinhibiting
peptide (LOM-MIP), a novel biologically active neuropeptide from
Locusta migratoria.;
Regul. Pept. 36:111-119(1991).
Regul. Pept. 36:111-119(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OVIDUCT.
-!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBDESOPHAGEAL GANGLION.
PIR; A60065; AKLQIM...
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01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
LOCUSTAMYOINHIBITING PEPTIDE (LOM-MIP).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tranheata; Hexapoda; Insecta; Petrygota; Neoptera; Orthopteroida; Orthoptera; Orthoptera; Acridomorpha; Acridoidea; Acridoidea; Locusta.
Q10582
P81886
P80430
P41486
P81010
P25419
P21142
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P41841
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P19344
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P12677
P166294
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P42993
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P42564
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P81815
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CLP_THICU
CLP_THICU
EAR1_BANRE
FIBB_PAPAN
FIBB_PAPAN
FIBB_THEGE
CXTA_TECTOR
OXYT_CYPCA
OXYT_CYPCA
OXYT_CYPCA
ULAL_TENTA
BIOA_SALIY
GAO_DACDE
IGAO_DACDE
IGAO_CARVI
ANTEL
CARVA
ALI2_CARVA
ALI3_CARVA
A
                                                                                                                                                                                         UNO6_CLOPA
FAR3_HAECO
FAR3_PANRE
                                        FAR3_HOMAM
FUSS_FUSSO
HTE_TENMO
LCK3_LEUMA
RPCH_PANBO
FIBB_MACFU
ISOT_CYPCA
OXYT_RABIT
                                                                                                                                                   OXYT_RAJCL
FAR4_HIRME
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LMIP_LOCMI
P31799;
 LMIP_LOCMI
 calliphora
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vibrio fisc
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macropus eu
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P19913 pseudomonas
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P42296
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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GFRP_MOUSE
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FAR1_CALVO
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LUXE_VIBFI
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TRPI_PSEPU
ALL7_CYDPO
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GAR2_PROCI
UNO6_PINPS
ACT_CARMA
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OXYA_SCYCA
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OXYE_SCYCA
UPA6_HUMAN
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UPA6_HUMAN
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UPA1_HUMAN
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Maximum Match 100%
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ALL5_CYDPO
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Gapop 10.0 , Gapext 0.5
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-!- COFACTOR: MOLYBDENUM.
-!- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
                                                                                                                      Gaps
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01-FEB-1991 (Rel. 17, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
CARBON MONOXIDE DEHYDROGENASE LARGE CHAIN (EC 1.2.99.2) (FRAGMENT).
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Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152.335.34(1989).
-!- CATALITIC ACTIVITY: CO + H(2)O + ACCEPTOR = CO(2) + REDUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R., "Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytochi-like peptides isolated from the spotted dogfish (Scyliorhinus caniculus)."; Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
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Bacteria; Proteobacteria; beta subdivision; Comamonadaceae;
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                                                                             DB 1; Length 9;
8.8e+04;
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  AMIDATION.
387D7DD4472AB6C3 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                            9 AA.
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1060 MW;
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VARIANT 2 2 2
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                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
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Matches 3; Conserv
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AA ;
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MEDLINE; 95062247
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P42996;
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MOD_RES
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Acher R., Chauvet J., Chauvet M.-T.;

"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";

Eur. J. Biochem. 29:12-19(1972).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol.NOV-1995 (Rel. 32, Last annotation update)
ASPAROCIN (ASPARGTOCIN).
Squalus acanthias (Spiny dogfish).
Elkaryota: Metazoa: Chordata: Craniata: Vertebrata: Chondrichthyes;
Elasmobranchii; Squalea: Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ULAH_HUMAN STANDARD; PRT; 9 AA.
p31934;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1995 (Rel. 32, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 94) (FRAGMENT).
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Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;

Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;

"Identification of 2 new neurohypophyseal hormones, valitocin oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, spiny dog-fish (Squalus acanthias).";

C. R. Acad. Sci., D. Sci. Nat. 274.313-316(1972).

-I- SIMILABITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

INTERPO. IPR000981;
-:- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
-:- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PUTERPRO: 1PR000981; -.
PRAM: PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM: 1.
                                                                                                                                                                                                                                                                                                                                Score 15; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 0; Indels
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9 AA; 996 MW; 17F8376EB444404B CRC64;
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                AMIDATION
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66.7%;
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Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichtyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
                                                                                                                      MEDLINE; 95009907.

Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;

Separation and sequencing of familiar and novel murine proteins
using preparative two-dimensional gel electrophoresis.";

Electrophoresis 15:735-745(1994).

--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.0, ITS MW IS: 32 KDA.
                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P32) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. INTERPRO; IPR000981; -.
                                                                                                                                                                                                                                                                                              Score 14; DB 1; Length 9;
Pred. No. 8.8e+04;
1 Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1; Length 9;
                                                                                                                                                                                                                                                       7E73EAB6D05B1AAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17EDD76EB44449DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 8.8e+04;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA.
                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM, PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                     30.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%;
                                                                                                                                                                                                                                                       9 AA; 1102 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1016 MW;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hormone; Amidation.
                                                                                                              TISSUE-FIBROBLAST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PITUITARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHASVATOCIN.
                                                                                                                                                                                                                                                                                                                                                                                    :||
5 IQD 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXYF_SCYCA
ID OXYF_SCYCA
AC P42997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UPA6_HUMAN
P30092;
                                                                                                                                                                                                                                                                                                                                                                   4 VQD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YLN 3
                                                                                                                                                                                                                                        NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YFN
                                                                                             SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
UPA6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC AC
                                                                                                                                                                                                                                                                                                                                                                                               Op
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pollen coat of Brassica napus.";
Planta 208:588-598(1999).
-!- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
SPECIFIC PLASTIDIAL LIPID ORGANELLE.
-!- TISSUE SPECIFICITY: TAPETUM OF ANTHERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Composition and role of tapetal lipid bodies in the biogenesis of the
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus (Rape).
Eukaryota, Viridiplantee, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; eudicotyledons; core eudicots, Rosidae; eurosids II;
Brassicales, Brassicaceae; Brassica.
                                                                                        MEDLINE; 94147969.

Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
Tissot J.-D., Bairoch A., Appel R.D., Hochstrasser D.F.;

"Human liver protein map: update 1993.";
Electrophoresis 14:1216-1222(1993).

"I MISCELLANBOOWS: ON THE ZD-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.5, ITS MM IS: 12 KDA.
SWISS-2DPAGE; P31934; HUMAN.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.4%; Score 14; DB 1; Length 8; llarity 60.0%; Pred. No. 8.8e+04; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                  Length 9;
                                                                                                                                                                                                                                                                                    F1CC7B172AB6DDCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;
                                                                                                                                                                                                                                                                                                                                 32.6%; Score 15; DB 1; Lot 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PLASTIDIAL LIPID-ASSOCIATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                       /FTId=VAR_000001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 AA.
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(Rel. 30, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. TOPAZ; TISSUE-TAPETUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 38, Created)
                                                                                                                                                                                                                                                                                    990 MM;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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Best Local Similarity
3; Conserve
 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
`-haq 3; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 99349136.
                                                                                                                                                                                                                                                                                    9 AA;
                                                                           TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |:|
1 VIDVN 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 VODLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1999
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999
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01-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                     111
4 QDL 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UF02_MOUSE
ID UF02_MOUSE
AC P38640;
                                                                                                                                                                                                                                                                                                                                                                                               ODL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLP_BRANA
P81707:
                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE.
                                                                                                                                                                                                                       NON_TER
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PLP_BRANA

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Gaps

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124 E

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Caps

8 AA.

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"Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
I- MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 4.9, TIS MW IS: 65 KDA.
                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 2) (FRAGMENT).
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                           MEDLINE; 93092937.
Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C01772C455BB06DA CRC64;
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.1%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         944 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.1
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE.
MEDLINE; 92195954.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
8
8 AA;
                                                                                                                                                                                                                                                                                                          TISSUE=PLASMA;
       |: |
2 YMGWMD 7
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2 QESNV 6
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                                                                                                           UPA1_HUMAN
P30087;
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                                                                                                                                                                                                                                                                          [1]
SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
UNSURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P42562,
                                                                                           UPA1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAR3_HIRME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MILTON: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
-!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION
AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION
IN THE BRAIN IS NOT CLEAR.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                                                            "Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992)
-!- MISCELLANBOUGS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5, ITS MW IS: 48 KDA.
SWISS-2DPAGE; P30092; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macropus eugenii (Tammar wallaby), and Jasyurus viverrinus (Southeastern quoll). Basyurus viverrinus (Southeastern quoll). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 88234141.
Fan Z.W., Eng J., Shaw G., Yalow R.S.;
"Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
0
.01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 14) (FRAGMENT).
                                                                                                                                                                                           Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 13; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.1%; Score 12; DB 1; Length 8; 33.3%; Pred. No. 8.8e+04; Live 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SULFATATION.
AMIDATION.
DDCAA68378768B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                          935 MW; 5282F2CAA8676447 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A43001; A43001.
PIR; PQ0012; PQ0012.
PNCERPC; IPR001651; -.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Sulfatation; Hormone.
                                                                                                                                                                                                                                                                                                                                                                                                                             28.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD_RES 2 2
MOD_RES 8 8
SEQUENCE ~ 8 AA; 1064 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Conservative
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Best Local Similarity 33.3
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHOLECYSTOKININ (CCK).
                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                            TISSUE=PLASMA;
MEDLINE; 93092937.
                                                                                                                                                                                                                                                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 LAPGDV 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marsupials."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
CCKN_MACEU
ID CCKN_MACEU
                                                                                                                                                                                                                                                                                                                                                          NON_TER
SEQUENCE
                                                                                                                                            SEQUENCE.
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                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Indentification of Reamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                          Hirudo medicinalis (Medicinal leech).
Eukaryota: Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Score 12; DB 1; Length 8;
Pred. No. 8.8e+04;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 11; DB 1; Length 4;
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD_RES 4 4 AMIDATION.
SEQUENCE 4 AA; 598 MW; 69D4073B3000000 CRC64;
                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEFTIDE YLRF-AMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.9%; Scor.
100.0%; Pred. No. .
0; Mismatches
                                                                                                                                                                                                                                                4 AA.
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PRCT_PERAM RESULT

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                                                                                                                                                                                                 Cowden C., Stretton A.O.W.;
"AF2, an Ascaris neuropeptide: isolation, sequence, and bloactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                  MALDE A.G., Shaw C., Bowman J.W.;

"The EMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the free-living nematode. Panagrellus redivivus (Nematoda, Rhabditida).";
Parasitology 109:351-356(1944).

-I- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.

-I- TSSUE SPECTERCITY: FOUND IN THE NERVE CORDS AND A VARIETY OF GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.

-I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1998) to the SWISS-PROT data bank.
-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                          Ascaris suum (Pig roundworm) (Ascaris lumbricoldes), and Panagrellus redivivus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridode; Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN (P35) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23.9%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 8.8e+04; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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69D4073B5B11E350 CRC64;
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01-JUL-1993 (Rel. 26, Last sequence update) 01-FEB-1996 (Rel. 33, Last annotation update) FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
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SWISS-2DPAGE; P99025; MOUSE.
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Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
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                                                                                                                                                                                                                                                                                                  SPECIES=P.REDIVIVUS;
MEDLINE; 95060998.
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Matches 2; Conserv
                                                                                                                                                                                         MEDLINE; 93324431.
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                                                                                                                                                                   SPECIES-A.SUUM;
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P99025;
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NON_TER
SEQUENCE
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MEDLINE; 76074708.
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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O'Shea M., Adams M.E.;
"Pentapeptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stangler J., Diroksen H., Keller R.;
Stangler J., Diroksen H., Keller R.;
"Identification and immunocytochemical localization of proctolin
pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).

-!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.

-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
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                                                                                                                                                                                                     Limulus polyphemus (Atlantic horseshoe crab), and Carcinus maenas (Common shore crab) (Green crab). Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pletrygota: Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
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                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                          5 AA.
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                                                                                                                                                                                       Periplaneta americana (American cockroach),
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                                                                          PRT;
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P31890;
01-JUL-1993 (Rel. 26, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Life Sci. 17:1253-1256(1975).
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                                                                          STANDARD;
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SPECIES-L. POLYPHEMUS;
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Best Local Similarity
Local 2; Conserve
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PIR; A60411; A60411.
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MEDLINE; 86232789.
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                                                                          PERAM
                                                                                                                                                                  PROCTOLIN.
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2 YL 3
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P01373;
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Best Local Si
Matches 2;
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SEQUENCE.
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FAR2_CALVO
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFWRFAMIDE 1.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera; Endopteryota; Diptera; Brachyceryota; Opestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE, 92082847.

Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.;

"Structure and biological activity of crustacean gastrointestinal peptides identified with antibodies to gastrin/cholecystokinin.";

Biochimie 73:1233-1239(1991).

-i FOWGTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.

-i - SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.

PIR; A48398; A483998.
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-!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rehfeld J.F., Thorpe A.; "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly
                                                                                                                                                                                                                                                                                             Nephrops norvegicus (Norway lobster).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

Nephropoidea; Nephropidae; Nephrops.
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MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%; Score 11; DB 1; Length 9; 100.0%; Pred. No. 8.8e+04; iive 0; Mismatches 0; Indels
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29D00699CAB6C6C7 CRC64;
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                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
GASTRIN/CHOLECYSTOKININ-LIKE PEPTIDE D1.
                                                                                                                                                             9 AA.
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9 AA; 1169 MW;
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Best Local Similarity
Matches 2; Conserv
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TISSUE=STOMACH;
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ID FAR1_CALVO
1 YL 2
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2 YL 3
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SEQUENCE
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P24816;
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Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridea; Calliphora.
                                                                                                                                                                                                                                                                                                                           Calliphora vomitoria (Blue blowfly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Oestroidea; Calliphoridae; Calliphora.
                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-1- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
-1- SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly Calliphora vomitoria.";

Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly Calliphora vomitoria";
                                                Indels
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             Length 9;
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29D00699CAB6C5A7 CRC64;
             DB 1; Le
8.8e+04;
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Pred. No. 8.8e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                         (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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Last annotation update)
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             Score 11;
Pred. No.
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100.0%; Pre
23.9%; Scor.
100.0%; Pre
0; )
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01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last anno
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MOD_RES 9 9
SEQUENCE 9 AA; 1128 MW
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                                                  Conservative
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nes 2; Conserv
             Query Match
Best Local Similarity
Matches 2; Conserv
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Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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 MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
calliphora vomitoria.",

Proc. Natl. Acad. Sci. U.S. A. 89:2326-2330(1992).

-! SIMILARITY: BELONGS TO THE FARP (FWRFAMIDE RELATED PEPTIDE)
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P41862;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIPMRFANDE 7.
CALLIPMRFANDE 7.
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Pred. No. 8.8e+04;
                                                                                                                                                                                                                              Length 9;
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96D10699CAB6D865 CRC64;
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39D10699CAB6D867 CRC64;
                                                                                                                                                                                                                            Score 11; DB 1; L. Pred. No. 8.8e+04;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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9 AA; 1058 MW;
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                                                                                                                                                   Neuropeptide; Amidation.
MOD_RES 9 9
SEQUENCE 9 AA; 1068 MW
                                                                                                                                                                                                                                                            Conservative
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Best Local Similarity
'-hos 2; Conserve
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Best Local Similarity
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FAR7_CALVO
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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Calliphora vomitoria (Blue blowfiy).

Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;

PLETYGOTA; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Oestroidea; Calliphoridae; Calliphora.
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Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
-!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED SALIVARY GLAND OF CALLIPHORA.
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Fehffeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated callifmRFamides) from the blowfly
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                                                                                                                                                   DB 1; Length 9;
8.8e+04;
hes 0; Indels
                                                                                         AMIDATION.
2F0B0699CAB6C5A7 CRC64;
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31730699CAB6D457 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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                                           FAMILY.
PIR; C41978; C41978.
Neuropeptide; Amidation.
MOD_RES
SEQUENCE 9 AA; 1114 MW;
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MOD_RES 9 9
SEQUENCE 9 AA; 1182 MW
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Matches 2; Conserv
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P41859;
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Vibrio fischeri.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea; Calliphoridae; Calliphora.
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Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
calliphora vomitoria.".

Proc. Natl. Acad. Sci. U.S. A. 89:2326-2330(1992).

Proc. Natl. Acad. Sci. U.S. A. 89:2326-2330(1992).
                                                                Rehfeld J.F., Thorpe A.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
(calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
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                                              MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                          23.9%; Score 11; DB 1; Length 9; 100.0%; Pred. No. 8.8e+04; ive 0; Mismatches 0; Indels
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                                                                                                                                                      AMIDATION.
E1D10699CAB6D86A CRC64;
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22D10699C87AB6D8 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRFAMIDE 13.
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                                                                                                                                                                                                                                                                                                   9 AA.
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                                                                                                                                                               9 AA: 1081 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation.
MOD_RES 9 9
SEQUENCE 9 AA: 1028 MM
                                     TISSUE=THORACIC GANGLION;
                                                                                                                                  PIR; G41978; G41978.
Neuropeptide; Amidation.
MOD_RES 9 9 9
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Best Local Similarity
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Best Local Similarity
2; Conserva
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P24272;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 site for the lux operon.";
J. Bacteriol. 172:6797-6802(1990).

-! FUNCTION: ACYL-PROTEIN SYNTHETAGE ACTIVATES TETRADECANOIC ACID.

IT IS A COMPONENT OF THE FATTY ACID REDUCTASE COMPLEX RESPONSIBLE FOR CONVERTING TETRADECANOIC ACID TO THE ALDEHYDE WHICH SERVES AS SUBSTRATE IN THE LOCIFERASE-CATALYZED REACTION.

-!- CATALYIC ACTIVITY: ATP + AN ACID + PROTEIN = AMP + PYROPHOSPHATE + AN ACYL-PROTEIN THIOLESTER.

-!- PATHWAY: SECOND STEP IN THE BIOLUMINESCENT FATTY ACID REDUCTASE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last annotation update)
TRYPSIN-MODULATING OOSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycerygota; Opestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";
Regul: Pept. 50:61-72(1994).
-:- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGOT WHICH INDIRECTLY REDUCES THE VITELLOGENIN CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCTTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                 Swartzman E., Rapoor S., Graham A.F., Meighen E.A.;
"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENT.

DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94211930.
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
LONG-CHAIN-FATTY-ACID--LUCIFERIN-COMPONENT LIGASE (EC 6.2.1.19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6AA3303000000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10; DB 1; Ler
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                            (ACYL-PROTEIN SYNTHETASE) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M62812; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.7%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER 1 1 1
SEQUENCE 3 AA; 374 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Luminescence; Ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 91072226
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30-MAY-2000 (Rel. 39, Last annotation update)
                     Cydia pomonella (Codling moth).
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuropeptide; Amidation.
                                                                                                                                                                                                                                    Local Similarity
nes 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 2; Conserv
                                                                                        TISSUE=LARVA;
                                                                                                                                                                                                                                                                                          4 DFGL 7
                                                                                                                                                                                                                                                                                                                                               FAR2_PROCL P38498;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 DLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DRN 3
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                                                                                                                                                                                                                                                                     DLNL
                                                                                                                                                                                                                           Query Match
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                                                                              SEQUENCE
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UNO6_PINPS
                                                                                                                                                                                                                                     Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                              Gaps
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1- FUNCTION: ACTUTATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDUCECLYCEROL PHOSPHATE), TRYPT IS BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.

-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
                                                                                                                                                                                                                                                                                                                       MEDLINE; 89333826.
Eberly L., Crawford I.P.;
"DNA sequence of the tryptophan synthase genes of Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iryptophan biosynthesis; Transcription regulation; Activator;
                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.7%; Score 10; DB 1; Length 6; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                       Length 6;
                     61E72451B7642000 CRC64;
                                                                                                                                                                                                 01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
TRPBA OPERON TRANSCRIPTIONAL ACTIVATOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA; 683 MW; 77672AA1EDD6F000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                     21.7%; Score 10; DB 1; Le
100.0%; Pred. No. 8.8e+04;
tive 0; Mismatches 0;
                                                                                                                                                                              6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 39, Created)
(Rel. 39, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PS00044; HTH_LYSR_FAMILY; PARTIAL
                                                                                                                                                                              PRT;
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EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X13299; CAA31660.1; -.
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Best Local Similarity 100.vv
Thes 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                     Biochimie 71:521-531(1989).
                     695 MW;
                                                                            Conservative
                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000847
                                                      Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                        Pseudomonas putida.
                                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=PPG1 C1S;
                     6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALL7_CYDPO
P82158;
                                                                                                                                                                            TRPI_PSEPU P36414;
                                                                                                NF 9
                                                                                                                     S
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                     SEQUENCE
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            Hormone
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Gaps
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Peptides 4:137-143(1993).
-I-FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
-I-FUNCTION: OF SEMI-ISOLATED HEARTS. INCREASES THE AMPLITUDE OF
CONTRACTIONS OF SEMI-ISOLATED HEARTS. IN ABDOMINAL EXTENSOR MUSCLE.
EXCITATORY POSTSYNAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Lepidoptera, Glossata, Ditrysia,
Tortricoidea, Tortricidae, Olethreutinae, Cydia.
                                                                                                                                                                                           MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).
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01-0CT-1994 (Rel. 30, Last sequence update)
01-0NT-1995 (Rel. 32, Last annotation update)
CARDIOEXCITATORY FMRFANIDE HOWOLOG DF2.

Procambarus clarkii (Red swamp crayfish).

Eukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mercier A.J., Orchard I., Tebrugge V., Skerrett M.; "Isolation of two FMRFamide-related peptides from crayfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.7%; Score 10; DB 1; Length 7; 50.0%; Pred. No. 8.8e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.7%; Score 10; DB 1; Length 7; 66.7%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                      Neuropeptide; Amidation.

MOD_RES 7 7 7 AMIDATION.

SEQUENCE 7 AA; 873 MW; 672879CABB569350 CRC64;
                                                                                                                                                                                                                                                                                                                                                        -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AMIDATION. 69D40729C4540AC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Astacoidea; Cambaridae; Procambarus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UN06_PINPS STANDARD; F
P81675;
15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-PERICARDIAL ORGANS; MEDLINE; 93248032.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA; 967 MW;
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us-09-529-121-9.lim9.rsp

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30-MAY-2000
30-MAY-2000
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                                               AKH_MELML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LN 3
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SEQUENCE
                                                                                                                                                                                       SEQUENCE.
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                                  AKH_MELML
                                                δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A transaldolase. An enzyme implicated in crab steroidogenesis.";
Endocrine 5:23-32(1996).
-!- FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED
IN VARIOUS TYPES OF CELLS.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- STELMIAND PI OF THIS PROTEIN IS:
6.8, ITS MW IS: 46 KDA.
-!- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N141) (FRAGMENT).
Pinus pinaster (Maritime pinaster (Maritime Pinus Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinasceae; Pinus.
                                                                                                MEDLINE; 99274088.
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Seperation and characterization of needle and xylem maritime pine
                                                                                                                                                     Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.6, ITS MW IS: 25 KDA.
                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S.,
Baghdassarian D.;
                                                                                                                                                                                                                                                                                                                                                                                                                      Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 1; Length 8;
Pred. No. 8.8e+04;
3; Mismatches · 0; Indels
                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                       Score 10; DB 1; Length 7; Pred. No. 8.8e+04; 1; Mismatches 1; Indels
                                                                                                                                                                                                         7 AA; 823 MW; 69D76724486B5740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1424005AB2CAAEB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                          8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00406; ACTINS_1; PARTIAL.
PROSITE; PS00432; ACTINS_2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.7%;
25.0%;
                                                                                                                                                                                                                                       21.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                976 MW;
                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 50.0
انامع 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 21.7
Best Local Similarity 25.0
Matches 1; Conservative
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR000279;
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                                                                                                                                                                                                                                                                                                                                                                                                             ACTIN (FRAGMENT).
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                                                                                       TISSUE-NEEDLE;
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P80709;
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SEQUENCE
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Gaede G.; "A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."; Blochem. J. 275:671-677(1991).
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Bukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIO1. Chem. Hoppe-Seyler 373:133-142(1992).

-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA CANDIACA AFFER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR; S15422; S15422.
PIR; S21663; S21663.
                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=M.MELOLONTHA, AND G.STERCOROSUS; TISSUE=CORPORA CARDIACA; MEDLINE; 91248100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                 Geotrupes stercorosus (Dor beetle), and
Pachnoda marginata (Flower beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
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Pred. No. 8.8e+04;
                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                          Melolontha melolontha (Cockchafer),
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100.0%; Pred
0; }
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Neuropeptide; Amidation; Flight.
                                              01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last seq
01-FEB-1994 (Rel. 28, Last ann
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(Rel. 39, Last anno
                                                                                                                                       ADIPOKINETIC HORMONE (AKH)
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STANDARD;
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Best Local Similarity
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P82156;
30-MAY-2000 (
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Gaps

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"Serum antibody responses of cats to soluble whole cell antigens of feline porphyromonas gingivalis.";
Vet. Microbiol. 73:37-49(2000).
-!- SIMILARITY: TO P.GINGIVALIS HEMAGGLUTININ A.
Antigen. 8
NON_TER. 8
SEQUENCE 8 AA; 989 MW; 9554540326CB476D CRC64;
                                                                                                                                 Ouery Match 21.7%: Score 10; DB 1; Length 8; Best Local Similarity 40.0%; Pred. No. 8.8e+04; Matches 2; Conservative 1; Mismatches 2; Indels
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Job time: 4567 sec
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Kukaryota: Metazoca: Chordata; Craniata: Vertebrata; Euteleostomi;
Lepidosauria: Squamata: Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Bothrops.
TISSUE-LARVA;

MEDLINE; 98054539.

MEDLINE; 98054539.

Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

"I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

Neuropeptide; Amidation.

MOD_RES 8 8

SEQUENCE 8 AA; 898 MW; 922879GABB58640D CRC64;
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0
                                                                                                                                                                          21.7%; Score 10; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
44 KDA IMMUNGENIC PROTEIN (FRAGEMENT).
                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
10-bEC-1998 (Rel. 37, Last annotation update)
ANGIOTENSIN-LIKE PEPTIDE II (FRAGMENT).
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MEDLINE; 20198497.
Norris J.M., Love D.N.;
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 2; Conserva
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P81886;
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Q10582;
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SEQUENCE
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ANG2_BOTJA
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us-09-529-121-9.lim9.rsp

| CEA derived HLA-A2 SHC phosphopeptide Membrane dipeptida Immunogenic peptid | HIV pol protein de Carcinoembryonic a | Sequence used to d Immunogenic peptid WT1 derived immuno WT1 derived immuno | WT1 derived immuno WT1 derived immuno WT1 derived immuno Peptide mimetic of | Desmoglein cell ad Peptide mimetic of Desmoglein cell ad | Peptide fragment (Peptide fragment (| HIV(B35)GAG-8, num Control peptide 92 | SH2 domain binding SH2 domain binding | SH2 domain binding Synthetic polypept Carcinoembryonic a T cell epitope/HHC | Desmoglein cell ad | Endothelin antagon Endothelin C-termi Human secreted pro | Hepatitis C virus- HLA-Al HCV antigen | Human leucocyte an Immunogenic peptid | Tumour antigen pro HLA binding peptid | Human NEDD8 protei 4-Aminobenzoyl-Tyr | Interleukin-6 anta Peptide antagonist | Peptide antagonist | Viral inhibiting p | MCF peptide #32. B. thuringiensis t | Peptide comprising Antigen fragment 8 | MHC class I restri | Peptide comprising | SH2 binding peptid | SH2 binding peptid | Antigenic P60 pept | Immunogenic peptid | Carcinoembryonic a | eptide antagonis | 176-18 | | | | ··. | |
|--|---------------------------------------|--|--|--|---------------------------------------|--|---------------------------------------|---|--------------------|--|--|---|---|--|---|-----------------------------|-----------------------------|--|--|--|---------------------------|--------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------------------------------------|--|---------------|----------|--|--|
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| 23 50. 23 50. 23 50. | 23 50. | 22 47. 22 47. 22 47. 22 47. | 23 22 47.8 24 22 47.8 25 22 47.8 26 21 45.7 | 21 45. 21 45. | 21 45. | 21 45. | 21 45. | 21 45. 21 45. 21 45. 21 45. | 21 45. | 20 43. 20 43. 20 43. | 20 43. 20 43. | 20 43. | 20 43. | 20 43. 19 41. | 19 4 1. 19 4 1. | 19 41. | 19 41. | 19 41. 19 41. | 19 41. 19 41. | 19 41. | 19 41. | 19 41. | 19 41. | 19 41. | 19 41. | 19 41. | 18 39. | 18 39. | | | RESULT 1 | Y09526 ID Y09526 standard; peptide; | . 9 |
| 4.5 Compugen Ltd. | | ; Search time 107.12 Seconds (without alignments) 2.873 Million cell updates/sec | | | es | ters: 61695 | | | | neseqp/AA1980.DAT:* neseqp/AA1981.DAT:* | neseqp/AA1982.DAT:* neseqp/AA1983.DAT:* | neseqp/AA1984.DAT:* neseqp/AA1985.DAT:* | neseqp/AA1986.DAT:* neseqp/AA1987.DAT:* | neseqp/AA1989.DAT:* eneseqp/AA1989.DAT:* | eneseqp/AA1990.DAT:* eneseqp/AA1991.DAT:* | eneseqp/AA1992.DAT:* | eneseqp/AA1994.DAT:* | gcgdata/geneseq/geneseqp/AA1995.DAT:* gcgdata/geneseq/geneseqp/AA1996.DAT:* | 'gcgdata/geneseq/genesegp/AA1997.DAT:* 'gcgdata/geneseq/genesegp/AA1998.DAT:* | eneseqp/AA1999.DAT:* eneseqp/AA2000.DAT:* | icted by chance to have a | s of the result being pr | | | | Description | Carcinoembryonic a | Carcinoembryonic a Immunogenic peptid | immunogenic peptid Peptide antagonist | – | Jas | Peptide comprising Elastase inhibitor | Human carcina-embr CEA synthetic pept |
| GenCore version Copyright (c) 1993 - 2000 | protein search, using sw model | December 16, 2000, 03:07:19 | US-09-529-121-9 46 1 YLNVQDENL 9 | BLOSUM62 Gapop 10.0 , Gapext 0.5 | 268485 seqs, 34193795 residues | hits satisfying chosen parameters | length: 0 length: 9 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries | 36.4 | , | <pre>3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:* 4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:*</pre> | /SIDS6/gcgdata/geneseq/geneseqp/AA1984.DAT:/SIDS6/gcgdata/geneseq/geneseqp/AA1985.DAT: | SIDS6/gcgdata/geneseq/geneseqp/AA1986.DAT:* |): /SIDS6/gcgdata/geneseq/ge .0: /SIDS6/gcgdata/geneseq/g | .1: /SIDS6/gcgdata/geneseq/g 2: /SIDS6/gcgdata/geneseq/g | 3: /SIDS6/gcgdata/geneseq/g | 5: /SIDS6/gcgdata/geneseq/g | .b: /SIDS6/gcgdata/geneseq/g | /SIDS6/gcgdata/geneseg/ /SIDS6/gcgdata/geneseg/ | /SIDS6/ | the number of | than or equal | ; | SUMMARIES 8 | ery | Watch Length DB ID | 9 20 | 55.2 9 20 Y47685 | 5 18 | 8 17 8 20 | 9 11 | 9 16 9 16 | 9 18 9 19 |
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13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                               or artigonists (Ib) of human carcinoembryonal artigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                       describes peptides (A) that comprise agonists (Ia)
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                                                     Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                            Peptide agonists and antagonists of carcinoembryonal antigen
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Pred. No. 2.1e+05;
1; Mismatches 2; Indels
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                                 Carcinoembryonic antigen peptide agonist SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                   5; Page 53; 72pp; English.
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Matches 6; Conservative
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or artagonists (ID) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but cEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic peptide having a human leukocyte antigen binding motif #2296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tunmour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 26; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 53; 72pp; English.
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                                                                                                                                 98WO-US19794.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                    Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-326544/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 5; Conser
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1 ylsgadinl
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W09919478-A1.
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                                                                                                                                 22-SEP-1998;
                                                                                                                                                                                                  10-0CT-1997;
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                                                                22-APR-1999
                                                                                                                                                                                                                                                                                                                                 Barzaga E,
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Southwood

Sette A,

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having a human major histocompatibility complex (MHC) class I (also having a human major histocompatibility complex (MHC) class I (also having a human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cyctotoxic T cell response against the antigen from which the peptide is derived.

Cyctoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tummour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) are prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or useful diagnostically, and can be used to induce a cytotoxic T cell vith the peptide e.g. to produce CTLEs x vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide antagonist (FCE 28883) of cellular mitogenesis and motogenesis.
                                                                                                                        New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                            Y45390 to Y48214 represent specifically claimed immunogenic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide antagonist; mitogenesis; motogenesis; proliferative disease; cancer; tumour; phosphotyrosine; motif; SH2 domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.2%; Score 24; DB 20; Length 9; llarity 57.1%; Pred. No. 2.1e+05; Conservative 2; Mismatches 1; Indels
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                            Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "C-terminal amide"
                            Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                Claim 1; Page 125; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W45373 standard; peptide; 5 AA.
                         Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-EP00595
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                                                                        WPI; 1999-551214/46.
                         Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 4; Conserv
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|3 ylhiqs1 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                            Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W45373;
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W45373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HA-AZ.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The pheroautically and for immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                             New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 24; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 1; Indels
                                                Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapeutically and for immunisation as above.
                                              Celis E,
                                                                                                                                                                                                                  Claim 1; Page 119; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y47858 standard; Peptide; 9 AA.
                                              Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.2%;
57.1%;
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(EPIM-) EPIMMUNE INC.
                                                                                            WPI; 1999-551214/46.
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Best Local Similarity
Matches 4; Conserv
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3 ylhiqs1 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Forssmann W,
Staendker L;
                 MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YLNVQD
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                                                                                                                Peptide(s)
associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staendker
                                     Patel DV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                      formula:
                     Gordeev
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Y25497
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                                                                                                                                                                                                                                                              a phosphorylated tyrosine residue, which can bind to a cytosolic signal transducer and inhibit binding to a receptor tyrosine kinase or to another tyrosine phosphorylated transducer. It can interfere with cell motility, cell proliferation, cell invasiveness and tubulogenosis. It can be used in the control or treatment of proliferative diseases such as cancer, tumour growth and/or metastasis, and psoriasis, and in the control or treatment of inflammatory, allergic, autoimmune, viral and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Core peptide; src homology region 2 binding peptide; SH2; cell growth; differentiation; regulation; receptor tyrosine kinase pathway; cancer; signal transduction pathway; non-insulin dependent diabetes; insulin-resistant diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphotyrosine,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                  The present sequence represents a specifically claimed peptide with
                                                                                                                                                     treating e.g. proliferative, inflammatory, allergic, auto:immune,
                                                                                                                                    New peptide with phosphorylated tyrosine residue - is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "opt. selected from tyrosine, phosphotyrc
tyrosine isosteres, and phosphotyrosine
isosteres"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and phosphotyrosine
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tyrosine isosteres, and phosp
isosteres"
                                       Corradi F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 18; Le
Pred. No. 2.1e+05;
1; Mismatches 0;
                                       Comoglio P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                         viral and cardiovascular diseases
                                                                                                                                                                                                           Claim 11; Page 72; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (AFFY-) AFFYMAX TECHNOLOGIES NV.
(PHAA ) PHARMACIA & UPJOHN SPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
80.0%;
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                                     Battistini C,
Giordano P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SH2 binding peptide #16.
                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
                                                                                            WPI; 1997-424973/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W12586 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1:111
1 yvnvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1997
                                     Bardelli A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-AUG-1996
                                                           Rosa S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W12586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Insulin-like growth factor binding protein; IBP; immunoprotective; anti-inflammatory; cytostatic; treatment; muscle loss; shrinkage; wastepoporosis; diabetees; amyloid lateral sclerosis; neuropathy; inflammation; cancer; neoplastic disease; growth disturbance; muscle; bone apparatus; wound healing; bone healing; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27 = phosphotycosine or its isostere;
28 = asparagine or its isostere;
the amino terminus is acylated, and the peptide is less than 14
residues in length, with the proviso that if 27 is phosphotyrosine
and 28 is asparagine, then the peptide is not GDGZ7XZ8XPLL.
These SH2 binding peptides are used to treat of diagnose diseases
associated with aberrant cell growth, differentiation or regulation
which is associated with defects in receptor tyrosine kinase pathways,
by partially blocking or inhibiting a cellular signal transduction
pathway. The disease may be cancer, a developmental or differentiation
disease or insulin-resistant (or non-insulin dependent) diabetes.
                                                                                                                                                                                                                                                                                                                                                                                2 (SH2)
to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                      which bind to SH2 domains \cdot are used to treat diseases with aberrant cell growth, differentiation or regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis; nervous system; lymph gland; stomach; intestinal tract
                                                                                                                                                                                                                                                                                                                                                                         The sequences given in W12571-614 represent src homology region binding peptides which contain a core peptide which corresponds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                      associated with aberrant cell growth, differentiation or regassociated with defects in receptor tyrosine kinase pathways
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 23; DB 17; Length 8; Pred. No. 2.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insulin-like growth factor binding protein fragment #32.
   Kim MH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mostafavi H, Obendorf M,
Hart CP,
                                                                                                                                                                                                                                                                                                             Claim 14; Page 118; 203pp; English
, Gordon E, Grove JR,
Szardenings AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y25497 standard; peptide; 8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               = any D- or L- amino acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97DE-1057250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z7-X-Z8-X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kling L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FORS/) FORSSMANN W.
                                                                                                   WPI; 1996-371373/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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page 34; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-060954/08.
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||||
1 lgvqdl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LNVQDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                        Claim 6;
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R69827;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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R69827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
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                                                                                                                                                  protein (IBP) constructed using the formula R1-C-X1-PNC-X2-QC-X3-CMCV-X2-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3-QC-X3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bones, muscles, nervous systems, lymph glands, stomach/intestinal tracts, inmune systems, for diabetes, inflammatory and neoplastic processes and also as a marker for cancer. This sequence represents a specific claimed example of a peptide which can occupy the R2 position of the IBP of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                      This invention describes a novel insulin-like growth factor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Elastase; inflammation; genetic diseases; neoplasm; tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified human elastase inhibitor - with therapeutic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23; DB 20; Length 8;
Pred. No. 2.1e+05;
!; Mismatches 1; Indels
                                        An insulin-like growth factor binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human elastase inhibitor peptide.
                                                                                        Claim 10; Page 18; 26pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R06899 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0 Best Local Similarity 66.7 Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnostic applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BLOO-) CENT BLOOD RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YLNVQD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||||:
3 yfnvqn 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nvention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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R06899
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This peptide is a tyrosine-contg, mol. representing a site of tyrosine phosphorylation. The peptides of the invention comprise a portion of the intracellular region of the human hepatocyte growth factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
This is a constituent peptide of a purified human elastase inhibitor (EI) which is capable of forming a covalent complex with elastase and acting as an inhibitor of the elastinolytic activity of elastase. The EI is useful in the treatment of conditions such as cystic fibrosis or bronchiectasis. The Abs may be used e.g. to diagnose rheumatological diseases, idiopathic diseases and inflammatory diseases or as a diagnostic tool for e.g. neoplastic or genetic diseases. The corresp. gene may be used in gene replacement therapy. See also R06900-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular region; human hepatocyte growth factor; hHGF; receptor; cytosolic signal transducer binding; cell proliferation; movement; extracelllular matrix invasion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide(s) which bind to a cytosolic signal transducer - used for interfering with pathways leading to cell proliferation and motility, for treating neoplastic disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 23; DB 11; Length 9; 83.3%; Pred. No. 2.1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide comprising a part of hHGFR intracellular region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "optionally phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FARM ) FARMITALIA ERBA SRL CARLO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 10; Page 64; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R69827 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Gln-OH'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "H-Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94WO-EP01943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93GB-0013528
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T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                   Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                          96EP-0203670
96EP-0201145
                                                                                                                                                                       97WO-NL00229
                               11-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YLNVQDLNL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: :|||
| ylsganlnl
                                                                                                              Homo sapiens
                                                                                                                                                                      28-APR-1997;
                                                                                                                                                                                          23-DEC-1996;
26-APR-1996;
                                                                                                                                WO9741440-A1
                                                                                                                                                    06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W77134;
             W39723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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    δý
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(HHGFR), and can generally reproduce potential recognition motifs for the SH2 domains of intracellular (cytosolic) signal inducers. The peptides can interfer with pathways leading to cell proliferation, movement and extracellular matrix invasion. They can be used to inhibit growth of neoplastic cells and to prevent metastatic spreading.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding human monocyte elastase inhibitor - used to develop prods. for diagnosis and therapy of conditions involving elastase
                                                                                                             ;
0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptides given in R64148-58 are tryptic digests of human monocyte elastase inhibitor (hMEI) (R64159), and were used to design oligonucleotide probes for the isolation of the hMEI gene (Q75377).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 23; DB 16; Length 9; 83.3%; Pred. No. 2.1e+05; ive 0; Mismatches 1; Indels
                                                                                        Score 23; DB 16; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                              Elastase inhibitor; monocyte; probe; hybridization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Column 25-26; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W39723 standard; peptide; 9 AA.
                                                                                                                                                                                                 R64152 standard; Peptide; 9 AA.
                                                                                        50.0%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                          89US-0314383
                                                                                                                                                                                                                                                                                                                                                                            89US-0314383.
                                                                                                                                                                                                                                                          Elastase inhibitor peptide
                                                                                                                                                                                                                                                                                                                                                                                                           (BLOO-) CENT BLOOD RES INC
                                                                                                                                                                                                                                        07-AUG-1995 (first entry)
                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or elastase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1995-021883/03
                                                                                                                                                                                                                                                                                                                                                                                                                             Remold-O'Donnell E;
                                                                                        Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ||||
|gvgdl:6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LNVQDL 7
                                                                                                                              1 YLNVQ 5
                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1989;
06-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                         23-FEB-1989;
                                                                                                                                                                                                                                                                                                                    US5370991-A.
                                                                                                                                                                                                                                                                                                                                       06-DEC-1994
                                                                                                                                         |:||
| S yvnvq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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W39723
                                                                                                                                                                               10
                                                                                                                                                                               RESULT
R64152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability chast indicule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides W39430-W39734 are used in a novel method for the selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                           the
                                                                                                            Van Der Burg SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                Method of selecting T cell peptide epitope(s) - by measuring stability of HLA class I-peptide complexes on intact B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23; DB 18; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrosinase; tyrosinase cytotoxic lymphocyte response; cytotoxic T lymphocyte; cysteine-depleted; melanoma.
                                                                                                         Toes REM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                 (SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
                                                                                                                                                                                                                                                                                                                                                         Example 3; Page 85; 109pp; English.
                                                                                                         Offringa R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEA synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W77134 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC Class I allele HLA-A2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-NOV-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Conservative
(UYLE-) RIJKSUNIV LEIDEN
                                                                                                     Kast WM, Melief CJM,
                                                                                                                                                                            WPI; 1997-549891/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (UEA). The peptides can bind to a human carcinoembryonic antigen (HEA), HLA-A2.1 and are used to examplify the method of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (MPCs) pretreated with presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated composition can then be administered to the patient. The activated CTLS with be used for treating cancers, immune disorders, viral infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SHC phosphopeptide; binding; src homology 2 domain; SH2 domain; Grb2; signal transduction protein; non-phosphorylated; inhibition; treatment; hyper-proliferative disease; human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hepatitis, bacterial infection, fungal infection, malaria or
                                                                               Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHC phosphopeptide capable of binding to the SH2 domain of Grb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%; Score 23; DB 19; Length 9; 55.6%; Pred. No. 2.1e+05; ive 2; Mismatches 2; Indels
  Tsai V;
Southwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "phosphorylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                      Example 6; Page 75; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W46895 standard; peptide; 9 AA.
Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97WO-US12501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-0021858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEOU ) UNIV GEORGETOWN.
                                     WPI; 1998-437445/37
Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                               presenting cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YLNVQDLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ylsganlnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9802176-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JAN-1998.
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W46895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W46895
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The peptide epitope W77119-W77138 were created for human tumour-specific cytocoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific timunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                                                                                       Disease specific immunogen – comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepetitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                        Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23; DB 19; L. Pred. No. 2.1e+05; 2; Mismatches 2;
                                                                                                                                                                                                                                                                        Kittlesen D,
                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                              (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50.0%;
55.6%;
                                                                                                                                        98WO-US01592.
                                                                                                                                                                                    97US-0037781.
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                                                                                                                                                                                                                                                                        Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                               WPI; 1998-437388/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YLNVQDLNL 9
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| ylsganin| 9
                                                                                                                                                                                                                                                                     Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                       WO9833810-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-JAN-1998;
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                                                                                                                                                                                    30-JAN-1997;
                                                                                                                                          29-JAN-1998;
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                                                                                                06-AUG-1998
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                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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W70045;

RESULT 13 W70045

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Example 6; Page 144; 193pp; English.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a SHC phosphopeptide that is capable of binding to the str homology 2 (SH2) domain of GTb2. GTb2 is a signal transduction protein. The specification describes a non-phosphorylated peptide (W46896) that binds to the SH2 domain of Grb2 with affinity similar to, or greater than, that of the present sequence. This non-phosphorylated peptide contains a tyrosine residue that has not been modified by phosphate or similar charged group. The non-phosphorylated peptide is used to inhibit a signal transduction process that involves binding of a phosphorylated protein or peptide to the SH2 domain of a signal transduction protein, particularly GTb2. It is used specifically for treatment of hyper-proliferative diseases, especially
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Pred. No. 2.1e+05;
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26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide having a human leukocyte antigen binding motif #2266.
The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue or for treating an organ or tissue pathology, where the organ or versue is selected from prostate, lung, skin, retina, pancreas, gut, meaning and administrate of liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). Y48618 to Y49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                 Gaps
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ID Y47655 standard; Peptide; 9 AA.
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                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                    Query Match
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us-09-529-121-9.lim9.rag

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vaccines
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                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat shock protein; HSP; complex; denatured protein matrix; antigen; vaccine; allergic disease; treatment; susceptibility; Th2; skin rash; allergic reaction; asthma; pol protein.
e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytocoxic T cell response, by contacting a cytocoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthesizing heat shock protein complexes using a denatured protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel method for synthesizing heat shock
                                                                                                                                                                                                          ;
0
                                                                                                                                                                                Length 9;
                                                                                                                                                                             Score 23; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                HIV pol protein derived peptide fragment #14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1C; 33pp; English.
                                                                                                                                                                                                                                                                                                                                Y25242 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYNE-) UNIV NEW MEXICO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0986234.
97US-0985548.
                                                                                                                                                                              50.0%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US25734
                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                             Query Match 50.0
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wallen ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-394912/33.
                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                ||: :|||
| ylsganln| 9
                                                                                                                                       Ä
                                                                                                                                                                                                                                   1 YLNVQDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9929182-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                     03-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moseley PL,
                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                          Y25242;
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                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoinmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides (A) that comprise agonists (Ia)
require isolation from a portion of the tumour itself. This represents a peptide fragment derived from the HIV pol protein used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or antagonists (1b) of human carcinoembryonal antigen (CEA). (1a) are used in vaccines to kill or inhibit carcinoma cells that express CEA or
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                  Score 23; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen peptide agonist CAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide agonists and antagonists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y09525 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zaremba
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                                                                                                                                                                                  55.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Conservative
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                                                                                                                                                 Query Match
Best Local Similarity
5; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                   1 YLNVQDLNL 9
                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                | | :|| |
| ylalqdsgl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09919478-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                             sednence
                                                     which is
                                                                                                         Sequence
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(EPIM-) EPIMMUNE INC.
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                                                                                                                                                    Kubo RT,
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                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YLNVQDLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :|: | |||
| flskgylnl
                                                   Homo sapiens
                                                                  W09945954-A1
                                                                                                    13-MAR-1998;
                                                                                                                     13-MAR-1998;
                                                                                   16-SEP-1999.
                                           Synthetic.
                                                                                                                                                    Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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ID Y9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide having a human leukocyte antigen binding motif #2143.
                                                                                                                                                                                                                                                                                                                                                     Six degenerate oligonucleotide primer sets were made to correspond to regions of amino acids highly conserved among previously described g protein alpha subunits. The primers were used for PCR with DNA from a taste cell library as template. Partial clones and further PCR primers were used to isolate a composite gustatory alpha subunit clone or gustducin gene clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                         Taste modifying agent; ligand; antiligand; binding activity; taste; taste receptor cells; sweet; bitter; sweet; salty; sour;
                                                                                                         Sequence used to design PCR primer for rat gustducin alpha subunit.
                                                                                                                                                                                                                                                                                                      New gustducin alpha subunit protein – used for identifying taste modifying agents which mimic or inhibit sweet, bitter, salty or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22; DB 14; Length 6;
Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 10; 50pp; English.
                                                        R42432 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y47532 standard; Peptide; 9 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 47.8%;
                                                                                                                                                                                                            93WO-US03279
                                                                                                                                                                                                                            92US-0868353
                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                            (MARG/) MARGOLSKEE R F.
                                                                                                                                                                                                                                                                             WPI; 1993-351746/44.
N-PSDB; Q51100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
               6
1 YLNVQDLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
          ||: :|||
1 ylsganlnl
                                                                                                                                                                                                                                                             Margolskee RF;
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1 flnkgd 6
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                                                                                                                                          amplification
                                                                                                                                                                                                           08-APR-1993;
                                                                                                                                                                                                                            09-APR-1992;
                                                                                        24-MAY-1994
                                                                                                                                                                          WO9321337-A.
                                                                                                                                                                                           28-OCT-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1999
                                                                                                                                                                                                                                                                                                                       sour tastes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                         R42432;
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having a human major histocompatibility complex (MHC) class I delico known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intext foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The product of the immunogenic peptides are also useful
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immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenic peptides with HLA binding motif, useful in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145390 to 148214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WT1 derived immunogenic peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 113; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y98547 standard; Peptide; 9 AA.
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55.6%;
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Best Local Similarity 55.00,
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Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer
                                                                 99WO-US22819
                                                                                         98US-0164223
99US-0276484
                                                                                                                                                                        Gaiger A, Cheever M;
                                                                                                                                 (CORI-) CORIXA CORP.
                                                                                                                                                                                                WPI; 2000-293107/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 4; Conserv
                                                                                                                                              (GAIG/) GAIGER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
              WO200018795-A2.
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                                                                 30-SEP-1999;
                                                                                           30-SEP-1998;
                                                                                                        25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-JUL-2000
                                        06-APR-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WTI, or variants of the immunogenic portion retaining the ability to react with WTI-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WTI polypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides, mimetros or polypuclectides can be included with a carrier/excipient in pharmaceutical compositions or with a conspecific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for WTI or a cell compositions with wTI expression, e.g. leukemia (especially associated with WTI expression, e.g. leukemia (especially cure/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 breast, lung, thyroid or gastrointestinal cancer, or a melanomal. Y99501 to Y98811 represent polypeptide sequences, and A13848 to A13862 represent PCR primers, used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WT1; immunotherapy; immunogenic; malignant disease; cancer; leukaemia; metastatic disease; mouse; human; Wilm's tumour; immune response;
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                                                                                                                                                                                                                                                            Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WT1 derived immunogenic peptide SEQ ID NO:101.
                                                                                                                                                                                                                                                                                                                Claim 4; Page 153; 193pp; English.
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                                                                                                                              98US-0164223.
99US-0276484.
                                                                                                    99WO-US22819
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                                                                                                                                                                                                           Gaiger A, Cheever M;
                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                    WPI; 2000-293107/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                   (GAIG/) GAIGER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
                                                  WO200018795-A2.
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1 dvrdln 6
                           Homo sapiens
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                                                                                                     30-SEP-1999;
                                                                                                                              30-SEP-1998;
25-MAR-1999;
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                                                                            06-APR-2000
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 vaccine.
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The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, Wilm's Tumour gene product polypeptide, Wil, (or variants of the immunogenic portion retaining the ability to react with WTI-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WTI comprising 16 consecutive amino acids (aa) or less of a native WTI comprising 16 consecutive amino acids (aa) or less of a native WTI comprising 16 consecutive amino acids (aa) or less of a native WTI comprising 16 consecutive amino acids (aa) or less of a native WTI companies. The polypeptides are useful therapeutically and to manufacture medicaments for enhancel compositions or with a non-specific immune response enhancer (e.g. an adjuvant or achievement or preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to compositions and vaccines can be administered to human patients to compositions and vaccines can be administered to human patients to composition and vaccines can be administered to human patients to composition and vaccines can be administered to human patients or associated with WTI expression, e.g. leukemia (especially acute/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501 to Y98811 represent polypeptide sequences, and A1386 to A13862 represent con the paremental control co
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Claim 4; Page 158; 193pp; English.
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3 NVQDLN 8
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1 dvrdln 6
              30-SEP-1998;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
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25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 25
Y98783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antiscra and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 compositions. The polypeptides are useful therapeutically and to patients. The polypeptides are useful therapeutically and to patients. The polypeptides, mimetics or polynucleotides can be included to patients. The polypeptides, mimetics or polynucleotides can be included to non-specific immune response enhancer (e.g. an adjuvant or enhancer or preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response specific for WT1 or a cell expressing WT1, useful to inhibit the development of malignant diseases associated with WT1 expression, e.g. leukemia) or cancer (especially compositions and acid or systemic confortion or gastrointestinal cancer, or a melanoma). Y98501 core Y98811 represent polypeptide sequences, and Al3848 to Al3862 represent
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PCR primers, used in the exemplification of the present invention
                                                                                                                                                                             Novel polypeptides comprising an immunogenic portion of a native polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer
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                                                                                                                                                                                                                               Claim 4; Page 174; 193pp; English
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                         99WO-US22819
                                                 98US-0164223
                                                              99US-0276484
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Best Local Similarity 66.7
Matches 4; Conservative
                                                                                                                            Gaiger A, Cheever M;
                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                     WPI; 2000-293107/25
                                                                                                    (GAIG/) GAIGER A.
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2 dvrdln 7
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                         30-SEP-1999;
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                                                              25-MAR-1999;
                                                  30-SEP-1998;
06-APR-2000.
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The present invention describes polypeptides (1) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WIT, (or variants of the immunogenic portion retaining the ability to react with WIT-specific antisers and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WIT comprising 16 consecutive amino acids (aa) or less of a native WIT conjypeptide. The polypeptides are useful therapeutically and to manufacture medicaments for enhancing/inducing an immune response in patients. The polypeptides winentics or polynocleotides can be included on specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to enhance or induce an immune response enhance to enhance an immune response specific for WIT or a cell expressing WIT, useful to inhibit the development of malignant diseases associated with WIT expression, e.g. leukemia (especially acute/chronic myeloid leukemia or acute lymphocytic leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). Y98501 to Y98811 represent polypeptide sequences, and A13862 represent
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                                                                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 182; 193pp; English
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98US-0164223.
99US-0276484.
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99US-0276484
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                                                                                                                      (CORI-) CORIXA CORP. (GAIG/) GAIGER A.
                                                                                                                                                                                                                                                 Gaiger A, Cheever
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Matches 4; Conser
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gamma-chain of cytokine receptors, and interacts with a cytokine or a gamma-chain partner receptor chain of a heterodimeric cytokine ereceptor. They inhibit signal transduction mediated by cytokine: receptor. In they inhibit signal transduction mediated by cytokine: receptor. In they inhibit or suppress cytokine-mediated immune responses, growth, proliferation, function and activity of cells. Particularly they are used for treatment or prevention of lymphoma, leukeemia, allergy are used for treatment or prevention of lymphoma, leukeemia, allergy multiple sclerosis or myasthenia gravis), graft vs. host disease and transplant or graft rejection. They inhibit function of interleukin (IL)-2, -4, -7, -9, -13 and -15 (the receptors for which include a common gamma -chain), so function as immunosuppressants by reducing
                                                                                                                                                                                                                                                                   The peptide mimetics W61734-W61756 and W77001-W77014 mimic a loop on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Modulation; nonclassical cadherin mediated cell adhesion; CAR; inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin-1; cadherin-6; cadherin-1; cadherin-1; cadherin-1; cadherin-1; cadherin-1; cadherin-1; racherin, pb-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmocalin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3192.
                                                                           New peptide(s) mimicking a loop in the gamma chain of cytokine receptors - inhibit signal transduction through these receptors, useful as immunosuppressants for treating or preventing e.g. leukaemia, autoimmune disease, graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.7%; Score 21; DB 19; Length 6; 66.7%; Pred. No. 2.1e+05; Live 2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                 Claim 2; Page 28; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T and B cells.
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98US-0187859.
99US-0234395.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
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Modified-site
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06-NOV-1998;
20-JAN-1999;
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| lnlqnl (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9957149-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LNVQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1999
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes polypeptides (I) comprising an immunogenic portion of a native Wilm's Tumour gene product polypeptide, WT1, (or variants of the immunogenic portion retaining the ability to react with WT1-specific antisera and/or T-cell lines or clones) and comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive amino acids (aa) or less of a native WT1 comprising 16 consecutive medicaments for enhancing/inducing an immune response in patients. The polypeptides, minetics or polynucleotides can be included on on-specific immune response enhancer (e.g. an adjuvant or enhancer preferentially enhancing a T cell response) in vaccines. Pharmaceutical compositions and vaccines can be administered to human patients to compositions and vaccines can be administered to human patients to compositions and vaccines can be administered to human patients to compositions and vaccines can be administered to human patients to composition and vaccines can be administered to human patients to composition and vaccines can be administered to human patients of associated with WT1 expression, e.g. leukemia) or cancer (especially breast, lung, thyroid or gastrointestinal cancer, or a melanoma). F98501 cor 98811 represent polypeptide sequences, and A13848 to A13862 represent cor correct c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide mimetic; gamma-chain; cytokine receptor; signal transduction; autoimmune disease; graft vs. host disease; transplant rejection; graft rejection; interleukin; immunosuppressant; T cell; B cell.
                                                                                                                                                                                                        Novel polypeptides comprising an immunogenic portion of a native WT1 polypeptide, useful for inhibiting the development of malignant diseases associated with WT1 expression e.g. leukemia or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 22; DB 21; Length 9; Pred. No. 2.1e+05; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide mimetic of cytokine receptor gamma chain 14.
                                                                                                                                                                                                                                                                                                                  Claim 4; Page 187; 193pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W61747 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autolmmune disease; graft vs. graft rejection; interleukin;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                 Galger A, Cheever M;
                                                                                                                                                      WPI; 2000-293107/25.
                (CORI-) CORIXA CORP. (GAIG/) GAIGER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
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2 dvrdln 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1998
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The peptide mimetics W61734-W61756 and W77001-W77014 mimic a loop on the gamma-chain of gytokine receptors, and interacts with a cytokine or a gamma-chain partner receptor chain of a heterodimeric cytokine receptor. They inhibit signal transduction mediated by cytokine:receptor binding (of cytokines that bind to receptors with a gamma-chain). They are used to inhibit or suppress cytokine-mediated immune responses, growth, proliferation, function and activity of cells. Particularly they are used for treatment or prevention of lymphoma, leukaemia, allergy (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus, multiple sclerosis or myasthenia gravis), graft vs. host disease and transplant or graft rejection. They inhibit function of interleukin (L1)-2, -4, -7, -9, -13 and -15 (the receptors for which include a common proliferation of T and B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..8
/note= "the terminal residues are condensed with each
    other to form a cyclic peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibition; cadherin extracellular domain; cell adhesion recognition; OB-cadherin-7; cadherin-7; cadherin-7; cadherin-7; cadherin-12; cadherin-12; cadherin-12; cadherin-12; cadherin-13; T-cadherin; PB-cadherin; cadherin related neuronal receptor; LI-cadherin; protocadherin; desmoglein; desmoclin; calcium binding; cancer; tumour; obesity; rheumatoid arthritis; multiple sclerosis; diabetes; metastasis; neurological disease; cyclic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Desmoglein cell adhesion recognition cyclic peptide SEQ ID NO:3195.
                                                                                                                                                                                                      New peptide(s) mimicking a loop in the gamma chain of cytokine receptors - inhibit signal transduction through these receptors, useful as immunosuppressants for treating or preventing e.g. leukaemia, autoimmune disease, graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modulation; nonclassical cadherin mediated cell adhesion; CAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 19; Length 8; Pred. No. 2.1e+05; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                              Claim 8; Page 29; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y63743 standard; Peptide; 8 AA.
                                                      (UYJE-) UNIV JEFFERSON THOMAS.
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  97US-0036941.
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Best Local Similarity 60...
                                                                                                        RM;
                                                                                                        Townsend
                                                                                                                                                    WPI; 1998-446944/38
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07-FEB-1997;
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2 lnlqn1 '
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                                                                                                     Korngold R,
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Comprising peptides which comprise a nonclassical cadherin cell adhesion

Comprisition (CAR) sequence. The MAs can be used for modulating

conclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

conclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

confamily, inhibiting metastasis of a cancer in a mammal, inhibiting

confidences in a mammal, inducing apoptosis in a nonclassical cadherin-

confidences in a mammal, enhancing delivery to the

contral nervous system, treating a demyelinating neurological disease,

contral nervous system, treating a demyelinating neurological disease,

conclassical cadherin-expressing cells, inhibiting synaptic stability in

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

conclastic can also be used for treating e.g. psoriasis, arthritis,

age-related macular degeneration, multiple sclerosis and diabetes. The

products can also be used for detection and diagnosis and in

concreactors. Y60592 to X64572 represent specifically claimed peptides,

concauting can be used for detection and diagnosis and in

concreactors. Y60592 to Y64572 represent specifically claimed peptides,

concentral represent invention.
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                                                                                                                                                                                                   New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide mimetic of cytokine receptor gamma chain 31.
                                                                                                                                                                                                                                                                                                                         Claim 90; Page 208; 252pp; English
                                                 (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                   Byers S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W77008 standard; peptide; 8 AA.
99US-0264516.
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                                                                                                   Gour BJ,
                                                                                                                                                  WPI; 2000-038791/03
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Best Local Similarity
Matches 4; Conserv
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08-MAR-1999;
                                                                                                   Blaschuk OW,
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WPI; 1994-302678/37.
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                                                                                                                                             (CYTE-) CYTEL CORP
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                                                                                                                                                                                                                                                                                                                                                                                                        9 AA;
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                                                                                         05-MAR-1993;
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29-NOV-1993;
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             WO9420127-A.
                                        15-SEP-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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R59233
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                                                                                                                                                                                                                                                     The present invention describes cadherin modulating agents (MA)

comprising peptides which comprise a nonclassical cadherin cell adhesion

cecognition (CAR) sequence. The MAs can be used for modulating

nonclassical cadherin-mediated functions. They can be used for e.g.

inhibiting adhesion of nonclassical-cadherin expressing cells in a

can mammal, enhancing delivery of a drug through the skin of a mammal,

can mammal, inhibiting metastasis of a cancer in a mammal, inhibiting

can giogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-

expressing cell, preventing or treating obesity in a mammal, stimulating

contral nervous system, treating a demyelinating neurological disease,

increasing vasopermeability in a mammal, enhancing adhesion of

conclassical cadherin-expressing cells, inhibiting synaptic stability in

a mammal, or preventing pregnancy in a mammal. They can also be used for

c.g. enhancing or directing neurite outgrowth, facilitating wound healing

cor reducing scar tissue, or enhancing adhesion of foreign tissue in a

conclassical table macular degeneration, multiple scloresis and diabetes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          products can also be used for detection and diagnosis and in
bioreactors. Y60592 to Y64572 represent specifically claimed peptides,
and Y64573 to Y64643 and 233183 to 233186 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                   New cadherin modulating agents, used for modulating nonclassical cadherin-mediated functions for treating e.g. cancers, obesity, rheumatoid arthritis, multiple sclerosis, diabetes or a neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HVI; corc antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor;
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Pred. No. 2.1e+05;
); Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide fragment (1.0384) of HBV binds HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention.
                                                                                                                                                                                                                                  Claim 90; Page 208; 252pp; English.
                                                                                          (ADHE-) ADHEREX TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R59112 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.78;
                                    98US-0187859.
99US-0234395.
99US-0264516.
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                            98US-0073040.
99WO-CA00363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human leukocyte antigen
                                                                                                                  Gour BJ,
                                                                                                                                           WPI; 2000-038791/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA;
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                                     06-NOV-1998;
20-JAN-1999;
                                                                08-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; epitope; immunogenic target protein; PSA; HBVc; HBVs; EBV; HTVI; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor;
                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide fragment (1.0164) of HIV binds HLA-A2.1.
                                                                                                                                                                                                                                                                    Sidney J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Page 100; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R59233 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                 Grey HM, Kast WM, Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immunodeficiency virus.
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93US-0073205.
93US-0159184.
                                                          93US-0027146.
93US-0073205.
93US-0159184.
94WO-US02353
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Gaps

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Length 9; Indels

DB 16; I 2.1e+05;

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Peptides R70066-7 are control peptides in an assay for stimulation of vytocoxic T cells (CTLS) by epitopes from the heptitis B virus (HBV) polymerase (HBpol) (see R70044-59). The HBpol peptides can be used, prophylactically as vaccines, together with, or conjugated to, HBV helper epitopes (R70060-4). The peptides can be used, particularly ex vivo, to stimulate CTL cells,which cells can be reintroduced into patients who have chronic or acute HBV infections or are carriers, especially in treatments to prevent conversion from acute to chronic infections.
                                                                                                                                                                                                                                                                                                                                             Hepatitis B virus polymerase; cytotoxic T cell response; prophylactic; vaccine; chronic; acute HBV infection; carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides inducing cytotoxic T lymphocytes to hepatitis B virus - are regions of HB polymerase protein, for treating acute and chronic infections
                                                                                                                                                                                                                                                                                                                 Control peptide 927.30 for HBV epitope stimulation of T-cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 16; Length 9;
Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                                            45.7%; Score 21; DB 100.0%; Pred. No. 2.1 iive 0; Mismatches
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                                                                                                                                                                                                                           R70067 standard; peptide; 9 AA.
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                                                                                           4; Conservative
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Best Local Similarity
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                                                             Query Match
Best Local Similarity
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                  AA;
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2 lnlqnlnv 9
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                  Seguence
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                                                                                         Matches
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                                                                                                                                          R59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (R71293). R59233 has an IC50 of 0 and the sequence occurs at position 614 in the HIV POL protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R70596 is a peptide fragment derived from an HIV (Human Immunodeficiency Virus) protein and is capable of binding to a human lymphocyte antigen. The peptide can induce killer cells which target HIV-infected cells. It is also useful in the prevention and treatment of HIV and AIDS. Anti-HIV vaccines may incorporate the peptides, or may incorporate a vector (such as vaccinia or BCG) contg. DNA encoding the peptides.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-binding peptide fragments from HIV proteins - induce killer cells which target HIV-infected cells and can be incorporated into anti-HIV vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA; human lymphocyte antigen; HIV; human immunodeficiency virus; binding peptide; induce killer cell; prevention; treatment; AIDS; autoimmune disease syndrome; vaccine.
                                                       Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or autoimmune diseases.
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Pred. No. 2.1e+05;
3; Mismatches 1; Indels
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 Sidney J;
                                                                                                                  Example 5; Page 105; 138pp; English.
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 Sette A,
                                                                                                                                                                                                                                                                                                                45.7%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                             4; Conservative
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                             WPI; 1994-302678/37
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 Kast WM,
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   9 AA;
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2 lnlgnlnv 9
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19-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                      09-OCT-1992
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                                                                                  Synthetic
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                                                                                                                  O-Malonyl-tyrosine; derivative; signal transduction; binding; Src; Pl-3 kinase; SH2 domain; Grb2; SH-PTP2; ligand; cancer; therapy; diabetes; immune dysfunction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH2 domain; binding; inhibition; interaction; site specific;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New O-malonyl-tyrosine derivs. - useful as protein-tyrosine phosphatase inhibitors
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                                                                                                                                                                                                                                                                                                                              "O-malonyltyrosyl derivative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yan X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH2 domain binding inhibiting peptide SEQ ID NO:60.
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Pred. No. 2.1e+05;
1; Mismatches 2
                                                                                                                                                                                                                                                                                      "Acylated N-terminus"
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                                                                                                                                                                                                                                                                                                                                                                    /note= "amidated C-terminus"
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                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                Peptide against SH-PTP2 SH2 domain
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Best Local Similarity 62.5%;
Matches 5; Conservative
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                                      06-JUL-1999 (first entry)
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| lnxidldl 8
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                                                                                                                                                                                                     Synthetic
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method has been developed of inhibiting a site-specific interaction between a first molecule having an SH2 domain and a second molecule that between a first molecule having an SH2 domain and a second molecule that interacts with the SH2 domain. The method comprises contacting the first complexity and RH and the septide containing a sequence of formula: RH-MET-R3-Met (1), where RH = phosphotyrosine (PTyr) or a phosphotyrosine analogue having a hydrolysis-resistant phosphorous complexy, and RB = any amino acid. W78501 to W78521 represent specifically claimed examples of the peptides described. The peptides are useful for modulating both cellular growth to control unwanted cell proliferation in e.g selected malignancies and for metabolic control in e.g. diabetes, by inhibiting signal transduction molecules such as protein tyrosine concogene products and the insulin receptor. The peptides are also useful for for tracting and for studying the enzymatic mechanisms of PTPase activity and the metabolic and blochemical roles of PTPases. W78702 represent other peptides given in the present invention, but
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signal transduction; protein tyrosine kinase; phosphotyrosine; growth factor receptor; oncogene; cellular growth; cell proliferation; metabolic control; dlabetes; PTK; proto-oncogene; insulin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inhibiting site-specific SH2 domain interaction - with peptide containing phosphotyrosine or phosphotyrosine mimic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 19; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: December 16, 2000, 03:07:20 Job time: 8061 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 53; 70pp; English.
                                                                                                                                                                                                                                                                                           /note= "unspecified"
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (JOSL-) JOSLIN DIABETES CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0408604.
91US-0722359.
92US-0959949.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-494822/42
                                                                                                                                                                                                                                                     Misc-difference
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December 16, 2000, 02:00:58; Search time 113.2 Seconds (without alignments)
7.424 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                             297973
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                        297973 seqs, 93374136 residues
                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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48
1 YLSGACLNL 9
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

| SPTREMBL_14:* : sp_archea:* : sp_archeria:* : sp_fund:* | Sp_numan:* Sp_numan:* Sp_nuvertebrate:* Sp_mamal:* | sp_organelle:* sp_phage:* sp_plant:* | <pre>sp_rodent:* sp_vertus:* sp_vertebrate:* sp_unclassified:*</pre> |
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | Description | Q9ved2 drosophila | Q9v3k8 drosophila | Q15142 homo sapien | Q15141 homo sapien | Q15140 homo sapien | Q31147 mus musculu | Q9sht3 arabidopsis | 075098 homo sapien | 009705 lassa virus | Q27167 paramecium | 037322 heliothis a | Q22960 caenorhabdi | 094038 candida alb | Q9tp68 homo sapien | 074484 schizosacch | P93818 arabidopsis | Q9xb13 mycobacteri | Q41716 xanthium sp | Q41717 xanthium sp |
|-----------|---|--------|-----------------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | | | | D2 | К8 | 42 | 41 | 40 | 47 | HT3 | 86 | 705 | 29 | 322 | 09 | 38 | 68 | 84 | 818 | 13 | 716 | 717 |
| S | | | ID | Q9VED2 | Q9V3K8 | 015142 | 015141 | 015140 | 031147 | Q9SHT3 | 075098 | 009705 | 027167 | 037322 | 0229 | 0940 | Q9TP | 0744 | P93818 | Q9XB13 | 041716 | 041717 |
| | | | DB | ß | S | 4 | 4 | 4 | 7 | 10 | 4 | 12 | ٠, | 12 | Ŋ | m | 7 | m | 10 | 7 | 10 | 10 |
| | | | Match Length DB | 344 | 1624 | 3638 | 4292 | 4302 | 91 | 265 | 375 | 2218 | 2395 | 82 | 114 | 348 | 362 | 363 | 453 | 514 | 648 | 648 |
| | æ | Query | Match | 76.0 | 75.0 | 72.9 | 72.9 | 72.9 | 70.8 | 70.8 | 70.8 | 70.8 | 70.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 |
| | | | Score | 36.5 | 36 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 |
| | | Result | NO. | H | 7 | m | 4 | Ś | 9 | 7 | & | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 |

| Q42767 gossyplum h Q42768 gossyplum h Q92su3 bassia scop O25380 helicobacte O4670 pneumocysti O9y253 lymphocytic O9tp21 ambystoma m Q89173 variola vir Q36114 trichoniscu Q36113 trichoniscu Q36113 trichoniscu Q9404 eptatretus O9wy5 mus musculu Q989p2 arabidopsis O07868 streptococc O95327 homo sapien | 093770 ovis aries 093827 candida alb 074624 trichoderma 09surl arabidopsis 061715 caenorhabdi 076258 caenorhabdi 023174 arabidopsis 092qf7 arabidopsis 09rmc9 acinetobact 093676 sulfolobus |
|---|---|
| 10 042767 110 042768 110 042768 12 025380 2 025380 3 074670 097225 7 097221 12 089173 12 089173 8 036113 9 036113 10 099084 11 098745 11 098745 11 098368 | 7 030770 3 093827 3 074624 10 095UR1 5 061715 5 076258 10 023174 10 092077 2 09RMC9 |
| 6559 6559 6559 10017 22009 1148 1168 2250 2250 2260 3300 323 | 333 3362 3370 3370 5388 6089 |
| 668 88 88 88 88 88 88 88 88 88 88 88 88 | 66.7 66.7 66.7 66.7 66.7 66.7 66.7 66.7 |
| | 2222222222 22222222222 |
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ALIGNMENTS

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Q15142
Q15142;
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          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RA MEDLINE; CLIDENDE, C. HOLT R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Ra George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gorger S. T., PH.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkov C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Brandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Gablish R.D., Brownes M., Dugan-Roches S., Dunkov B.C., Dunn P.,
Bordson K., Doup L.E., Downes M., Dugan-Roches S., Dunkov B.C.,
RA God B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Hortin N.J., Evangelista C.C., Ferriacra S., Fleischmann W.,
RA God F., God J., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kanp D., Li X.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai X.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai X.,
Alali M., Kalush F., Karpen G.H., Neclod M.D., Moshefi A.
Lux, Mattel B., Modira C.D., Kraft C., Kraft C., Karnison J.A., Moshefi A.
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L,
RA Merkulov G., Milshina N.V., Mobarty C., Morris J., Moshrefi A.
Nelazzolo M., Pittman G.S., Pan S., Pollard J., Puri, V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
L., Rayerer D., Saunders R.D.C., Scheeler F., Shen H.,
L., L., Rayerer D., Saunders R.D.C., Scheeler F., Shen H.,
L., L., Rayerer D., Sunders R.D.C., Scheeler F., Shen H.,
L., L., L., L., L., L., Sumpson M., Skupski M.P., Sales S., Shen H.,
L., L., Stanger R.D., Stanger
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
A Svirskas K., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ped J., Yah R.F., Zaveri J. S., Zhang G., Zhang G.,
Zheng X.H., Zhong F.W., Zhong W., Zhu S., Zhu X., Smith H.O.,
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
The genome sequence of Drosophila melanogaster.";
EMBL: AE003720; AAF55493.1:
                                                                                                                                                                                                                                                                                                                                                   ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Fukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta;
Pterygota, Neoptera, Endopterygota, Diptera; Brachycera, Muscomorpha,
Ephydroidea; Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                               5; Length 344;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                          39318 MW; 3ECAA947157719C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                            76.0%; Score 36.5; DB 75.0%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1624 AA.
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                          FLYBASE; FBgn0038567; CG14316.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CG2995 PROTEIN.
CG2995 OR EG:BACR37P7.2.
                                                                                                                                                                                                                                                                                                                                                                                                 134 YLSGAPLKCLNL 145
                                                                                                                                                                                                                                                                                                                                                                               1 YLSGA---CLNL 9
                                                                                                                                                                                                                                                             344 AA;
                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 20196006.
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                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V3K8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q9V3K8
   pp
                                                                                                                                                                                                                                                                                                                                                                               δ
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woorley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhan K., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE: 94273192.
Ward C.J., Peral B., Hughes J., Thomas S., Gamble V., MacCarthy A.B., Sloane-Stranley J., Buckle V.J., Kearney L., Higgs D.R., Ratcliffe P.J., Harris P.C., Roelfsema J.H., Spruit L.L., Saris J.J., Baucok-Carter P.T., Maheshwar M.M., Cordeiro I., Santos H., Cabral P., Sampson J.R., Janssen B., Hesseling-Janssen A.L.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The polycystic kidney disease 1 gene encodes a 14 kb transcript and lies within a duplicated region on chromosome 16. The European Polycystic Kidney Disease Consortium [published errata appear in Cell 1994, Aug 26;78(4):following 724 and 1995 Jun 30;81(7):following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Burn T.C., Connors T.D., Dackowski W.R., Petry L.R., Van Raay T.J., Millholland J., Venet M., Miller G., Hakim R.M., Doggett N.A., Landes G.M., Klinger K.W., Qian F., Onuchic L.F., Watnick T., Germino G.G.;
                                                                                                                                                                                                                                                                                                                                                      Madueno E., de Pablos B., Modolell J.; "Sequencing the distal X chromosome of Drosophila melanogaster."; Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benos P.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE003417; AAF45.87.1; -.
EMBL; AL050231; CAB65850.1; -.
FLYBASE; FEGRO029516; CG2995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1624 AA; 179964 MW; AAA34BAFCDAE5121 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%; Score 36; DB 5;
66.7%; Pred. No. 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLYCYSTIC KIDNEY DISEASE-ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT; 3638 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                          Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR001214; -. INTERPRO; IPR002110; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00023; ank; 5. PFAM; PF00856; SET; 1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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1170].";
Cell 77:881-894(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 9473192.
MEDLINE; 9473192.
Mard C.J., Peral B., Hughes J., Thomas S., Gamble V., MacCarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L., Higgs D.R.,
Ratcilffe P.J., Harris P.C., Roelfsama J.H., Spruit L.L., Saris J.J.,
Dauwerse H.G., Peters D.J.M., Breuning M.H., Nellist M.,
Brook-Carter P.T., Maheshwar M.M., Cordeiro I., Santos H., Cabral P.,
Sampson J.R., Janssen B., Hesseling-Janssen A.L.W.,
Halley D.J.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hughes J., Ward C.J., Peral B., Aspinwall R., Clark K., Millan J.L., Gamble V., Harris P.C.;
"The polycystic kidney disease 1 (PKD1) gene encodes a novel protein with multiple cell recognition domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
"Analysis of the genomic sequence for the autosomal dominant polycystic kidney disease (PKD1) gene predicts the presence of a leucine-rich repeat. The American PKD1 Consortium (APKD1 Consortium) ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 4; Length 3638;
Pred. No. 2.3e+02;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0500; POLYCYSTIN.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 3638 AA; 392182 MW; 8267F06B5E04B0D1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 4292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                            lum. Mol. Genet. 4:575-582(1995).
sMBL; L39891; AAB59488.1; -.
INTERPRO; IPR000203; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.9%;
75.0%;
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                                                                                                                                                                                                                                                                                                   PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                         PF01462; LRRNT; 1.
PF01463; LRRCT; 1.
PF0147; PLAT; 1.
PF01825; GPS; 1.
PF02010; REJ; 1.
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                                                                                                                                                                                                                                                                                                                    PF00560; LRR; 1.
PF00801; PKD; 11.
                                                                                                                                                                                                                                                            INTERPRO; IPR001611; -. INTERPRO; IPR002859; -.
                                                                                                                                                                                                                                       IPR001304; -.
                                                                                                                                                             INTERPRO; IPR000434; -.
                                                                                                                                                                             INTERPRO; IPR000483; -.
                                                                                                                                                                                                                     INTERPRO; IPR001024; -.
                                                                                                                                        INTERPRO; IPR000372; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cell 77:881-894(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1740 YLEGRCLN 1747
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                                                              Consortium).
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PFAM;
PFAM;
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PFAM;
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ward C.J., Peral B., Hughes J., Thomas S., Gamble V., MacCarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L., Higgs D.R., Ratcliffe P.J., Harris P.C., Roelfsema J.H., Spruit L.L., Saris J.J., Dauwerse H.G., Peters D.J.M., Breuning M.H., Nellist M., Brook-Carter P.T., Maheshwar M.M., Cordeiro I., Santos H., Cabral P., Sampson J.R., Janssen B., Hesseling Janssen A.L.W., Halley D.J.J.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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75.0%; Pred. No. 2.7e+02;
Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-JUN-2000 (TrEMBLrel. 14, Last annotation update) POLYCYSTIC KIDNEY DISEASE 1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 4302 AA.
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             MAC. CENEL. 10:121-100(1293)

EMBL; L4361; AAC41765.1; -

EMBL; L43601; AAC41765.1; JOINED.

EMBL; L43602; AAC41765.1; JOINED.

EMBL; L43605; AAC41765.1; JOINED.

EMBL; L43610; AAC41765.1; JOINED.

EMBL; L43610; AAC41765.1; JOINED.

EMBL; L43618; AAC41765.1; JOINED.
Genet. 10:151-160(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.vv.,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRRNT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRR; 2.
PKD; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF01477; PLAT; 1.
PFAM; PF01822; WSC; 1.
PFAM; PF01825; GPS; 1.
PFAM; PF02010; REJ; 1.
                                                                                                                                                                                                                                                                            INTERPRO; IPR000434; -. INTERPRO; IPR000483; -.
                                                                                                                                                                                                                                                                                                                              INTERPRO; IPROOD601; -. INTERPRO; IPRO01024; -. INTERPRO; IPRO01052; -. INTERPRO; IPRO01304; -.
                                                                                                                                                                                                                          INTERPRO; IPR000203; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR002859;
INTERPRO; IPR002889;
                                                                                                                                                                                                                                                          INTERPRO; IPR000372;
                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001611;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF01462;
PFAM; PF01463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00801;
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Gaps

; 0

Length 91; Indels

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SEQUENCE FROW. n.n.
STRAIN-CV. COLUMBIA,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shenning C.M., Koo, H., Moffat K.S.,
Buell C.Y., Mason T.M., Lee J.J., Ronning C.M., Koo, H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome II of Arabidopsis thaliana.";
"Sequence and A.J. Tallon L.J.
"Sealzberg S.L., Fraser C.M., Venter J. Tallon L.J.
"Sequence and A.J. Tallon L.J.
"Sealzberg S.L. Tallon L.J.
"Sealzberg S.L., Fraser C.M., Venter J. Tallon L.J.
"Sequence and A.J. Tallon L.J.
"Sequence and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 98360089.

Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;

"Identification of high-molecular-weight proteins with multiple EGF-
like motifs by motif-trap screening.";

Genomics 51:27 34(1998).

EMBL; AB031542; BAA32470.1; -.

HSSP; P02468; ITLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 34; DB 10; Length 265;
Pred. No. 31;
                              E14021DAB93E95E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
AT2G05410 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                               Score 34; DB 7;
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                  265 AA
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                                                                                                                                                                                                                                                                                                                                                  PRT;
           1
10747 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.8%;
66.7%;
                                                                                               70.8%;
85.7%;
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08,
14,
                                                                     Query Match
Best Local Similarity 85.,.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6; Conservative
                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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           1
91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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|151 YLKTACMNL 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YLSGACLNL 9
                                                                                                                                                                                                                   1 YLSGACL 7
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      NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                       09SHT3;
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                                                                                                                                                                                                                                                                                                                                                Q9SHT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEGF9
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075098
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      SO
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                                                                Hughes J., Ward C.J., Peral B., Aspinwall R., Clark K., Millan J.L., Gamble V., Harris P.C.;
"The polycystic kidney disease 1 (PKD1) gene encodes a novel protein with multiple cell recognition domains.";
Nat. Genet. 10:151-160(1995).
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRODEOS; POLYCYSTIN.
PROSITE; PS00202; RUBREDOXIN; UNKNOWN_1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 4302 AA; 462436 MW; 97472CA1981FB51A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                       Harris P.C.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L33243; AAC37576.1; -.
                                                                                                                                                                                                                                                   Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 4; 1
Pred. No. 2.7e+02;
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01-NOV-1996 (TrEMBLrel. 01, Last sequ
01-MAX-2000 (TrEMBLrel. 13, Last ann
MHC C6/G2 (QA-2) PROTEIN (FRAGMENT).
MHUS MUSCULUS (MOUSE).
EUKATYOLA; Metazoa; Chordata; Craniat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.9%; Scc...
75.0%; Pred
0; 1
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Immunogenetics 21:343-353(1985).
EMBL; MI4833, AAA39566.1; -.
INTERPRO: IPRO01039; -.
PFAM; PF00129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PF00059; lectin_c; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01462; LRRNT; 1.
PF01463; LRRCT; 1.
PF01477; PLAT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPR000203; -.
INTERPRO; IPR000372; -.
INTERPRO; IPR000434; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00560; LRR; 2. PF00801; PKD; 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002889; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01825; GPS; 1
PF02010; REJ; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR000601;
INTERPRO; IPR001024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPR000483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR001304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO; IPR002859;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR001052;
SEQUENCE FROM N.A.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 85206117.
                                                                                                                                                                                     [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                   Harris P.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rogers J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM;
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PFAM;
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F10G2.9.
Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heliothis armigera entomopoxvirus (HaEPV).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae.
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                                                                                 Scott J., Leeck C., Forney J.;
"Analysis of the micronuclear B type surface protein gene in
Paramecium tetraurelia.";
Nucleic Acids Res. 22:5079-5084(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.8%; Score 34; DB 5; Length 2395; 100.0%; Pred. No. 2.5e+02; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 85;
                                                                                                                                                                                                                                                                                                                                      EMBL; LU4/32, ...
INTERPO; IPR000550; -.
INTERPRO; IPR001680; -.
INTERPRO; IPR002895; -.
INTERPRO; IPR012895; -.
INTERPRO; IPR01289; -.
INTERPRO; IPR01289; -.
INTERPRO; IPR01289; -.
PROJITE; PS00641; RECEPTOR CYTOKINES_1; UNKNOWN_1.
PROSITE; PS00678; WD_REPEATS; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 AA; 9920 MW; D7A7449AD155389A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last annotation update)
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA.
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2; Mismatches
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STRAIN-CLONAL ISOLATE WT#2/011293;
STSTAINTHA A., OSDORNE R.J., Dall D.J.;
J. Gen. Virol. 0:0-0(1997).
EMBL; AF019224; AAB96627.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                       Scott J.M., Leeck C.L., Forney
Genetics 133:189-198(1993).
EMBL: U07663; AAA81947 1; -.
EMBL: L04795; AAA16710.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 05, C
(TrEMBLrel. 05, I
(TrEMBLrel. 05, I
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71.4%;
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Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
     SEQUENCE FROM N.A. STRAIN=STOCK 51; MEDLINE; 95098630.
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     STRAIN-STOCK 51;
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Virology 235:414-418(1997).

EMBL: U303044; AAD50401.1; -

EMBL: U730045; PR001005; -
                                                                                                                                                                                                                                                                                       Gaps
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MEDLINE; 97201617.
Lukashevich I.S., Djavani M., Shapiro K., Sanchez A., Ravkov E.,
Lukashevich I.S., Salvato M.S.;
"The Lassa fever virus L gene: nucleotide sequence, comparison, and
precipitation of a predicted 250 KDa protein with monospecific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lassa virus.
Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2000 (TREMBLrel. 13, Last annotation update)
51B TYPE SURFACE PROFIN.
Paramecium tetraurelia.
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
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Pred. No. 2.3e+02;
                                                                                                                                                                                                                               Score 34; DB 4; Length 375;
Pred. No. 43;
1; Mismatches 0; Indels
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SEQUENCE 2218 AA; 253429 MW; F325C51F96ED2EA6 CRC64;
                                                                                                                                                        375 AA; 40803 MW; 84D1746CA8E3B172 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
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0
INTERPRO; IPR002561; -.
INTERPRO; IPR002049; -.
PPGM; PF00053; laminin_EGF; 4.
PROSITE; PS00022; EGE_1; UNKNOWN_1.
PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2218 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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85.7%;
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85.7%;
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Best Local Similarity 85.77
                                                                                                                                                                                                                               Query Match 70.8
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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86 LTGACLN 92
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SEQUENCE
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EMBL; AL033501; CAA21988.1; -. INTERPRO; IPR002085; -. INTERPRO; IPR002328; -.
                                        INTERPRO; IPRO02328; -.
PFAM; PF00107; adh_zinc; 1.
PROSITE; PS00059; ADH_ZINC; 1.
Oxidoreductase; Zinc.
SEQUENCE 348 AA; 36807 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%;
66.7%;
                                                                                                                                                                                       68.8%;
62.5%;
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                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 5; Conserv
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Best Local Similarity
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SEQUENCE FROM N.A.
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93 WENGSCEN 100
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Q9TP68
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                                                                               Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Graxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Bightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 97435544.

Tait E., Simon M.C., King S., Brown A.J., Gow N.A.R., Shaw D.J.;

"A Candida ablicans genome project: cosmid contigs, physical mapping, and gene isolation.";
Fungal Genet. Biol. 21:308-314(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; Length 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     P.; to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=1161;
Taylor K., Harris D.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrell B.G., Rajandream M.A.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F9830BB98EA84E89 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%; Score 33; DB 55.6%; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13337 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-2000 (TrEMBLrel. 13, ALCOHOL DEHYDROGENASE II. CA41C10.04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (JUL-1996) to th
EMBL; U64836; AAB04834.1;
INTERPRO; IPR001628; -.
INTERPRO; IPR002219; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 55.v.
5; Conservative
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                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00105; zf-C4; SEQUENCE 114 AA; 1:
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=BRISTOL N2;
Murray J., Wohldmann
Submitted (JUL-1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                             STRAIN-BRISTOL N2;
MEDLINE; 94150718.
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47 YMAGNCFNL 55
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7:07.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 01-7.7; 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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DJ377H14.9 (MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS I, F (CDA12)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              ;
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SEQUENCE FROM N.A.
STRAIN=972;
Lyne M., Rajandream M.A., Barrell B.G., Murphy L., Harris D.;
                                                                                                                                                                             Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 362,
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AL022723; CAB46623.1; -.
INTERPRO; IPRO00495; -.
INTERPRO; IPRO01039; -.
INTERPRO; IPRO03006; -.
PFAM; PF00047; 19; 1.
PFAM; PF00047; 19; 1.
348 AA; 36807 MW; 3D6E67538522ADCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40578 MW; 970D072C813A07E2 CRC64;
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Schizosaccharomycetaceae; Schizosaccharomyces.
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Pred. No. 65;
                                                                                                                                                                             3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 AA.
                                                                                                                                                                             DB
63;
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SPCC1906.01.
                                                                                                                                                                             Score 33;
Pred. No.
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RECUENCE FROM N.A.

RECUENCE FROM N.A.

RECUENCE FROM N.A.

RECUENCE FROM N.A.

RECUENCE FROM S., Kato K., Nakai K., Okayama H., Nojima H.;

RECUENCE S., Kato K., Nakai K., Okayama H., Nojima H.;

RECUENCE S., Kato K., Nakai K., Okayama H., Nojima H.;

RECUENCE S., RECUENCE S., RECUENCE S., RECUENCE S., RECUENCE S., RECUENCE S., RECUENCE PROCRESSION (BY SIMILARITY).

RECUENCE C. - CATALYTIC ACTIVITY: GTP + ALPHA-D-MANNOSE I-PHOSPHATE =

DIPHOSPHATE + GDP-MANNOSE I-PHOSPHATE =

DIPHOSPHATE + GDP-MANNOSE I-PHOSPHORYLASE (RFBF).

CC. -I- SIMILARITY: TO S. TYPHIMURIUM CDP-GLUCOSE PYROPHOSPHORYLASE (RFBF).

BEBL; ALOSISS: CAA20770.1; -

DR FEMBL; BROO132; hexapep; 1.

PEMM; PEOOLS; hexapep; 1.

PEMM; PEOOLS; hexapep; 1.

PEMM; PEOOLS; hexapep; 1.

PEMM; PEOOLS; NUCLECTICITYLETARSFERASES; UNKNOWN.1.

PERM; PEOOLS; Nucleotidyltransferase; Kinase; Cell cycle.

FT CONFLICT 175 176 GI -> VL (IN REF. 2).

SEQUENCE 363 AA; 39719 MW; 55F55FF0EDDITCOZ CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 68.8%; Score 33; DB 3; Length 363; Best Local Similarity 66.7%; Pred. No. 65; Matches 6; Conservative 1; Mismatches 2; Indels
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Search completed: December 16, 2000, 02:01:00 Job time: 5934 sec

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| | 100 July 100 | | | |
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2000, 01:51:16; Search time 91.14 Seconds (without alignments) 6.267 Million cell updates/sec Run on:

US-09-529-121-5 48 1 YLSGACLNL 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

182106 seqs, 63460219 residues Searched:

182106 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_65:* Database

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| SUMMARIES | Description | A36319 carcinoembryonic a | | breast cancer | breast cancer | dihydrolipoami | | polycystic ki | | | | | | 8 | | | T18230 alcohol dehydrogen | histocompati | | mannose-1-ph | T42371 probable mannose-1 | | | I64229 dihydrolipoamide d | | 58 acetolactate | acetolactate | YCMU acetolactate synth | |
|-----------|----------------|---------------------------|------|---------------|---------------|----------------|-----|---------------|----|-----|-----|------|------|------|------|------|---------------------------|--------------|------|--------------|---------------------------|------|------|---------------------------|------|-----------------|--------------|-------------------------|---|
| | DB ID | 2 A3 | | | 2 I | | | | | | | | | | | | | | | | | | | | | | | | |
| | Length D | 702 | 3328 | 3329 | 3329 | 57 | 314 | 4302 | 91 | 219 | 451 | 2395 | 114 | 261 | 263 | 345 | 348 | 348 | 362 | 363 | 363 | 368 | 457 | 457 | 637 | 629 | 629 | 670 | , |
| æ | Query Match | 75.0 | 75.0 | 75.0 | 75.0 | | | | | | | 70.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 8.89 | 68.8 | 8.89 | 68.8 | 68.89 | 68.8 | 68.89 | 68.8 | 68.8 | |
| | Score | 36 | 36 | 36 | 36 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | |
| | Result No. | 1 | 7 | m | ₹ | S | Q | 7 | 80 | đ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | |

| genome polyprotein 6R protein - vario | RNA-binding ribonu | ribonuclease HI (E A35R protein – var | beta-crystallin Bl | beta-crystallin Bl | conserved hypothet | hypothetical prote | fructokinase (EC 2 | probable peptidyl- | hypothetical prote | hypothetical prote | hypothetical prote | hypothetical prote | creatine transport |
|--|--------------------|--|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| RRXPLC T28576 | н36851 | B81260 H72167 | CYRTB1 | S07264 | D70081 | S26008 | S44256 | T38464 | T05598 | T47407 | T33045 | T46460 | G02277 |
| 7 7 | ~ | 0 0 | - | ~ | 7 | ~ | 7 | ~ | 7 | ~ | 7 | 7 | 7 |
| 2210 | 140 | 146 146 | 249 | 253 | 276 | 277 | 288 | 362 | 370 | 378 | 378 | 420 | 426 |
| 68.8 | 66.7 | 66.7 | 2.99 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 |
| 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| 30 | 32 | 3 3 4 3 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

Carcinoembryonic antigen precursor - human
N;Alternate names: CEA; meconium antigen 100
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 16.5 Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000
C;Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098;
R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shive
Mol. Cell. Biol. 10, 2738-2748, 1990
A;Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its p
A;Accession: A36319 A; Molecule type: DNA
A; Residues: 1-702 <SCH)
A; Cross references: GB:M17303; NID:g178676; PIDN:AAB59513.1; PID:g178677
A; Cross references: GB:M17303; NID:g178676; PIDN:AAB59513.1; PID:g178677
A; Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-T
B; Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P.
Mol. Cell. Biol. 7, 3321-3320, 1987
A; Title: Isolation and characterization of full-length functional cDNA clones for hum
A; Reference number: A27773; MUID:88038876

A; Molecule type: mRNA
A; Residues: 1-702 <BEA>
A; Residues: 1-702 <BEA>
A; Residues: 1-703 <BEA>
A; Cross-references: GB: M29540; NID: g180222; PIDN: AAA51967.1; PID: g180223
B; Barnett, T.; Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A; Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA an A; Reference number: A31037; MUID: 89122014
A; Accession: A31037

A; Molecule type: mRNA
A; Residues; 1-702 < BARP
A; Residues; 1-702 < BE.M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
A; Note: the authors translated the codon GTG for residue 130 as Leu
R; Oikawa, S.; Nakazato, H.; Kosaki, G.
Biochem. Biophys: Res. Commun. 142, S11-518, 1987
A; Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from CDNA
A; Reference number: A25845, MUID:87128144
A; Residues: 5-702 < OIK>
A; Reference number: S08106
A; Reference number: S08106
A; Recession: S08106
A; Residues: 5-302 < OIZ>
A; Residues: 5-302 < OIZ

A;Cross-references: EMBL:X16455; NID:g29854; PIDN:CAA34474.1; PID:g825638 R;Barnett, T.

Ribathett, 1. submitted to the EMBL Data Library, September 1991 A:Description: Genomic DNA sequence upstream of the translational start of the carcin A:Reference number: S31737

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ANOTE: expression of Brca2 detected in midgestation embryos and adult testis, thymus C; Superfamily: breast cancer tumor suppressor BRCA2 C; Keywords: tumor suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;McAllister, K.A.; Haugen-Strano, A.; Hagevik, S.; Collins, N.K.; Brownlee, H.; Futr submitted to the EMBL Data Library, February 1997
A;Description: Characterization of the mouse and rat homologs of the BRCA2 breast can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dreast cancer tumor suppressor Brca2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
C;Accession: T30904
R;Connor, F.; Smith, A.; Wooster, R.; Stratton, M.; Dixon, A.; Campbell, E.; Tait, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U65594; NID:g1743859; PID:g1743860; PIDN:AAC23702.1
A;Experimental source: strain C57B1/6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-3329 <MCA>
A;Cross-references: EMBL:U89652; NID:92443438; PID:92443439; PIDN:AAB71377.1
A;Experimental source: strain CD1; 129Sv; ICR Swiss
                                                                                                                                breast cancer tumor suppressor Brca2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast cancer susceptibility protein BRCA2 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                               R;Sharan, S.K.; Bradley, A. Genomics 40, 234-241, 1997
A;TitLe: Muribne Brca2: sequence, map position, and expression pattern.
A;Reference number: 220894; MUID:97237041
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Pred. No. 1.2e+02;
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Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: BRCA2
C;Superfamily: breast cancer tumor suppressor BRCA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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77.8%;
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Best Local Similarity 77.0
From Tr. Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-3328 <SHA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: Brca2
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T30904
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88.9%; Pred. No. 3
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Best Local Similarity 88.۶۰
ما 8; Conservative
                                                                              A: Residues: 1-141 <BA2>
                      A; Molecule type: DNA
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C;Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
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75.0%;
                                                                          72.9%;
87.5%;
                                                                     Query Match 72.9
Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity
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R; Allen, A.G.; Perham, R.N.
FEBS Lett. 287, 206-210, 1991
A; Title: Two lipoyl domains in the dihydrolipoamide acetyltransferase chain of the pyruv A; Reference number: S16988; WUID:91348216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology C;Reywords: FAD: flavoprotein; lipoamide; NAD; oxidoreductase; redox-active disulfide; F;ll-39/Region: beta-alpha-beta FAD nucleotide-binding fold F;47-52/Disulfide bonds: redox-active #status predicted
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Hum. Mol. Genet. 6, 291-300, 1997
A:Title: Cloning, chromosomal mapping and expression pattern of the mouse Brca2 gene.
A:Reference number: 220931; MUID:97217789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterococcus faecalis (fragment)
                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-3329 <CON>
A;Cross-references: EMBL:UB2270; NID:g1854950; PID:g1854951; PIDN:AAB48306.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein YMR241w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM9408.03
C;Species: Saccharomyces cerevisiae
C;Date: 27-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.Alternate names: pyruvate dehydrogenase multienzyme complex chain E3
C.Species: Enterococcus faecalis
C.Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 30-Jun-1997
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 332. Pred, No. 1.2e+02;
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A; Residues: 1-57 <ALL>
A; Note: the source is designated as Streptococcus faecalis C; Genetics:
                                                                                                                                                                                                                                                            tumor suppressor BRCA2
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Pred. No. 4;
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R; Gentles, S; Bowman, S.
R; Boultted to the EMBL Data Library, March 1995
A; Reference number: $56053
A; Accession: $56055
A; Molecule type: DNA
A; Residues: 1-314 <GEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dihydrolipoamide dehydrogenase (EC 1.8.1.4)
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Best Local Similarity 77.87
France 7; Conservative
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Matches 5; Conservative
                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                             C; Keywords: tumor suppressor
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42 YIGGVCLNV 50
                                                                                                                                                                                                                                                          Superfamily: breast
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A;Map position: 13R
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YLSGACLNL
                                                                        A; Accession: T30904
                                                                                                                                                                                                                                    A; Map position: 5
                                                                                                                                                                                                               A; Gene: Brca2
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A; Molecule type: mRNA
A; Residues: 1-70, E; 72-137, Q', 139-252, A', 254-301, D', 303-690, P', 692-738, R', 740-7
5-1975, V', 1977-3389, Q', 3389-2890, HV', 3883-4003, HV', 4006-4302 CALE>
A; Cross-references: GB: U24497; NIDS: 9799334; PIDN: AAC50128.1; PID: 9799335; GB: U24499
R; Ward, C.J.; Peral, B.; Hughes, J.; Thomas, S.; Gamble, V.; MacCarthy, A.B.; Sloane-aris, J.J.; Dauwerse, H.G.; Peters, D.J.M.; Breuning, M.H.; Nellist, M.; Brook-Carter W.; van den Ouwelland, A.M.W.; Eussen, B.; Verhoef, S.; Lindhout, D.; Halley, D.J.J.
Cell 77, 881-894, 1994
A; Title: The polycystic kidney disease 1 gene encodes a 14 kb transcript and lies wit A; Accession: A44604
A; MUD: 94273192
A; Accession: A44604
A; Status: significant sequence differences
A; Status: significant sequence differences
A; Cross-references: GB: L33243
A; Cross-references: GB: L33243
A; Cross-references: GB: L33243
B; Ward, C.J.; Peral, B.; Hughes, J.; Thomas, S.; Gamble, V.; MacCarthy, A.B.; Sloane-aris, J.J.; Dauwerse, H.G.; Peters, D.J.M.; Breuning, M.H.; Nellist, M.; Brook-Carter W.; van den Ouwelland, A.M.W.; Eussen, B.; Verhoef, S.; Lindhout, D.; Halley, D.J.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: GDB:PKD1
A;Cross-references: GDB:120293; OMIM:173900; OMIM:601313
A;Map position: 16p13.3-16p13.3
C;Superfamily: human polycystic kidney disease protein 1; proteoglycan carboxyl-termi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Reference number: A. 83971
A. Accession: A. 83971
A. Accession: A. 83971
A. Accession: A. 83971
A. Molecule: L. 4302
A. Molecule: L. 4302
A. Molecule: L. 4302
A. Molecule: L. 4302
A. Cross-references: GB:L33243; NID:g904222; PIDN:AAC37576.1; PID:g904223
B. Cross-references: GB:L33243; NID:g904222; PIDN:AAC37576.1; PID:g904223
B. A. Torosian. B. 289-298, 1995
A. Tric Bolycystic kidney disease: the complete structure of the PKD1 gene and 1ts par. Reference number: A56520; MUID:95254638
A. Reference number: A56520
A. Status: preliminary; nucleic acid sequence not shown
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F:24-4302/Product: polycystic kidney disease protein 1 #status predicted <MAT>
F:123-170/Domain: proteoglycan carboxyl-terminal homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                               A38971
polycystic kidney disease protein 1 precursor - human
polycystic kidney disease protein 1 precursor - human
C;Species: Homo sapiens (man)
C;Species: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 08-Oct-1999
C;Accession: A38971; A56520; A44604
S;Harris, P.C.
submitted to GenBank, May 1995
                                                                                                      Gaps
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A;Contents: annotation; erratum
A;Note: this is a revision to the sequence from reference A44604
         Length 314;
                                                                                                 Indels
         5
         Score 35; DB;
Pred. No. 20;
0; Mismatches
DB
20;
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A;Contents: annotation; erratum
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Length 4302;

Score 35; DB 2; 1 Pred. No. 2.3e+02;

Gaps

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Length 451; Indels

5

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A.Reference number: S15235; MUID:91194546
A.Recession: S15236
A.Accession: S15236
A.Accession: S15236
A.Accession: S15236
A.Recission: S15236
A.Residues: 1-451 
A.Residues: 1-451 
A.Cross-references: EMBL:X54201; NID:945324; PIDN:CAA38122.1; PID:945326
C.Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homolog
C.Reywords: FAD; flavoprotein; NADP; oxidoreductase
C.Reywords: FAD; flavoprotein; NADP; oxidoreductase
F:8-443/Domain: dihydrolipoamide dehydrogenase homology <br/>
ADLD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Molecule type: DNA
A;Residues: 1-2335 -SSCO.
A;Cross-references: EMBL:U07603; NID:g467226; PIDN:AAA81947.1; PID:g467227
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Mesidues: 1-114 <MUR>
A; Cross-references: EMBL:U64836; PIDN:AAB04834.1; GSPDB:GN00023; CESP:F10G2.9
A; Experimental source: strain Bristol N2; clone F10G2
C; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: GESP:F10G2.9
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29869
R;Murray, J.; Wohldmann, P.
Submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid F10G2.
A;Reference number: Z20701
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Pred. No. 2.1e+02;
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100.0%; Pred. No. ...
0; Mismatches
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Pred. No. 44;
2; Mismatches
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55.6%;
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A;Introns: 472/3; 1310/3; 1821/3
C;Superfamily: G surface protein
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 55.00,
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Best Local Similarity
Matches 6; Conserv
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A; Introns: 61/3; 94/3
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892 YLSGAC 897
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B49181
beta B2-crystallin - chicken
C; Species: Gallus gallus (chicken)
C; Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
C; Accession: B49181
R; Sawada, K.; Agata, K.; Eguchi, G.
Exp. Eye Res. 55, 879-887, 1992
A; Title: Crystallin gene expression in the process of lentoidogenesis in cultures of chickener number: A49181; MUD:93137981
A; Reference number: A49181; MUD:93137981
A; Reference number: A9181
A; Residues: 1-219 cSAW>
A; Cossion: B49181
A; Molecule type: nucleic acid
A; Residues: 1-219 cSAW>
A; Cross-references: GB: S52330; NID: 9264001; PIDN:AAB25042.1; PID: 9264002
A; Experimental source: lens epithelial cells
A; Note: sequence extracted from NCBI backbone (NCBIN:123033, NCBIP:123034)
C; Superfamily: beta-crystallin
C; Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S15236
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Cr. Species: Mus musculus (house mouse)
Cr. Species: Mus musculus (house mouse)
Cr. Species: Musculus (house mouse)
Cr. Species: J. H.
Immunogenetics J. 343-353, 1985
A. Title: Family organization of mouse H-2 class I genes.
A. Reference number: 154413; MUID:85206117
A. Recession: 168703
A. Rocession: 168703
A. Rocession: 168703
A. Rocession: 168703
A. Rocession: 191 < RES.
A. Cross-references: GB:M14833; NID:g199298; PIDN:AAA39566.1; PID:g554214
Cross-references: GB:M14833; NID:g199298; pidn:AaA39566.1; PID:g554214
Cross-references: GB:M14833; NID:g199298; pidn:AaA39566.1; Pid:g554214
Cross-references: GB:M14833; NID:g199298; pidn:AaAa39566.1; Pid:g554214
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       Indels
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   2;
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Pred. No. 9.8;
       Mismatches
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87.5%; Pred. No. ;
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85.7%;
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Best Local Similarity 85.7
Matches 6; Conservative
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Matches 7; Conservative
       Conservative
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34 LSGACPNL 41
                                                                       1 YLSGACLN 8
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68 YLEGACL 74
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Gaps

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Indels

Length 2395;

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S07114.

MHC class I histocompatibility antigen Ch28 alpha chain precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Species: Pant-1997 *sequence_revision 19-Mar-1997 *text_change 21-Jan-2000
C;Accession: S07114
R;Lawlor, D. A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A;Title: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A;Reference number: S06424; MUID:88319000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-345 < LAW>
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Reywords: glycoprotein; membrane protein
F; 217-282/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 2;
Pred. No. 54;
0; Mismatches
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Job time: 7638 sec
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66.7%;
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Matches 6; Conservative
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180 YLEGECLEL 188
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206 ISGACMN 212
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A; Status: preliminary
   2 LSGACLN 8
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B:Ma, T.: Yang, B.: Verkman, A.S.
Biochem. Biophys. Res. Commun. 240, 324-328, 1997
Biochem. Biophys. Res. Commun. 240, 324-328, 1997
A.Title: Cloning of a novel water and urea-permeable aquaporin from mouse expressed strc. A:Reference number: JC5806; MJID:98049830
A:Rocession: JC5806
A:Molecule type: mRNA
A:Residues: 1-261 <AAA>
A:Cross references: DDBJ:AF018952; NID:92353796; PIDN:AAB68847.1; PID:92353797
C:Comment: This protein functions as a mercurial-sensitive water channel.
C:Superfamily: lens fiber membrane major intrinsic protein
C:Superfamily: lens fiber membrane major intrinsic protein
C:Superfamily: NPA motif
F:320-212/Region: NPA motif
F:35.139/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
C;Accession: JC5622
R;Ishlbashi, K.; Kuwahara, M.; Kageyama, Y.; Tohsaka, A.; Marumo, F.; Sasaki, S.
Blochem. Blophys. Res. Commun. 237, 714-718, 1997
A;Title: Cloning and functional expression of a second new aquaporin abundantly expresse A;Reference number: JC56,22; MUID: 97445104
A;Reference number: JC56,22; MUID: 97445104
A;Accession: JC56622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-263 <ISH>
A; Residues: 1-263 <ISH>
A; Cross-references: DDBJ-AB005547; NID:92346967; PIDN:BAA21918.1; PID:92346968
C; Comment: This protein is a water channel protein which plays a role in the regulation
C; Superfamily: lens fiber membrane major intrinsic protein
C; Superfamily: lens fiber membrane major intrinsic protein
F; 39-59/Domain: transmembrane #status predicted <TM1>
F; 65-84/Domain: transmembrane #status predicted <TM2>
F; 94-96/Region: NPA motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                       C.Species: Mus musculus (house mouse)
C.Date: 27-Jan-1998 #sequence_revision 13-Mar-1998 #text_change 13-Aug-1999
                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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231-250/Domain: transmembrane #status predicted <TM6>
141/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Score 33; DB 2; Length 114;
Pred. No. 19;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 2; Length 261;
Pred. No. 41;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.8%; Score 33; DB 2; Length 263; 71.4%; Pred. No. 42; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;109-130/Domain: transmembrane #status predicted <TM3>F;159-179/Domain: transmembrane #status predicted <TM4>F;182-204/Domain: transmembrane #status predicted <TM5>
68.8%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 68.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 71.44
Matches 5; Conservative
                                                             Conservative
Query Match
Best Local Similarity
Matches 5; Conserv
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47 YMAGNCFNL 55
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204 ISGACMN 210
                                                                                                                 1 YLSGACLNL 9
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Gaps

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Length 345; 3; Indels

us-09-529-121-5.rsp

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

December 16, 2000, 03:05:20 ; Search time 69.45 Seconds (without alignments) 4.140 Million cell updates/sec Run on:

US-09-529-121-5 48

1 YLSGACLNL 9 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

87993 seqs, 31947931 residues Searched:

87993 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| | \$ | Description | P06731 homo sapien | | Q04013 saccharomyc | | gallu | pseudon | P56404 mus musculu | P56405 rattus norv | | | тасаса | | haemo | _ | _ | | | P14240 lymphocytic | | P02523 rattus norv | - | | _ | | | P53796 homo sapien | 009028 rattus norv | P51513 homo sapien | P55931 sus scrofa | | 528 bacte | 0x2 rattu | Q02779 homo sapien |
|-----------|---|-------------|--------------------|------------|--------------------|------------|------------|------------|--------------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--------------------|-----------|--------------------|------------|------------|------------|------------|------------|--------------------|--------------------|--------------------|-------------------|------------|------------|-----------|--------------------|
| SUMMARIES | £ | #D | CCEM_HUMAN | BRC2_MOUSE | YM78_YEAST | PKD1_HUMAN | CRB2_CHICK | GSHR_PSEAE | AOP8_MOUSE | AQP8_RAT | 1C28_PANTR | ADH1_PICST | HLAF_MACMU | HLAF_HUMAN | Y093_HAEIN | DLDH_MYCGE | DLDH_MYCPN | ILV2_BRANA | ILVB_ARATH | RRPO_LYCVA | VA31_VARV | CRB1_RAT | CRB1_BOVIN | YXKO_BACSU | YM06_MARPO | SCRK_PEDPE | YAV6_SCHPO | NTCS_HUMAN | GAAP_RAT | NOA1_HUMAN | ETFD_PIG | ETFD_HUMAN | TSPE_BPP22 | NAH5_RAT | M3KA_HUMAN |
| | 2 | | | | | | | 7 | | - | • | | - | | | | | | | 7 | | | | | | | | | | | 7 | ٦ | Н | - | |
| | 1000 | reng cu | 702 | 3329 | 314 | 4303 | 218 | 451 | 261 | 263 | 346 | 348 | 348 | 362 | 368 | 457 | 457 | 637 | 670 | 2210 | 140 | 248 | 252 | 276 | 277 | 288 | 362 | 426 | 440 | 510 | 607 | 617 | 667 | 868 | 954 |
| ø | Query | | 75.0 | 75.0 | 72.9 | 72.9 | 70.8 | 70.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 8.89 | 68.8 | 8.89 | 68.8 | 68.8 | 68.8 | 68.8 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 66.7 | 9 |
| | o L | 3CO1 6 | 36 | 36 | 32 | 35 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| | Result | 2 | 1 | 7 | m | 4 | 2 | 9 | 7 | 80 | Q | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 | 30 | 31 | 32 | 33 |

| Q27171 paramecium P03132 adeno-assoc P82010 beta vulgar P14430 mus musculu P14428 mus musculu P14427 mus musculu P00991 mus musculu P009991 mus musculu | P3000 peacoundias P36295 herpes simp P10238 herpes simp Q00157 ictalurid h P42701 homo sapien |
|---|---|
| DYHC_PARTE VNCA_AAV2 AX2_BETVU HAIB_MOUSE HAIA_MOUSE HAIW_MOUSE HAIW_MOUSE | 1263 HSV11 1E63 HSV11 1E63 HSV11 VG58 HSV11 112R HUMAN |
| | |
| 4540 536 326 328 368 368 | 511 512 599 662 |
| 665 665 665 665 665 665 665 665 665 665 | 64.6 64.6 64.6 64.6 |
| 31 31.5 31 31 31 31 31 | 31131 |
| 33334 333 4433 1403 1503 1503 1503 1503 1503 1503 1503 15 | 4 4 4 4 5 4 4 3 2 1 |

ALIGNMENTS

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COMPRISING 60% CARBOHYDRATE. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 7 IG-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC ANTIGEN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M59709; ... NOT_ANNOTATED_COS.
EMBL; M59709; ... NOT_ANNOTATED_COS.
EMBL; M59709; ... NOT_ANNOTATED_COS.
EMBL; M2940; AAA51967.1; ...
EMBL; M1542; AAA51967.1; ...
EMBL; M1542; AAA51972.1; ...
PIR, A36319; A36319.
MIM; 114800; ...
PITERPRO, IPRO03006; ...
PFRAM; PF00047; ig; 7.

Immunoglobulin domain; Glycoprotein; GPI-anchor; Membrane; Signal.
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REMOVED IN MATURE FORM.
IG-LIKE DOMAIN 1.
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IG-LIKE DOMAIN 5.
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IG-LIKE DOMAIN 6.
IG-LIKE DOMAIN 7.
N-LINKED (GLCNAC. ..) (POT N-LINKED (GLCNAC. ...) (POT
                                                                                                                                       DATABASE: NAME=PROW; NOTE=CD guide CD66e entry; WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD66E.HTM".
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M59255; AAA62835.1; JOINED.
M59257; AAA62835.1; JOINED.
M59257; AAA62835.1; JOINED.
M59259; AAA62835.1; JOINED.
M59259; AAA62835.1; JOINED.
M59269; AAA662835.1; JOINED.
M59260; AAA662835.1; JOINED.
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McAllister K.A., Ramachandran S., Haugen-Strano A., Fiedorek F.T. Jr.,
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Hamm. Genome 8:30-541(1997).

-!- FUNCTION: MAY PARTICIPATE IN A PATHWAY ASSOCIATED WITH THE ACTIVATION OF DOUBLE-STRAND BREAK REPAIR AND/OR HOWOLOGOUS RECOMBINATION (BY SIMILARITY).

-! SUBDUIT: INTERACTS WITH RAD51 (BY SIMILARITY).

-!- TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST EXPRESSION IN CEREBELLUM, TESTIS, ILEUM, APPENDIX, EPIDYWIS, OVARY AND MAMMARY GLAND. NO EXPRESSION IN LING.

-!- DEVELOPMENTAL STAGE: IN THE MAMMARY GLAND, EXPRESSION INCREASES
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"Brca2 is coordinately regulated with Brcal during proliferation and
differentiation in mammary epithelial cells.";
Proc. Natl. Acad. Sci. U.S.A. 93:13078-13083(1996).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Connor F., Smith A., Wooster R., Stratton M., Dixon A., Campbell F
Tait T.M., Freeman T., Ashworth A.;
"Cloning, chromosomal mapping and expression pattern of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sharan S.K., Bradley A.; "Murine Brca2: sequence, map position, and expression pattern."; Genomics 40:234-241(1997).
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MISSING (IN REF. 4). ; 6299AE26CDDBDB5C CRC64;
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BRC2_MOUSE

D BRC2_MOUSE

AC P97929; P97383; 035922;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DC-1998 (Rel. 37, Last sequence update)

DT 0-CT-2000 (Rel. 40, Last annotation update)

DF 0-CT-2000 (Rel. 40, Last annotation update)

DF 0-CT-2000 (Rel. 40, Last annotation update)

DF 0-CT-2000 (Rel. 40, Last annotation update)
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Pred. No. 1
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SEQUENCE OF 18-200 FROM N.A.
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Best Local Similarity 88.>
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MEDLINE; 97384941.
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MEDLINE; 97237041.
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                 S - - F ( IN STRAINS C57BL/6 AND 129/SV).

T - > P ( IN STRAIN 199/SV).

H - > P ( IN STRAIN 199/SV).

I - > V ( IN STRAIN C57BL/6).

I - > V ( IN STRAIN C57BL/6).

GF - > RI ( IN STRAIN C57BL/6).

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E - > F ( IN STRAIN C57BL/6).
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BRCA2 5.
BRCA2 6.
BRCA2 7.
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PROSITE; PS50138; BRCA2_REPEAT; 6.
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DRAMATICALLY DURING PREGNANCY
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INTERPRO; IPR002093; -.
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01-0CT-1996 (Rel. 34, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTIC KIDNEY DISEASE
PROTEIN 1).
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPORHETICAL 34.2 KDA PROTEIN IN CUSI-RPL20A INTERGENIC REGION.
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Pred. No. 13;
0; Mismatches 1; Indels
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INTERPRO; IPR01993: -
PFAM, PF00153; mito_carr; 2.
Hypothetical protein.
SEQUENCE 314 AA; 34184 MW; EB483C715D195BED CRC64;
                                              314 AA.
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                                              PRT;
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87.5%;
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Best Local Similarity 87.5
المراجعة 7; Conservative
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                                                                                                                                                                               XMR241W OR YM9408.03
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P98161;
                                           YM78_YEAST
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RESULT 3
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PKD1_HUMAN
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Gaps

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Indels

2;

Pred. No. 69; Score 36;

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Conservative

YLSGACLNL 9

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Query Match Best Local Similarity Matches 7; Conserv

75.0%; 77.8%;

DB 1; Length 3329;

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Ravine D.;
                                                                     Maccarthy A.B., Sloane-Stanley J., Buckle V.J., Kearney L.,
Higgs D.R., Ratcliffe P.J., Harris P.C., Roelfsema J.H.,
Spruit L.L., Saris J.J., Dauwerse H.G., Peters D.J.M.,
Breuning M.H., Nellist M., Brook-Carter P.T., Maheshwar M.M.,
Cordeiro I., Santos H., Cabral P., Sampson J.R., Janssen B.,
Hesseling-Janssen A.L.W., van den Ouweland A.M.W., Eussen B.,
The polycystic kidney disease I gene encodes a 14 kb transcript and
lies within a duplicated region on chromosome 16. The European
Polycystic Kidney Disease Consortium.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS T-2760; P-2761; V-2763; T-2764; Q-2791; T-2826; L-3008 & L-3064.
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"An unusual pattern of mutation in the duplicated portion of PKD1 revealed by use of a novel strategy for mutation detection.";
Hum. Mol. Genet. 6:1473-1481(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Three novel mutations of the PKD1 gene in Italian families with autosomal dominant polycystic kidney disease."; Hum. Mutat. 10:164-167(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Constantinides R., Xenophontos S., Neophytou P., Nomura S., Pierides A., Constantinou-Deltas C.D.; "New amino acid polymorphism, Ala/Val4058, in exon 45 of the polycystic kidney disease I gene: evolution of alleles.";
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                                                      Ward C.J., Peral B., Hughes J., Thomas S., Gamble V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene reveals six novel mutations." Am. J. Hum. Genet. 58:86-96(1996).
SEQUENCE OF 2769-4303 FROM N.A.
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DISEASE: DEFECTS IN PKD1 ARE THE CAUSE OF AUTOSOMAL DOMINANT POLYCYGTIC KIDNEY DISEASE (ADPKD), A COMMON AUTOSOMAL DOMINANT GENETIC DISEASE AFFECTING ABOUT 1 OUT 1000 INDIVIDUALS. IT IS CHARACTERIZED BY PROGRESIVE FORMATION AND ENLARGEMENT OF CYSTS IN BOTH KIDNEYS, TYPTCALLY LEADING TO END-STAGE RENAL DISEASE IN ADULT LIFE. CYSTS ALSO OCCURS IN THE LIVER AND OTHER ORGANS. SIMILARITY: THE REPEATED LEUCING-RICH (LRR) SEGMENT IS FOUND IN MANY PROTEINS. NUMBER IN THIS PROTEIN: 2, FRAMED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00500; POLYCYSTIN.
PR05TIE; PS5041, C_TYPE_LECTIN_2; 1.
Signal; Leucine-repeat; Lectin; Repeat; Glycoprotein; Transmembrane; Disease mutation; Polymorphism; 3D-structure.
                                                                                                       (PKD).
                                                                                        LRR N-FLANK AND LRR C-FLANK.
SIMILARITY: CONTAINS 16 POLYCYSTIC KIDNEY DISEASE DOMAINS (PR SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN (ATYPICAL, THE POTENTIAL CALCIUM-BINDING SITE IS MISSING).
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
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MIM; 601313; -.
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PF01462; LRRNT; 1.
PF00801; PKD; 17.
PF01477; PLAT; 1.
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MEDLINE; 91194546.
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01-OCT-1994
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                                                                                                                                                                                                                                                                        RESULT 6
GSHR_PSEAE
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European Bioinformatics Institute. There are no restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES OF HIGHER ORDER. THE STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY).

-1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.

-1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sawada K., Agata K., Eguchi G.;
"Crystallin gene expression in the process of lentoidogenesis in cultures of chicken lens epithelial cells.";
Exp. Eye Res. 55.879-887(1992).
-i- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS OF THE VERTEBRATE EYE LENS.
                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                (POTENTIAL)
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                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                        POTENTIAL
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                                                                                                                                                                                                                                                       Length 4303;
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                                                                                                                                                                                                                                                               Pred. No. 1.3e+02;
0; Mismatches 2;
                                                                                                                                                                               (GLCNAC.
                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                       (GLCNAC.
                                                                                                                                                                                                                                       (GLCNAC
                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                            01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
BETA CRYSTALLIN B2 (BP).
                                                                                                                                                                                                                                                                                                                                               218 AA
                                                                                                                                                      SIMILARITY
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               POTENTIAL.
                                                                                                                                                     BY SIMILAR
BY SIMILAR
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N-LINKED (
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N-LINKED
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                                                                                                                                                                                                                                                       72.9%;
75.0%;
                                                                                                                                                                                                                                                                        6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
                                                                                              3580
3603
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Best Local Similarity
Matches 6; Conserv
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3560
3583
3674
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4055
4086
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Q05714;
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CARBOHYD
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                               PRANSMEM
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       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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-!- SUBUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.
-!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perry A.C.F., Ni Bhriain N., Brown N.L., Rouch D.A.; "Molecular characterization of the gor gene encoding glutathione reductase from Pseudomonas aeruginosa: determinants of substrate specificity among pyridine nucleotide-disulphide oxidoreductases."; Mol. Microbiol. 5:163-171(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - FUNCTION: MAINTAIN HIGH LEVELS OF REDUCED GLUTATHIONE IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 218;
                                                                                                                                                                                                                                                                                                                                                                       ACETYLATION (BY SIMILARITY).
N-TERMINAL ARM.
MOTIF 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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78C77D24CBB3F8E2 CRC64;
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(Rel. 30, Last annotation update)
REDUCTASE (EC 1.6.4.2) (GR) (GRASE).
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                                                                                                                                                                                                                                                                   PRUSITE; PS00225; CRYSTALLIN_BETAGAMMA; 3.

Eye lens protein; Duplication; Acetylation.

INIT_MET 0 0 BY SIMILARITY.

MOD_RES 1 1
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Pred. No. 15;
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(Rel. 20, Last sequ
(Rel. 30, Last anno
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ΜΣ
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87.5%;
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                                                                                                                                                                                                                                                       PFAM; PF00030; crystall; 2.
PROSITE; PS00225; CRYSTALLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               161
205
218
24929 1
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55
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119
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INTERPRO; IPR001064;
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9

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Transport; Transmembrane.
DOMAIN
TRANSMEM
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                                         DOMAIN
                                                              DOMAIN
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"Cloning of a novel water and urea-permeable aquaporin from mouse expressed strongly in colon, placenta, liver, and heart.";

Biochem. Biophys. Res. Comun. 246:324-328(1997).

-I-FINCTION: FORMS A WATER-SPECIFIC CHANNEL; MERCURY-SENSITIVE. ALSO PERMEABLE TO UREA BUT NOT TO GIVEGRAC.

-I-SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-I-TISSUE SPECIFICITY: COLON, LIVER, HEART AND PLACENTA.

-I-SIMILARITY: BELONGS TO THE TRANSMEMBRANE CHANNEL MIP FAMILY.
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                       FAD (FLAVIN PART) (BY SIMILARITY).
PROTON ACCEPTOR/DONOR (POTENTIAL).
2924599996DB98EA CRC64;
                                                                                                                                                                                                 ;
0
                                               PRINTS; PRO0368; FADPNR.
PRINTS; PR00411; PNDROTASEI.
PROSTE; PS00076; PYRIDINE_REDOX_1; 1.
Redox_active_center; Oxidoreductase; Flavoprotein; FAD; NADP.NP_END.
                                                                                                                                                                           Score 34; DB 1; Length 451;
Pred. No. 28;
2; Mismatches 2; Indels
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
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Last annotation update)
                                                                                                                                                                                                                                                                                             261 AA
                                                                                                                REDOX-ACTIVE.
                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                       292 302 E
436 436 P
451 AA; 49237 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00230; MIP; 1.
PRINTS; PR00783; MINTRINSICP.
PROSITE; PS00221; MIP; 1.
                                                                                                                                                                           70.8%;
55.6%;
                                                                                                                                                                Query Match
Best Local Similarity 55.00,
There 5; Conservative
 EMBL; X54201; CAA38122.1;
                                                                                                                                                                                                                                                                                             STANDARD;
          PIR; S15236; S15236.
HSSP; P00390; 1ALG.
INTERPRO; IPR001100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1195271; AQP8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000425; -.
                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, C
15-JUL-1998 (Rel. 36, I
30-MAY-2000 (Rel. 39, I
AQUAPORIN 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
57
84
105
128
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/6J;
MEDLINE; 98049830.
                                                                                                                                                                                                                                || | |:|:
37 YLGGTCVNV 45
                                                                                                                                                                                                                     1 YLSGACLNL 9
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P56404;
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TRANSMEM
                                                                                                                        NP_BIND
ACT_SITE
SEQUENCE
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Sato N., Hatakeyama K., Kihara I.;
"Molecular cloning of a new aquaprin from rat pancreas and liver.";
J. Biol. Chem. 272:30329-3033(1997).
-!- FUNCTION: FORMS A WATER-SPECIFIC CHANNEL; MERCURY-SENSITIVE. IT MAY HAVE AN IMPORTANT ROLE IN SPERMATOGENESIS, IN FERTILIZATION, AND IN THE SECRETION OF PANCRETIC JUICE AND SALIVA.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN SPERM, PANCREAS AND LIVER.
SOME EXPRESSION HAS BEEN FOUND IN SALIVARY GLAND AND ABSORPTIVE COLONIC EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N'LINKED (GLCNAC. . . ) (POTENTIAL).
W; 9CB48ACAIFB5E589 CRC64;
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Ishibashi K., Kuwahara M., Kageyama Y., Tohsaka A., Marumo F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and functional expression of a second new aquaporin abundantly expressed in testis.";
                                                                                                                                                                                                                                                                                                                       Length 261;
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER, AND PANCREAS; MEDLINE; 98043735.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 237:714-718(1997).
                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            263 AA
                                                                                                                                                                                                                                                                                                                                            Pred. No. 26;
2; Mismatches
                                                                                                                                                                                                                                                                                                                       Score 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-TESTIS;
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                                                                                                                                                                                                                               27797 MW;
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                                                                                                                                                                                                                                                                                                                 Query Match 68.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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156
177
177
183
204
228
249
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204 ISGACMN 210
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                                                      DOMAIN
TRANSMEM
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FAMILY.
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000097;
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DISULFID
DISULFID
CARBOHYD
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TRANSMEM
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ADH1_PICST
DD ADD1_PICST
DD ADD1_PICST
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Matches
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01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 335:268-271(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
B34AC8ACFA596BD2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lawlor D.A., Ward F.E., Ennis P.D., Jackson A.P., Parham P.; "HLA-A and B polymorphisms predate the divergence of humans and
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                Score 33; DB 1; Length 263;
Pred. No. 27;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 90201944.
LEWIOR D.A., Warren E., Ward F.E., Parham P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
                     POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
                                                                                                               EXTRACELLULAR (POTENTIAL)
   CYTOPLASMIC (POTENTIAL).
                                                                          CYTOPLASMIC (POTENTIAL).
                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC 1; Transmembrane; Glycoprotein; Signal.
SIGNAL 1
                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                  POTENTIAL.
                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                Query Match 68.8%;
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM, PF00129; MHC_I; 1.
PFAM, PF00047; 19; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M30685; AAA87973.1; -. HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                            28055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPR000495; -. INTERPRO; IPR001039; -. INTERPRO; IPR003006; -.
                                                                                                                                               185
206
230
251
263
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141
263 AA;
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206 ISGACMN 212
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39
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87
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110
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P16215;
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TRANSMEM
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TRANSMEM
                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
DOMAIN
TRANSMEM
                                                         PRANSMEM
                                                                                             FRANSMEM
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                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
                                                                                                                                                      BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

F83E882D5C2E0971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CBS 6054;
MEDLINE; 98207831.
Cho Jr., Jeffries T.W.;
Pitchia stipitis genes for alcohol dehydrogenase with fermentative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                       68.8%; Score 33; DB 1; Length 346; 66.7%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                             Indels
                                    EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                             .;
                                                                                            CONNECTING PEPTIDE
                                                                                                                                  CYTOPLASMIC TAIL.
                    CH28 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ALCOHOL DEHYDROGENASE I (EC 1.1.1.1) (ADH 2).
ADHI OR ADHIZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and respiratory functions.";
Appl. Environ. Microbiol. 64:1350-1358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA.
                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF008245; AAC49991.1; -.
EMBL; X13397; CAA73827.1; -.
INTERPRO; IPR002085. -.
INTERPRO; IPR002328; -.
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                                111
203
203
305
305
346
185
280
280
107
                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia stipitis (Yeast).
                                  22
112
204
206
306
330
122
224
107
346 AA;
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nes 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                    IRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA F ANTIGEN) (LEUKOCYTE ANTIGEN F).
DR PROBITE; PS00059; ADH_ZINC; 1.

KW Oxidoreductase; Zinc; 1.

KM Oxidoreductase; Zinc; 1.

FT METAL 44 44 42 INC (CATALYTIC) (BY SIMILARITY).

FT METAL 67 67 ZINC (CATALYTIC) (BY SIMILARITY).

FT METAL 101 101 ZINC (SECOND ATOM) (BY SIMILARITY).

FT METAL 104 104 ZINC (SECOND ATOM) (BY SIMILARITY).

FT METAL 112 ZINC (SECOND ATOM) (BY SIMILARITY).

FT METAL 112 ZINC (SECOND ATOM) (BY SIMILARITY).

154 154 ZINC (SATALYTIC) (BY SIMILARITY).

154 154 ZINC (SATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                             Gaps
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SIGNAL 1 21 BY SIMILARITY.
CHAIN 22 348 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

BEDLINE, 3246295.
Otting N., Bontrop R.E.;
"Characterization of the rhesus macaque (Macaca mulatta) equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 38:141-145(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                     Length 348;
                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
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                                                                                                                                                                                                                                                                                                                   DB 1;
34;
                                                                                                                                                                                                                                                                                                                 Score 33; DB:
Pred. No. 34;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                   68.8%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM; PF00129; MHC_I; 1.
PFAM; PF00047; 19; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; Z21819; CAA79885.1; -.
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HSSP; P03989; IHSA.
INTERPRO; IPR001495; -.
INTERPRO; IPR01039; -.
INTERPRO; IPR03006; -.
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Macaca.
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205
297
307
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93 WLNGSCLN 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of HLA-F.";
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.
MEDLINE; 90111605.
Geraghty D.E., Wei X., Orr H.T., Koller B.H.;
"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA ANTIGEN) (LEUKOCYTE ANTIGEN F) (CDA12).
HLA-F OR HLA-F OR HLA-5.4.
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lury D., Epstein H., Holmes N.;
The human class I MHC gene HLA-F is expressed in lymphocytes.";
Int. Immunol. 2:531-537(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                     CYTOPLASMIC TAIL.
BY SIMILARITY
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
77BD7E3B9B11E0F7 CRC64;
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                                                                                                                                                                                      Length 348;
                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALPHA CHAIN F. EXTRACELLULAR ALPHA-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             362 AA
                                                                                                                                                                                    DB
34;
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                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                      Score 33;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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X
                                                                                                                                                                                    68.8%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Exp. Med. 171:1-18(1990).
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PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X17093; CAA34947.1; -.
331
348
187
282
109
39300 N
                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A60384; A60384.
PIR; JL0147; JL0147.
HSSP; P03989; 1HSA.
MIM; 143110; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                              348 AA;
                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                              182 YLEGECLEL 190
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                                                                                                                                                                                                                                                                            1 YLSGACLNL 9
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308
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NP_BIND
ACT_SITE
CONFLICT
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                                                                                COMPLEX)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NP BIND
                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                          FIGURE: 95350630.

REDLINE: 95350630.

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weldman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
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                                                                    N-LINKED (GLCNAC. .) (BY SIMILARITY). BBDD041F820A34E1 CRC64;
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                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 368;
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SEQUENCE 368 AA; 42251 MW; C77F1C9EF043B89A CRC64;
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                            DB 1;
35;
                                      CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB 1;
Pred. No. 36;
                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL PROTEIN HI0093.
                                                                                                           Score 33; DB ]
Pred. No. 35;
0; Mismatches
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Science 269:496-512(1995).
-!- SIMILARITY: BELONGS TO THE CDAR FAMILY.
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100.0%; Pre
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66.78;
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SEQUENCE FROM N.A.
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ID Y093_HAEIN
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINS-ATC. 33730 / G-37;
STRAINS-ATC. 33530 / G-37;
STRAINS-ATC. 33530 / G-37;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchmann J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
The minimal gene complement of Mycoplasma genitalium.";
DLDH_MYCGE STANDARD; PRT; 457 AA.
P47513; Q49233;
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 33, Last annotation update)
DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) (E3 COMPONENT OF PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 175:7918-7930(1993).

-!- FUNCTION: LIPOAMIDE DEHYDROGENASE IS A COMPONENT OF THE ALPHA-KETOACID DEHYDROGENASE (BY SIMILARITY).

-KETOACID DEHYDROGENASE COMPLEXES (BY SIMILARITY).

-!- CATALYTIC ACTIVITY: DIHYDROLIPOAMIDE + NAD(+) = LIPOAMIDE + NADH.

-!- COFACTOR: FAD (BY SIMILARITY).

-!- SUBGENIT: HOMODIMER (BY SIMILARITY).

-!- SUBCELLUAR LOCATION: CYTOPLASMIC.

-!- MISCELLANEOUS: THE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.

-!- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE

OXIDOREDUCTASES CLASS-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM: PF00070: pyr_redax; 1.
PRINTS: PR00368; FADPAR.
PRINTS: PR00411; PNDRDTASEI.
PROSITE: PS00076: PYRLDIME.REDOX 1; 1.
Redox-active center; Glycolysis; Oxidoreductase; NAD; Flavoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REDOX ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
BY SIMILARITY.
EYKNM -> LSRWC (IN REF. 2).
ZAOB3F11370AD072 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 306-404 FROM N.A.
STRAIN-ATCC 33530 / G-37;
MEDLINE; 94075230.
PETERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                         Mycoplasma genitalium.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
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293
437
487
457 AA;
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Length 457;

Score 33; DB 1; Pred. No. 43;

68.8%; 55.6%;

Best Local Similarity

Query Match

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Job time: 8041 sec
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01-NOV-1997 (Rel. 35, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
DIHYDROLIPOAMIDE DEHYDROGENASE (EC 1.8.1.4) (E3 COMPONENT OF PYRUVATE
                                                                                                                                                                                                                                                                                                                                                                                                                    Herrmann R.; "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUCLEIC ACIDS RES. 24:4420-4449(1996).

"INCLEIC ACID MEDIANDE DEHYDROGENASE IS A COMPONENT OF THE ALPHA-
KETOACID DEHYDROGENASE COMPLEXES (BY SIMILARITY).

"ETOACID DEHYDROGENASE COMPLEXES (BY SIMILARITY).

"INCREMENT: HOMODIMER (BY SIMILARITY).

"INCREMENT: HOMODIMER (BY SIMILARITY).

"INCREMENT: HOMODIMER (BY SIMILARITY).

"INCREMENT: HE ACTIVE SITE IS A REDOX-ACTIVE DISULFIDE BOND.

"INCREMENT: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
OXIDOREDUCTASES CLASS-I.
 Gaps
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INTERPRO; IPR001100; -
PFAM, PF00070; pyr_redox; 1.
PRINTS; PR00411; PNDRTASEI.
PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
Redox-active center; Glycolysis; Oxidoreductase; NAD; Flavoprotein;
0;
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REDOX-ACTIVE (BY SIMILARITY).
FAD (FLAVIN PART) (BY SIMILARITY).
BY SIMILARITY).
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE; 97105885.
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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| SUMMARIES | | | Description | 0 Y09529 Carcinoembryonic a | | | 9 W70045 CEA derived HLA-A2 | | | 0 Y09526 Carcinoembryonic a | | | 0 P93499 Sequence of carcin | | |
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                               or artigonists (Tb) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune responses, e.g. in vaccinated subjects, to prevent an autoimmune percent of cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA response. Cytotoxic T sequence represents a specifically claimed example of (Ia).
                 present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides W39430-W39734 are used in a novel method for the selection of
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - by measuring the intact B cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                     Score 48; DB 20;
Pred. No. 2.1e+05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method of selecting T cell peptide epitope(s) stability of HLA class I-peptide complexes on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toes REM,
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SCI SEED CAPITAL INVESTMENTS BV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Page 85; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W39723 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
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96EP-0201145.
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Best Local Similarity 100.

Matches 9; Conservative
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                                                                                                                                                                                                                                                                                   Sequence
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with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC Class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The peptide epitope W77119-W77138 were created for human tumour-specific cytocoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a mative disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an anitigen with the same epitope, or with a different cross-reactive
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disease specific immunogen - comprises disease specific cytotoxic lymphocyte epitope used to elicit melanoma specific CTL response
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0
                                                                                                                              Length 9;
                                                                                                                           Score 36; DB 18; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        cytotoxic T lymphocyte; cysteine-depleted; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 19; L
Pred. No. 2.1e+05;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VIRGINIA PATENT FOUND,
                                                                                                                                                                                                                                                                                                                                                              CEA synthetic peptide epitope 1.
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                                                                                                                             75.0%;
88.9%;
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88.9%;
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                1 YLSGACLNL 9
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1 ylsqanini
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| ylsganlnl
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(first entry)

immunisation.

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Immunogenic peptide having a human leukocyte antigen binding motif #2266.
                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 118; 150pp; English.
                            Y47655 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                              WO9945954-A1.
                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                          01-DEC-1999
                                                                                                                                                                                                                                                                                                                           16-SEP-1999.
                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                    vaccine;
                                                             Y47655;
                 147655
                                                             antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCs) pretreated with pretreatment growth factors, and incubating the APCs with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contracting the cytocoxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprises class I MHC molecules. The pretreated APCs are incubated with the cytocoxic growth factors, thereby producing activated cTLs which are contacted with a carrier to form a composition. The activated composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, and DSC, hepatitis, bacterial infection, fungal infection, malaria or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human leukocyte antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an
                                                                                                                                                                   human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                     Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                      CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsai V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood S,
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                           W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sidney J,
                                                                                                                                                                                                                                                                                                                                                         98WO-US01959
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Best Local Similarity 88.3.
                                                                                                                                                                                                                                                                                                                                                                                                                      (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presenting cells
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                                                                                                                                                                                                                                                               Homo sapiens.
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RESULT
                W70045
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Southwood

Grey HM,

Celis E,

98WO-US05039. 98WO-US05039

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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also having a human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CE HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cepproses egainst the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and the particularly important in tumour rejection and in fighting viral infections are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) cor prevent viral infections and cancers in mammals (especially humans) corprevent viral infections as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
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Score 36; DB 19; Length 9; Pred. No. 2.1e+05; 0; Mismatches 1; Indels

75.0%; 88.9%;

1 YLSGACLNL 9

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16-SEP-1999.
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                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, panticularly for treating gastrointestinal, breast, panticularly for treating of prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                        Carcinoembryonic antigen; CEA; human; agonist; antagonist; mimune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                Peptide agonists and antagonists of carcinoembryonal antigen
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Pred. No. 2.1e+05;
Mismatches 1; Indels
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                                                                                     Carcinoembryonic antigen peptide agonist CAP-1.
                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                      Zaremba S;
                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 53; 72pp; English.
                     Y09525 standard; peptide; 9 AA.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                        Synthetic
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or antigonists (1b) of human carcinoembryonal antigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating asstrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA.specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but GEA-expressing cells). (Ia) are more active than native sequence (I) and generated recognize both (Ia) and native CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenic peptide having a human leukocyte antigen binding motif #1166.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
immune response; carcinoma; gastrointestinal; breast; pancreatic bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 20; Length 9;
Pred. No. 2.1e+05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-326544/27.
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Matches 8; Conserv
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1 ylsqadini
                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1998;
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The invention relates to a method for the production of non-immunogenic acid sequence of the protein. (b) identifying in the amino acid sequence of the protein, (b) identifying the amino acid sequence on or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins. e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the protein sequence of vaccine 2 708 VI.
                                                                                                                                                                                                         Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 20; Length 107;
Pred. No. 6;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P93499 standard; protein; 178 AA.
                                                                                                                                                                                                                                                                                             Example 4; Fig 19; 77pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90..178
∕note="domain B"
97GB-0016197.
97GB-0025270.
97US-0067235.
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88.9%;
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Best Local Similarity 88.5
                                                                                     (BIOV-) BIOVATION LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-349991/48.
                                                                                                                                                                  WPI; 1999-045301/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CITY ) CITY OF
  31-JUL-1997;
28-NOV-1997;
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                                             02-DEC-1997;
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Domain
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                                                                                                                                                                                                                            New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunoglobulin; therapeutic; streptokinase; vaccine; 708.
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                                                                                                                                               Southwood
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                                                                                                                                               Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides encoding the immunogenic peptitherapeutically and for immunisation as above.
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Pred. No. 0.51;
0; Mismatches
                                                                                                                                               Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein sequence of vaccine 2 708 Vl.
                                                                                                                                                                                                                                                                                           Claim 1; Page 76; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W86133 standard; Protein; 107 AA.
                                                                                                                                               Sidney J,
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97GB-0010480.
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                     98WO-US05039
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Matches 8; Conservative
                                                                                                      (EPIM-) EPIMMUNE INC
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                       13-MAR-1998;
                                                              13-MAR-1998;
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21-MAY-1997;
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Query Match
Best Local Similarity
Matches 8; Conserv
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                                                                                     468 AA;
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                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                      RESULT 12
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                 Carcinoembryonic antigen fragments – used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens.
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                                                               CEA fragments can be used in assays to determine the presence and amt. CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128~{\rm kD} antigen.
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                   Primer; amplify; polymerse chain reaction; PCR; human; blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CER; chimmeric protein; PRLA3 epitope; anti-PRLA3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New molecules which bind carcinoembryonic antigen - used for the diagnosis, and treatment of colorectal carcinoma and for isolation
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                                                                                                                                   Length 178;
                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stewart LMD;
                                                                                                                                  DB 10;
10;
                                                                                                                                                                                                                                                                                                 BGP (1-314)/CEA (490-643) chimaeric protein.
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                                                                                                                                                     Mismatches
                                                                                                                                  Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                         "CEA (490-643)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                     "BGP (1-314)"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                              Disclosure; page 4; 15pp; English
                                                                                                                                                                                                                                         R77436 standard; Protein; 468 AA.
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                                                                                                                                75.0%;
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                                                                                                                                                      Conservative
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/note=
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                                                                                                                        Query Match
Best Local Similarity
Local 8, Conserv?
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                                                                                                     178 AA
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                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                             Protein
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indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in R77435-38 are chimaeric proteins comprising portions of human bilary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRLA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biliary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody; colorectal carcinoma; monoclonal antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 16; Length 468;
Pred. No. 28;
0; Mismatches 1; Indels
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/note= "CEA (490-C-terminal)"
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315..493
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88.9%;
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Gaps

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Length 509;

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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer; amplify; polymerse chain reaction; PCR; human;
biliary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody;
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                                                                                                                                                    Score 36; DB 16;
Pred. No. 30;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               colorectal carcinoma; monoclonal antibody
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468..511
/note= "BGP (387-430)"
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88.9%;
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                                                                                                                                                    Query Match 75.0
Best Local Similarity 88.9
Matches 8; Conservative
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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
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bound carcinoembryonic antigen (CEA). These chimaeric proteins were
used to identify the PRIA3 epitope. The PRIA3 epitope was found to be
an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA
is no longer membrane bound did not react with anti-PRIA3 antibodies
indicating that the PRIA3 epitope is not present in non-membrane bound
hybrid proteins. Antibodies which recognise the PRIA3 epitope are used
                                                                                                                                                                                 Gaps
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                                                                                                                                                  DB 16; Length 493;
29;
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                                                                                                                                                 Score 36; DB 1
Pred. No. 29;
0; Mismatches
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470..509
/note= "BGP (391-430)"
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88.9%;
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315..46
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Best Local Similarity
Matches 8; Conserv
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396 ylsganlnl 404
                                                                                                       AA;
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Search completed: December 16, 2000, 00:51:15 Job time: 18775 sec

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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRLA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q71567 is the DNA sequence which encodes carcinoembryonic antigen (CEA)
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                                                                                                                                                      Score 36; DB 16; Length 511;
Pred. No. 30;
0; Mismatches 1; Indels
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Pred. No. 39;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinoembryonic antigen; CEA; neoplastic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                  Carcinoembryonic antigen glycoprotein.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conservative
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N-PSDB; Q71567.
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098866 spinacia ol
097221 pseudomonas
09772 escherichia
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09488 boophilus m
094629 oryza sativ
035835 rattus norv
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027396 babesia bov
028112 bos taurus
091rw2 orytclagus
031653 anser caeru
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Q83332 murine hepa
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homo sapien
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KIT.

Momo saplens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Q83349
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0974J3
0914J3
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01-MAY 2000 (TrEMBLrel. 13, Last sequence update)
01-MAY 2000 (TREMBLrel. 13, Last sequence update)
LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosouria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
C-TERMINUS OF THE VIRAL REPLICASE (FRAGMENT).
Cherry leaf roll virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.; "Long, nearly identical untranslated sequences at the 3' terminal regions of the genomic RNAs of cherry leafroll virus (walnut strain).";
                                                                                                                                                                                                                                                                                                                                                                                                Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
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                             Giebel L.B., Spritz R.A.;
"Mutation of the KIT (mast/stem cell growth factor receptor)
protononcogene in human piebaldism.";
EMBL; S58152; AAB19972.1; --
EMBL; S58152; AAB19972.1; --
EMBL; S58152; AAB19972.1; --
EMBL; S58155; AAB19972.1; JOINED.

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SEQUENCE 9 AA; 875 MW; D32C74087041AEBD CRC64;
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                                                                                                                                                            0; Indels
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EMBL; Z34265; CAA84019.1; -.
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Best Local Similarity
Matches 3; Conserv
         SEQUENCE FROM N.A. MEDLINE; 92020918.
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Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J., Schneider W.J.;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                 "The laying hen expresses two different low density lipoprotein receptor-related profess."
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT).
                                                                                                                                                                                                                                  Score 17; DB 13; Length 8;
Pred. No. 3e+05;
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
GINI1 PROFEIN (FRAGMENT).
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                                                                                   receptor-related proteins.";
J. Biol. Chem. 266:19079-19087(1991).
SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;
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Best Local Similarity 80.0%;
Matches 4; Conservative (
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Matches 3; Conservative
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SEQUENCE FROM N.A.
Urbach E., Chisholm S.W.;
"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1612-1630(1998).
EMBL; AF070193; AAD23233.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.; "Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and Limnodynastes terraereginae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Limnodynastes interioris (Giant banjo frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaee;
Prochlorococcus.
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Last annotation update)
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Pred. No. 3e+05;
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Plummer N.W., Medisler M.H.;
Plummer N.W., McBurney M.W., Medisler M.H.;
"Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Blol. Chem. 272:24008-24015(1997).
EMBL; U97673; ABB80916.1;
Ionic channel.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE.
MEDLINE; 92049376.
Shimsaki S., Gao L., Shimonaka M., Ling N.;
"Isolation and molecular cloning of insulin-like growth factor-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Verteborata; Euteleostomi;
Actinopterygii; Neopterygii; Telestei; Euteleostei; Acanthopterygii;
Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae;
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT (FRAGMENT).
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Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF061830; AAF06818.1; -. Oxidoreductase.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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1NSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-6, IGFBP-6.
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76C5B73B5051F6D8 CRC64;
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SEQUENCE 8 AA; 850 MW; 9FB2CEA37EA7687D CRC64;
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3e+05;
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Waeber G., Habener J.F.,
"Novel testis germ cell-specific transcript of the CREB gene contains an attentatively spliced exon with multiple in-frame stop codons."; Endocrinology 131:2010-2015(1992).
EMBL: X68994; CAA48780.1;
                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Drechsler M., Schumacher V., Friedrich S., Wildhardt G., Giesler Schroth A., Bodem J., Royer-Pokora B.;
"Genomic structure, Alternative transcripts and chromosomal localization of the human LIM domain binding protein 1 gene
                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 13; DB 4; Length 6; 100.0%; Pred. No. 3e+05; tive 0; Mismatches 0; Indels
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
NUCLEAR LIM INTERACTOR (FRAGMENT).
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Matches 2; Conservative
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Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015(1997).
EMBL; U97672; AAB80914.1;
MGD; MGI:103169; Scn8a.
                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
CALCYCLIN-ASSOCIATED PROTEIN, CAP50-CA2+/PHOSPHOLIPID-BINDING PROTEIN
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Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

A calcyclin-associated protein is a newly identified member of the Ca2+/Phospholipid-bloiding proteins, annexin family.";

J. Biol. Chem. 267:8912-8924(1992).

SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-ONV-1999 (TrEMBLrel. 12. Last annotation update)
soDIUM CHANNEL, VOLTAGE-GATED, TYPE VIII, ALPHA POLYPEPTIDE (TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Stewart P.M., Krozowski Z.S., Gupta A., Milford D.V., Howle A.J., Sheppard M.C., Whorwood C.B.; "Hypertension in the syndrome of apparent mineralocorticoid excess due to mutation of the 11 beta-hydroxysteroid dehydrogenase type 2 gene."; Lancet 347:88-91(1996).
EMBL: S80133; AAD14324.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gorski K., Huang X., Tseng S.-Y., Rattis F., Pardoll D., Tsuchiya H.; "Denditic cell requisation of DCL1 mRNA expression."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF192526; AAF04843.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
C-TYPE LECTIN DCL1 (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
IMMEDIATE-EARLY TRANSACTIVATOR 110 (FRAGMENT)
                                                                                                                                            9 AA; 1020 MW; CEFC2EB1F5B059C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA; 1029 MW; 797BB867740DDB04 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 9 AA; 994 MW; 342161AB172EBAB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=MP;
Gu W., Huang Q., Hayward G.S.;
J. Biomed. Sci. 2:105-130(1995).
EMBL; U18080; AAA75442.1;
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                           Ouery Match
Best Local Similarity
'-hag 2; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human herpesvirus 1.
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nes 2; Conserv
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NON_TER
SEQUENCE
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SEQUENCE
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7 CL 8
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Q9QZA8
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Q69473
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STRAIN-W,
MEDLINE; 8215599.
Takagi J.S., Ida N., Tokushige M., Sakamoto H., Shimura Y.;
"Cloning and nucleotide sequence of the aspartase gene of Escherichia
                                                                                                                                        Vuorio E.; "Evidence for insufficient chondrocytic differentiation during repair of full-thickness defects of articular cartilage.";
                                                                                                                                                                                                                                                                                                                                      Gaps
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PRO ALPHA 1 TYPE III COLLAGEN PROTEIN (FRAGMENT).
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                   SEQUENCE FROM N.A.
MEDLINE: 96377339.
Metsaranta M., Kujala U.M., Pelliniemi L., Osterman H., Aho H.,
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                                                                                                                                                                                                                                                                                                  27.1%; Score 13; DB 6; Length 8; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.1%; Score 13; DB 2; Length 9; 100.0%; Pred. No. 3e+05;
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EMBL; X02307; CAA26175.1; -.
SEQUENCE 9 AA; 1061 MW; 9DE21EA5B9C72EA1 CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
11. CBETAS-+HSD2 PROTEIN (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                               8 AA; 1028 MW; B859C7272EA77371 CRC64;
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                                                                                                                                                                                            Matrix Biol. 15:39-47(1996).
EMBL; S83371; AAD14433.1; -.
                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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Q99887;
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Q99887
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TISSUE-BLOOD;
MEDLINE; 90349591.
Chelf-Zahar B., Balloy C., Le Van Kim C., Blanchard D., Bailly P.,
Hermand P., Salmon C., Cartron J.-P., Colin'Y.;
"Molecular cloning and protein structure of a human blood group Rh
polypeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.; "Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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(TremBirel. 02, Last sequence update)
(TremBirel. 07, Last annotation update)
                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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                                                                  860 MW; 37D72878676729CB CRC64;
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EMBL, 297030; CAB09726.1; -
                                                                                                            DB 4;
3e+05;
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Pred. No. 3e+05;
1; Mismatches
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                                                                                                                                       Mismatches
                                                                                                            Score 12;
Pred. No.
                                                                                                                                                                                                                                                                                           Created)
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66.7%;
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50.0%;
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
RHCE PROTEIN (FRAGMENT).
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           Hum. Mol. Genet. 0:0-0(0).
EMBL; L32080; AAA73891.1;
NON_TER 1
NON_TER 8
SEQUENCE 8 AA; 860 MW;
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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  Caskey C.T.H.;
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01-FEB-1997 (
01-AUG-1998 (
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2 FLPG 5
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SEQUENCE
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095213;
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MEDLINE; 96400908.
Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
"Mosaic structure of plasmids from natural populations of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-PLACENTA;
Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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              Length 9;
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                                         0; Indels
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                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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              ore 13; DB 12;
red. No. 3e+05;
Mismatches 0
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              Score 13;
Pred. No.
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    27.1%; Sco.
100.0%; Pre
0;
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Genetics 143:1091-1100(1996).
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01-FEB-1997 (TrEMBLrel. 02,
01-FEB-1997 (TrEMBLrel. 02,
01-JAN-1999 (TrEMBLrel. 09,
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Q15901;
01-NOV-1996 (TrEMBLrel. 01,
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AAC44238.1;
AAC44239.1;
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AAC44242.1;
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                                         Conservative
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Query Match
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'-hac 2; Conserve
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nes 2; Conserv
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Plasmid IncFII R1
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U50658;
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U50660;
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3 LNI 5
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Matches
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Electrophoresis 19:142-151(1998).
EMBL; U40497; AAC60364.1; -.
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Best Local Similarity
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P82082;
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                                                                                                                                         Gaps
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MEDLINE; 99208049.
MEDLINE; 99208049.
"Heslewcod M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
"Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis.";
Electrophoresis 19:142-151(1998).
EMBL; U40496; AAC60363.1; -.
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Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.
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Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.; "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis.";
                                                                                                                                                                                                                                                                                        Erythrura gouldiae (Gouldian finch).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Passeriformes, Passeridae, Erythrura.
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                                                                                                                    Score 12; DB 7; Length 8;
Pred. No. 3e+05;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MYOGLOBIN (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA; 890 MW; C6C1F2C865B046DE CRC64;
                                                                                       5CA861B5AB58677B CRC64;
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                           Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
Mol. Immunol. 0:0-0(0).
EMBL; U62585; AAB18735.1; -.
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1; Mismatches
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50.0%;
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Best Local Similarity 66.70,
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MM
                                                                                                                                         Conservative
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Matches 2; Conserv
         SEQUENCE FROM N.A.
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8 AA;
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                    STRAIN-F-I/RGM;
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4 YSTG 7
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastes.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                            Gaps
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"Peptides from Australian frogs. The structure of the dynastins from
Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
Aust. J. Chem. 46:1235-1244(1993).
-!- MASS SPECTROMETRY: MW=772; METHOD=FAB.
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Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;

Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;

Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";

Aust. J. Chem. 46:1235-1244(1993).

-I- MASS SPECTROMETRY: MW=786; METHOD=FAB.

Amphibian skin.

SEQUENCE 8 AA; 786 MW; 7BS8772455B05728 CRC64;
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                                                                                   Length
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;
C6C1F2C865B046DE CRC64;
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                                                                                   Score 12; DB 13;
Pred. No. 3e+05;
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50.0%;
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66.7%;
     890 MM;
                                                                                                                                         Conservative
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SEQUENCE FROM N.A.
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4 ISG 6
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SEQUENCE
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SEQUENCE.
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1 MSG
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MEDLINE; 92040090.
PRETEINE; 92040090.
PRETEINE STATE T.J., de la Maza L.M.;
PRETEISON E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
"Functional and structural mapping of Chlamydia trachomatis species-specific major outer membrane protein epitopes by use of neutralizing monoclonal antibodies.";
Infect. Immun. 59:4147-4153(1991).
SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Raboudi N., Julian J., Rohde L.H., Carson D.D.;
Raboudi N., Julian J., Rohde L.H., Carson D.D.;
"Identification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95).";
J. Biol. Chem. 267:11930-11939(1992).
SEQUENCE 9 AA: 1008 MW; CB56D0544732C732 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN VARIABLE DOMAIN IV, MOMP VD IV.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE
    Score 12; DB 13; Length 8; Pred. No. 3e+05;
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                                               3; Indels
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25.0%;
50.0%;
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Best Local Similarity 66.7
Matches 2; Conservative
                                               Conservative
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    Query Match
Best Local Similarity
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MEDLINE; 92291065.
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Matches 2; Conserv
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7 ISG
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Q9R635;
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Q27396
ID Q27396
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALDESMON-PHOSPHORYLATION SITE.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
6-PHOSPHOFFUCTO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (FRAGMENT).
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                                                                                                                                                                                                                                                         Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77326; AAA96415.1; - GEBDZC865B05044 CRC64;
SEQUENCE 9 AA; 931 MW; 6D5BDZC865B05044 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAX-1999 (TrEMBLrel. 10, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                    6D5BD2C865B05044 CRC64;
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Pred. No. 3e+05;
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Best Local Similarity 66.7%;
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Izeta A., Smerdou C., Alonso S., Penzes 2., Mendez A., Plana-Duran J., Enjuanes L.;
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MEDLINE; 95159435.
Eleouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
"Complete sequence (20 kilobases) of the polyprotein-encoding gene 1 of transmissible gastroenteritis virus.";
Virology 206:817-822(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88078100.
Rasschaert D., Gelfi J., Laude H.;
Rasschaert D., Gelfi J., Laude H.;
Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization and expression.";
Biochimie 69:591-600(1987).
EMBL, AJOH1482; CAROMO525.1; --
SEQUENCE 7 AA, 927 MW, 69D6D7273B5726F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL FUSION PROTEIN.

Dorchine transmissible gastroenteritis virus.

Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.
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3e+05;
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MEDLINE; 91378498.

IKebe M., Hornick T.;

Ibetermination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C.";

Arch. Biochem. Blophys. 288:538-542(1991).

SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;
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MEDLINE: 81001892.
Dhar R., Chanock R.M., Lai C.J.;
"Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza viral mRNA deduced from cloned complete genomic sequences.";
Cell 21:495-500(1980).
EMBL; M25045; AAA43202.1; -.
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Quinn T.W., Wilson A.C.;
"Sequence evolution in and around the mitochondrial control region in
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
(UDORN/72) HEWAGGLUTININ (SEG 4) CDNA, 3' END (FRAGMENT).
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Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group.
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Pred. No. 3e+05;
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EMBL; X77190; CAA54411.1; -.
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Matches 2; Conservative
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CYTOCHROME B. (FRAGMENT).
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Gaps

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RA Hesslinger C., Sawers G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
CSTRAIN=W3110;
RA Hesslinger C., Fairhurst S.A., Sawers G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
BR Hesslinger C., Fairhurst S.A., Sawers G.;
RA Hesslinger C., Fairhurst S.A., Sawers G.;
RN Hesslinger C., Fairhurst S.A., Sawers G.;
FT NON_TER 1 1 1
SQ SEQUENCE 8 AA; 1000 MW; 3A505EB044140DC4 CRC64;

Query Match
Best Local Similarity 50.0%; Pred. No. 3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps
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Search completed: December 16, 2000, 04:22:13
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01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1991 (Rel. 17, Last annotation update)
SEX PHEROMONE CPD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Craig R.A., Clewell D.B.;
"Isolation and structure of bacterial sex pheromone, cPD1.";
Science 226:849-850(1984).
-! FUNCTION: CPD1 IS INVOLED IN THE CONJUGATIVE TRANSFER OF BACTERIOCIN PLASMID PPD1.
                   P38644
P81780
                                            PB1813
PB1814
PB1814
PB1170
PB11661
PB19145
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AL11_CARMA
DSIP_RABIT
FAR5_ASCSU
FAR6_CALVO
FIBB_MACFU
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MOSH_CLYJA
OXYA_SCYCA
OXYT_BUFRE
OXYT_RABIT
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FAR4_HIRME
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Stomopneutes variolaris (Sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Bucchinoidea; Diadematacea; Phymosomatoida; Stomechinidae;
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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=EGG JELLY;
MEDLINE; 92097763.
Yoshimo K.-I., Takao T., Shimonishi Y., Suzuki N.;
"Determination of the amino acid sequence of an intramolecular disulfide linkage-containing sperm-activating peptide by tandem mass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    spectrometry.";
FEBS Lett. 294:179-182(1991).
-I- FUNCTION: CRAUSE STIMULATION OF SPERM RESPIRATION AND MOTILITY
THROUGH INTRACELLURAR ALKALINIZATION, TRANSIENT ELEVATIONS OF
CAMP, CGMP AND CLACIUM LEYELS IN SPERM CELLS, AND TRANSIENT
ACTIVATION AND SUBSEQUENT INACTIVATION OF THE MEMBRANE FORM OF
GUANYLATE CYCLASE.
PIR; $19329; $19329.
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-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; A29477; A29477.
INTERPRO; IPR000981; -.
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Bukaryota; Metazoa; Arthropodá; Trachesta; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
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  Indels
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01-AUG-1990 (Rel. 15, Last sequence update)
1-DEC-1998 (Rel. 37, Last annotation update)
LOCUPRESSIN (DIURETIC NEUROPEPTIDE F1/F2).
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                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cyprinus carpio (Common carp).

Bekaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
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                                                                                                   INTERCHAIN (WITH C-6') (IN F2). INTERCHAIN (WITH C-1') (IN F2).
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                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                 Length 9;
                                                                                                                                          AMIDATION.
56EB176EB451A057 CRC64;
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9 AA; 969 MW; 17FF476EB455B04B CRC64;
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100.0%; Pred. No. 8.8e+04;
ive 0; Mismatches 0;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comp. Biochem. Physiol. 14:245-254(1965).
PFAM; PF00220; hormone4; 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
Hormone, Neuropeptide; Amidation.
6 IN F1.
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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01-NOV-1995 (Rel. 32, Last seq
01-NOV-1995 (Rel. 32, Last ann
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66.78;
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Raja clavata (Thornback
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 32, C
(Rel. 32, I
(Rel. 32, L
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INTERPRO; IPR000981; -
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DISULFID 1
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Best Local Similarity
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Best Local Similarity
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Gaps

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Starratt A.N., Brown B.E., \mbox{\tt "Structure of the pentapeptide proctolin, a proposed neurotransmitter}
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                                                                                                        MEDLINE: 92195954.

Evants B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Evants B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

"Identification of RFamide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

"IMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
01-NOV-1995 (Rel. 32, Last annotation update)
FMRRAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea; Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota: Metazoa; Arthropoda: Tracheata: Hexapoda: Insecta;
Pterygota: Neoptera: Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
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BOLLINE; 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                         AMIDATION.
69D4073B30000000 CRC64;
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; Pred. No. 8.8e+04;
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21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                    22.9%; Scor.
100.0%; Pred. No. o...
0; Mismatches
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Best Local Similarity
' Local 2; Conserva
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MEDLINE; 81225865.
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MEDLINE; 86232789.
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P01373;
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SEQUENCE
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Purification and characterization of an endo-polygalacturonase from the gut of West Indies sugarcane rootstalk borer weevil (Diaprepes abbreviatus L.) larvae.";
Comp. Blochem. Physiol. 118B:861-867(1997).
-!-CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-ALPHA-D-GALACTOSIDURONIC LINKAGES IN PECTAFE AND OTHER GALACTURONANS.
-!-INDUCTION: INHIBITED BY CITRUS PGIP.
-!-MISCELLANBOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
-!-SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                   Acher R., Chauvet J., Chauvet M.-T., Crepy D.; "Phylogeny of neurophyophyseal peptides: isolation of a new hormone, glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 36, Last annotation update)
8-MAY-2000 (Rel. 39, Last annotation update)
Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
Bukaryota; Metazoa; Arthropoda; Tracheata; Haxapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cuculiformia; Curculionidae; Entiminae; Entimini; Diaprepes.
                                                                                       the ray (Raia clavata)."; 333-39, blackin. Blochin. Blophys. Acta 107, 333-396(1965).
-!- FUNCTION: ANTIDIURETIC HORMONE.
-!- FUNILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. INTERPRO. 1 PRO00981. .
PRAM: PF00220; hormone4: 1.
PROSITE; PS00264: NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                            Score 13; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                         9 9 AA; 984 MW; 17E9C76EB455B04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA.
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(Rel. 32, Last sequence update)
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66.7%;
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50.0%;
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Best Local Similarity
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Best Local Similarity
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                    MEDLINE; 66123415.
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01-NOV-1995
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P81179;
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P42562;
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PGLR_DIAAB

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100.0%; Pre
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Matches 2; Conserv
                                                                 TISSUE=LIVER;
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P05487;
01-NOV-1988 (
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MEDLINE; 93324431.
Cowden C., Stretton A.O.W.;
APZ, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
Peptides 7:67-72(1986).
-!- FUNCATION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
PIR; A01644; HORDIAL
PIR; A016411: A60411.
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0
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                                                                                                                   0; Indels
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                                                                                                  Score 11; DB 1; Length 5; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.9%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 8.8e+04;
                                                                         5 AA; 649 MW; 71B7673B44600000 CRC64;
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69D4073B5B11E350 CRC64;
                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-EBB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 37, Created)
(Rel. 37, Last sequence update)
(Rel. 37, Last annotation update)
                                                                                           22.9%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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Best Local Similarity 100.
Matches 2; Conservative
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                                                                                                                                                                                                                                                                             Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                             Neuropeptide.
SEQUENCE 5
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P99025;
15-DEC-1998 (
15-DEC-1998 (
15-DEC-1998 (
                                                                                                                                                                                               FAR2_ASCSU
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2 YL 3
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SEQUENCE
                                                                                                                                   1 YL 2
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| YL 5
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GFRP_MOUSE
                                                                                                                                                                             RESULT 9
FAR2_ASCSU
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                                                                                                                                                                                                                                                                  Submitted (AUG-1998) to the SWISS-PROT data bank,
-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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"Isolation and structure of the bacterial sex pheromone, CAD1, that induces plasmid transfer in Streptococcus faecalis.";
FEBS Lett. 178:97-100(1984).

-I- FUNCTION: CAD1 IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PADA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEX PHEROMONE CADI.

Entercococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
Enterococcus.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X. Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA; 806 MW; 71B5B057273B4700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        047DD732C735B9C7 CRC64;
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Pred. No. 8.8e+04;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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01-NoV-1988 (Rel. 09, Last sequence update)
101-NOV-1995 (Rel. 32, Last annotation update)
ARG-CONOPRESSIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA.
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                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY).
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
SWISS-2DPAGE; P99025; MOUSE.
INIT_MET 0 0
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MEDLINE; 73031727.
Acher R., Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
                                                                                                                                                                                                                                                                                                                                                                    valitocin (Val8-
                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pallini V.; Submitted (SEP-1994) to the SWISS-PROT data bank. submitted (SEP-1994) to the SWISS-PROT data bank. -1. MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
                                                                                                                                                                                                                                                                                                                         ACHER R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Adentification of 2 new neurohypophyseal hormones, valitocin (Vallaciting aspartacin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
INTERPRO: IPRO00981;
INTERPRO: IPRO00981;
PROSITE: PSO0226; hormone4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
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01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.9%; Score 11; DB 1; Length 9; 28.6%; Pred. No. 8.8e+04; Live 2; Mismatches 3; Indels
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9 AA; 996 MW; 17F8376EB444404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA; 474 MW; 75BAA865AA800000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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100.0%; Pred. No. 8.8e+04;
iive 0; Mismatches 0;
OXYA_SQUAC STANDARD; PRT; 9 AA. P42999; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
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                                                                                            ASPARTOCIN (ASPARGTOCIN).
Squalus acanthias (Spiny dogfish).
                                                                                                                                                                                                                                                                        Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 22.9
Best Local Similarity 28.6
Matches 2; Conservative
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Best Local Similarity 100.
Matches 2; Conservative
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SEQUENCE
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P38005;
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Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from Conus geographus and Conus straitus venoms.";
J. Biol. Chem. 262:15821-15824(1987).
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Eukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinoidea, Echinoidea, Gnathostomata, Clypeasteroida,
Clypeasteridae, Clypeaster.
                                                                                                                                                                                                                                            Gray W.R., Olivers B.M., Cruz L.J.;
"Peptide toxins from venomous Conus snails.";
Annu. Rev. Biochem. 57:665-700(1988).
1- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; B28495; B28495.
INTERPRO; IPRO00981; -.
PRAM; PF00220; hormone4; 1.
PROSITE: PS00250; hormone4; 1.
Hormone; Amidation.
Conus striatus (Striated cone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
Neogastropoda; Conoidea; Conidae; Conus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.9%; Score 11; DB 1; Length 9; 50.0%; Pred. No. 8.8e+04; ative 1; Mismatches 0; Indels
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17EB176EB4540050 CRC64;
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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Best Local Similarity
Matches 1; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                                                       SEQUENCE.
MEDLINE; 88058932.
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P19853;
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MOD_RES SEQUENCE

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RESULT 13

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RESULT 14 OXYA_SQUAC

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"Isolation and identification of multiple neuropeptides of the
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250.727-734 (1997).
-i. FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 7 AMIDATION (POTENTIAL)
7 AA; 770 MW; 672879CDCB5DDB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                         30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last Sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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MOD_RES 7 7 AMIDATION (PC
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                                                                                                                                                                                                                                                             STANDARD;
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Matches 2; Conserv
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P81806;
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N = N
N = 3
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ALL3_CARMA
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Sarcophaga bullata (Grey flesh fly) (Noobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Peterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- DEVELOPMENTÂL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida; Mytiloida; Mytiloide; Mytiloide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-OVARY;
MEDLINE; 94211930.
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 6 AMIDATION.
6 AA; 621 MW; 72C9C6876DD81000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 10; DB 1; La
Pred. No. 8.8e+04;
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                                                                                                                                                                  01-JNN-1990 (Rel. 13, Created)
01-JNN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Mytilus edulis (Blue mussel).
                                                                                                         6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                         PRT;
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100.0%; Pie
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100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: TO MIP I.
PIR; B27696; B27696.
Hormone; Amidation.
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Best Local Similarity 100.
Matches 2; Conservative
                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=PEDAL GANGLION;
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Best Local Similarity
Matches 2; Conserva
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                                                                                              CIP2_MYTED
P13737;
01-JAN-1990 (
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SEQUENCE
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TMOF_SARBU
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CIP2_MYTED
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Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Score 10; DB 1; Length 7;
Pred. No. 8.8e+04;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.8%; Score 10; DB 1; Length 7; 50.0%; Pred. No. 8.8e+04; Live 0; Mismatches 2; Indels
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Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eubrachyura; Portunoidea; Portunidae; Carcinus
                                                                                                                                                                                                                                                                                                                                                       30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                    7 AA.
                                                                                                                                                                                                                                                                                                       PRT;
20.8%;
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Matches 2; Conserv
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Gaps

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Mismatches

Conservative

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"A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species."; Biochem. J. 275:671-677(1991).
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Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
Grade G., tructures of neuropeptides isolated from the corpora
"Primary structures of neuropeptides isolated from the corpora
cardiaca of various cetonid beetle species determined by
pulsed-liquid phase sequencing and tandem fast atom bombardment mass
                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.";
Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 25 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pli
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Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N141) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.8%; Score 10; DB 1; Length 7; ilarity 100.0%; Pred. No. 8.8e+04; Conservative 0; Mismatches 0; Indels
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AA.
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Medolontha melolontha (Cookcher),
Geotrupes stercorosus (Dor beetle),
Pachnoda marginata (Flower beetle).
                                                                                                                                                                                                                                                                                                                                             Pinus pinaster (Maritime pine).
                                                                                                                                                                                  STANDARD;
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Best Local Similarity
Matches 2; Conserv
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P81675;
  1 YLSG
                                                   3 YAFG
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and identification of multiple neuropeptides of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
7 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                          Carcinus maenas (Common shore crab) (Green crab).
Eukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinus maenas (Common shore crab) (Green crab).
Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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llarity 50.0%;
Conservative
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Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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ID ALL4_CARMA
AC P81807;
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YLSG 4
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ID ALLS_CARMA
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Eubrachyura; Portunoidea; Portunidae; Carcinus
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Best Local Similarity
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30-MAY-2000
30-MAY-2000
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P81811;
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ALL7_CARMA
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ID ALL8_C
AC P81811
DT 30-MAY
DT 30-MAY
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Spectrometry.";
Biol. Chem. Hoppe-Seyler 373:133-142(1992).

-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA

-!- FUNCTION: THIS HORMONE, RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAUSES RELEASE OF
DIGLYCERIDES FROM THE PAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR; S15422; S15422.
PIR; S21663; S21663.
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Carcinus maenas (Common shore crab) (Green crab).

Eukaryota: Metazoa; Arthropoda: Crustacea: Malacostraca;

Eumalacostraca; Bucarida: Decapoda: Plecyemata: Brachyura;

Eubrachyura: Portunoidea: Portunidae: Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                   Neuropeptide; Amidation; Flight.

MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

MOD_RES 8 AMIDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.8e+04;
                                                                                                                                                                                 Score 10; DB 1; Length 8; Pred. No. 8.8e+04;
                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.8%; Score 10; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                  867AB775AB544736 CRC64;
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                                                                                                                                                                                                                                                                                                                      30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 17.
                                                                                                                                                                                                                                                                                                    8 AA.
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                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                  20.8%; ; 100.0%;
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8 AA; 1022 MW;
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                                                                                             INTERPRO; IPR002047; -. PROSITE; PS00256; AKH; 1.
                                                                                                                                                                                                        Conservative
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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P81815;
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P81820;
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AL12_CARMA
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0
                                                                                                                       of the
                                                                                                                                            allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROPRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Nouropeptide; Amidation; Multigene family.
MOD_RES 8 AMIDATION (POTENTIAL).
SEQUENCE 8 AA; 858 WW; C82879D5AB46D865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Biochem. 250:727-734(1997).

-I. FUNCTION: MAY ACT AS A NEUROPTRANSMITTER OR NEUROMODULATOR. IS IMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
                           MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALL7_CARMA STANDARD; PRT; 8 AA.
P81809; P81810; P81804;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 7 [CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1].
CARCINUSTATIN 7 EDWATYOCA; Arthropoda; Crustacea; Malacostraca; Euwaryota; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura; Eubrachyura; Portunoidea; Portunidae; Carcinus.
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
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                                                                                                                 "Isolation and identification of multiple neuropeptides
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825 MW; 922879CDCB4775BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 1; Le
Pred. No. 8.8e+04;
0; Mismatches 0;
TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
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Pred. No. 8.8e+04;
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CARCINUSTATIN 6.
CARCINUSTATIN 1.
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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100.0%; Pre
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Lote C.J., Weiss J.B.;

"Identification in urine of a low-molecular-weight highly polar
glycopeptide containing cystein/j-galactose.";

Biochem. J. 123:25P-25P(1971).

-I- FUNCTION: THE IDENTITY OF THE GLYCOPROTEIN FROM WHICH THIS PEPTIDE
IS DERIVED IS UNRNOWN. NO PHYSIOLOGICAL FUNCTION HAS BEEN
ATTRIBUTED. AN ERYTHROCYTE MEMBRANE GLYCOPEPTIDE HAVING A
SIMILAR STRUCTURE HAS ALSO BEEN FOUND.
   01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRFAMIDE 8.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                           Rehfeld J.F., Thorpe A.,
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.",
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
                                                                                                                                                                             Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Pred. No. 8.8e+04;
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C2D87AA1F5B1EB1E CRC64;
                                                                                                                                                                                                                                                                                                                                                      AMIDATION.
72D40699CAA44DD8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
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                                                                                                                                                                                                                                                                                                                                                                     8 AA; 957 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity luv.
                                                                                                                                                                                                                                                                                                                               Neuropeptide; Amidation.
MOD_RES 8 8
SEQUENCE 8 AA; 957 MW:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Matches 2; Conserv
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MEDLINE; 72062338.
                                                                                                                                                           MEDLINE; 92196111
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CARBOHYD
SEQUENCE 8 AA
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P02729;
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                                                                                                                                                                                                           allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blochem. 250:727-734 (1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Blochem. 250:737-734(1997).
-1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR..
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                         Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
CARCINUSTATIN 8.

Carcinus maenas (Common shore crab) (Green crab).

Eukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                   Score 10; DB 1; Length 8;
Pred. No. 8.8e+04;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                        TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA.
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(Rel. 32, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuropeptide; Amidation; Multigene family.
MOD_RES 8 AMIDATION.
                                                                                                                                                                                                                                                                                Neuropeptide; Amidation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
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50.0%;
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50.0%;
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Best Local Similarity
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Best Local Similarity
'-hos 2; Conserve
                                                                                                                                         MEDLINE; 98121193
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P41863;
01-NOV-1995 (
01-NOV-1995 (
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P81812;
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SEQUENCE
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ALL9_CARMA RESULT

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FAR8_CALVO

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LEUCOKININ VIII (L-VIII).
Leucophaea maderae (Madeira cockroach)
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MOD_RES 8 8
SEQUENCE 8 AA; 902 MW:
                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                  01-FEB-1991
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Fernlund P.;
                                                                                                                                                                                      01-FEB-1991
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P08939;
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SG 4
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                                                                                  RESULT 33
LCK8_LEUMA
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Holman G.M., Cook B.J., Nachman R.J.;
Holman G.M., Cook B.J., Nachman M.J.;
Comp. Blochem. Physiol. 88C:27-30(1987).
I- FORCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
PIR: JS0315; JS0315.
Neuropeptide: Amidation.

AMIDATION.
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       01-MAY-1992 (Rel. 22, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
HYPERTREHALOSAEMIC FACTOR (HOTH) (HYPERTREHALOSEMIC NEUROPEPTIDE).
                                                                                                                                                                                                       Gacde G., Rosinski G.;

"The primary structure of the hypertrehalosemic neuropeptide from tenebrionid beetles: a novel member of the AKH/RPCH family.";

Peptides 11:455-459(1990).

-!- FUNCTION: HYPERTREHALOSAEMIC FACTORS ARE NEUROPEPTIDES THAT ELEVEL OF TREHALOSE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH (TREHALOSE IS THE MAJOR CARBOHYDRATE IN THE HEMOLYMPH (FREHALOSE IS THE MAJOR A43976; A43976; PIR; B43976; B43976.
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                                                                          Tenebrio molitor (Yellow mealworm), and Zophobas rugipes.
Bukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cuculiformia; Tenebrionidae; Tenebrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEUCONININ V (L.V).
LEUCOPIAna maderae (Madeira cockroach).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pletrygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 1; Length 8; Pred. No. 8.8e+04; 0; Indels
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784 MW; 736365A5B9C865B8 CRC64;
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Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
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100.0%; Pre
0; '
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1005 MW;
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Best Local Similarity 100.
Matches 2; Conservative
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                                                                                                                                                                              TISSUE=CORPORA CARDIACA; MEDLINE; 90341081.
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Best Local Similarity
Matches 2; Conserv
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P19987;
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LN —
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RESULT 32 LCK5_LEUMA

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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea; Pandaloidea;
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-1- FUNCTION: THIS HORMONE ADAPTS THE ANIMAL TO LIGHT BACKGROUNDS BY STIMULATING CONCENTRATION OF THE PIGMENT OF ITS RED BODY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helman G.M., Cook B.J., Nachman R.J.;
"Isolation, primary structure and synthesis of leucokinins VII and VIII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae.";
Comp. Biochem. Physiol. 88C:31-34(1987).
-!-FUNCTION: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE
ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
-!-SIMILARITY: TO THE OTHER LEUCOKININS.
-!-SIMILARITY: TO THE OTHER LEUCOKININS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structure of the red-pigment-concentrating hormone of the shrimp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Trachéata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
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01-FBS-1994 (Rel. 28, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
RED PIGMENT CONCENTRATING HORMONE (RECH).
Pandalus borealis (Northern red shrimp).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PYRROLIDONE CARBOXYLIC ACID.
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PIR; S07139; S07139.
INTERPRESO; IPR002047; -.
PROSITE; PS00256; AKH; 1.
Pigment; Hormone; Amidation.
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8 AA; 902 MW; 736365AB59CAADD8 CRC64;
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948 MW; 86786775B9C44736 CRC64;
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Pred. No. 8.8e+04;
0; Mismatches 0;
                                                                                                                               (Rel. 17, Last sequence update)
(Rel. 17, Last annotation update)
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01-0C7-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P50) (FRAGMENT).
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
Query Match 20.8\$; Score 10; DB 1; Length 8; Best Local Similarity 100.0\$; Pred. No. 8.8e+04; Matches 2; Conservative 0; Mismatches 0; Indels
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Job time: 4566 sec
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P38644;
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UF06_MOUSE
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J. Biol. Char. 260, 4856-4863, 1985 A; Title: Characterization of the bilin attachment sites in R-phycoerythrin. A; Reference number: A22565; MUID:85182601 A; Molecule type: protein A; Molecule type: protein A; Residues: 1-6 <KLO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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\begin{array}{c} \mathbf{x} \\ \mathbf{
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cytochrome oxidase
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actin I - malaria
T-cell receptor be
T-cell receptor be
T-cell receptor be
capsid protein VP-
phosphatidylethano
neuropeptide Grb-A
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                                                                                                                                                         Search time 89.11 Seconds (without alignments) 6.409 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
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                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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                                                                                                                                                              December 16, 2000, 03:35:12
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Maximum Match 100%
Listing first 75 summaries
                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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48
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length: 9
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Gaps

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RESULT

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C;Species: Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 07-May-1999
C;Accession: C61512
Mol. Blochem. Parasitol. 2, 135-150, 1981
A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-te A;Reference.number: A61512; MUD:81172836
                                                                                                                                                                                                                                                                                                                                                                                                cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-58p-1999 #sequence_revision 20-5ep-1999 #text_change 11-May-2000
C;Accession: T13818
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Tille: The main features of the craniate mitochondrial DNA between the NDI and the A;Reference number: Z17775; MUID:97398704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: Y09527; NID:e1011465; PID:e329906; PIDN: CAA70718.1
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C;Species: Stomopneustes variolus
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 18-Jun-1993
C;Accession: S13329
R;Yoshino, K.; Takao, T.; Shimonishi, Y.; Suzuki, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)
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       Score 15; DB 2; I
Pred. No. 1.8e+05;
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Pred. No. 1.8e+05;
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A;Molecule type: DNA
                                                                            0; Mismatches
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A Molecule type: protein
A Residues: 1-8 < HOL>
C Keywords: glycoprotein
                                      Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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Al2016
formylglycinamide ribonucleotide amidotransferase (EC 2.-.-.) - chicken (fragment)
C; Species; Gallus gallus (chicken)
C; Species; Gallus gallus
C; Species; Gallus Gallus
R; Choroki, S.; Hong, B.S.; Buchanan, J.M.
Fed. Proc. 35, 1549, 1976
A; Title: Amino acid sequence at glutamine active site for FGAR-amidotransferase.
A; Reference number: A91459
A; Reference number: A91459
A; Molecule type: protein
A; Residues: 1-7 < CHN
A; Residues: 1-7 < CHN
A; Residues: 1-7 < CHN
A; Residues: 1-5 < CHN
A; Residues: Lransferase
                                                                                        Trought receptor beta chain V-D-J region (121-1E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Dectes: Mus musculus (house mouse)
C;Accession: Pr0652
C;Accession: Pr0652
D;Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: Pr0509; MUD:91277601
A;Reference number: Pr0509; MUD:91277601
A;Status: translation not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Residues: 1-6 <FEE>
A;Residues: 1-6 <FEE>
A;Residues: T-cell receptor
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F2256
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6;
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Pred. No. 1.8e+05;
0; Mismatches 1;
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31.2%; 66.7%;

Conservative

Query Match Best Local Similarity Matches 2; Conserv

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35.4%; ilarity 75.0%; Conservative

Query Match Best Local Similarity Matches 3; Conserv

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SGAC 6

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C;Species: Plasmodium falciparum
C;Species: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Date: 03-Jun-1993 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: B45525
R;Wesseling, J.G.; Snijders, P.J.F.; van Someren, P.; Jansen, J.; Smits, M.A.; Schoen Mol. Biochem. Parasitol. 35, 167-176, 1989
A;Title: Stage-specific expression and genomic organization of the actin genes of the A;Reference number: A45525; MUID:89364996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional Sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601
A;Accession: PT0605
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0509; MUID:91277601
A;Accession: PT0593
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0593
R;Feeney, A.J.
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0605
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                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-5 <WES>
A; Cross-references: GB: J03988
A; Oross-references: GB: J03988
A; Note: the authors translated the codon GAA for residue 3 as
C; Comment: The actin I gene contains no introns.
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A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.2%; Score 14; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.8e+05; Matches 3; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A)Status: translation not shown
A)Molecule type: mRNA
A)Residues: 1-6 <FEE>
A)Experimental Source: newborn thymus, strain BALB/C
C)Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.2%; Score 14; DB 2; 1 66.7%; Pred. No. 1.8e+05;
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Matches 2; Conserv
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2 SGA 4
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C; Accession: 641946
R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A; Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge
A; Reference number: A41946; MUID:92049316
A; Reference number: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 1-9 <WHE>
C; Keywords: T-cell receptor
                 A;Title: Determination of the amino acid sequence of an intramolecular disulfide linkage A;Reference number: $19329; MUID:92097763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Homo sapiens (man)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C; Accession: PT0288
R; Yamada, M; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A; Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A; Reference number: PT0222; MUID:91108337
A; Molecule type: DNA
A; Molecule type: DNA
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Pred. No. 1.8e+05;
1; Mismatches 1; Indels
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-9 < YAM>
A; Experimental source: B lymphocyte
C; Keywords: heterotetramer; immunoglobulin
                                                                                                         A; Molecule type: protein
A; Residues: 1-9 <YOS>
F;3-8/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                        31.2%;
50.0%;
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ilarity 75.0%;
Conservative (
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Best Local Similarity 50.09
Matches 2; Conservative
FEBS Lett. 294, 179-182, 1991
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Best Local Similarity
Matches 3; Conserv
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Matches 3; Conserv
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5 YSSG 8
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Y protein - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Accession: 137263
R:Waeber, G.; Habener, J.F.
B:Waeber, G.; Habener, J.F.
A:Title: Novel testis germ cell-specific transcript of the CREB gene contains an alte A:Reference number: 137263; MUID:93010691
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipecies: Gryllus binaculatus (two-spotted cricket)
Cipecies: Gryllus binaculatus (two-spotted cricket)
Cipecies: Gryllus binaculatus (two-spotted cricket)
Cipecies: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
Cipecies: 26-Jan-1996 #sequence_revision 26-Jan-1996
Cipecies: 26-Jan-1996 #sequence_revision 26-Jan-1996
Cipecies: N.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A; Title. A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A; Reference number: A57444; MUID:95403341
A; Reference number: A57444; MUID:95403341
A; Molecule type: protein
A; Residues: 1-9 <LOR>
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 20-oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43599
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
A;Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice. A;Accession: S43956; MUID:94248036
A;Molecule type: DNA.
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                                                                                       29.2%; Score 14; DB 2; Le
100.0%; Pred. No. 1.8e+05;
tive 0; Mismatches 0;
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Pred. No. 1.8e+05;
1; Mismatches 1;
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100.0%; Pred. No. ...
... 0; Mismatches
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
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C; Keywords: brain
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C;Species: murine poliovirus, Theiler's encephalomyelitis virus
C;Species: murine poliovirus, Theiler's encephalomyelitis virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C;Accession: PL0184
R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.
J. Exp. Med. 170, 2037-2049, 1889
A;Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogenici
A;Reference number: PL0184; MUID:90063468
A;Mccession: PL0184
A;Mccession: PL0184
A;Mccession: PL0184
C;Keywords: capsid protein
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PN0043
phosphatidylethanol amine-binding protein - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C; Accession: PN0043
R; Kato, H.
R; 
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PT0654
PT0654
PT0654
C; Seclas receptor beta chain V-D-J region (121-1BK) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0654
R; Feeney, A.J. 4, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A; Reference number: PT0509; MUID:91277601
A; Accession: PT0654
A; Status: translation not shown
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-7 <FEE>
A; Residues: 1-7 <FEE>
A; Residues: 1-7 <FEE>
A; Experimental source: day 4 postnatal thymus, strain BALB/C
C; Keywords: T-cell receptor
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:Keywords: capsid protein
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acetylcholinesterase (EC 3.1.1.7) 5.6S form - Pacific electric ray (fragment)
C;Species: Torpedo californica (Pacific electric ray)
C;Date: 16-Mar-1990 #sequence_revision 16-Mar-1990 #text_change 08-Nov-1996
C;Accession: A34026
R;Gibney, G.; MacPhee-Quigley, K.; Thompson, B.; Vedvick, T.; Low, M.G.; Taylor, S.S.
J; Biol. Chem. 263; Il40-1144, 1988
A;Title: Divergence in primary structure between the molecular forms of acetylcholine A;Reference number: A34026; MUID:88087239
                                                                                                                                                                              S38516
mabinlin II chain A - Yunnan caper (fragments)
mabinlin II chain A - Yunnan caper (fragments)
C;Species: Capparis masaikai (Yunnan caper)
C;Species: Capparis masaikai (Yunnan caper)
C;Accession: S38516
E;Nirasawa, S.; Liu, X.; Nishino, T.; Kurihara, Y.
Biochim. Blophys. Acta 1202, 277-280, 1993
A;Title: Disulfide bridge structure of the heat-stable sweet protein mabinlin II.
A;Reference number: S38516; MUID:94002261
A;Accession: S38516
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NIR>
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C:Species: Gallus gallus (chicken)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
C:Accession: I50210
B:Kabrun, N.; Bunstead, N.; Hayman, M.J.; Enrietto, P.J.
Mol. Cell. Biol. 10, 4788-4794, 1990
A:Title: Characterization of a novel promoter insertion in the c-rel locus. A:Reference number: I50210; MUID:90355995
A:Accession: I50210
A:Accession: I50210
A:Accession: I50210
A:Accession: I50210
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Residues: 1-7 < KAB>
A:Residues: 1-7 < KAB>
A:Coss-references: GB:M55577; NID:9555438; PID:9211661
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llarity 100.0%; Pred. No. 1.8e+05;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 2; Conserv
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N;Alternate names: glutathione S-transferase class alpha 5
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
C;Accession: S71867
R;Roulmi, P.; Anglade, P.; Debrauwer, L.; Tulliez, J.
Biochem. J. 317, 879-884, 1996
A;Title: Characterization of pig liver glutathione S-transferases using HPLC-electrospra
A;Reference number: S71864; MUID:96332484
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A; Residues: 1-7 <ROU>
C; Comment: At least five species-independent classes of cytosolic glutathion transferase c; Complex: dimer
C; Complex: dimer
C; Complex: dimer
C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            laminin B1 - western wild mouse (fragment)
C;Species: Mus spretus (western wild mouse)
C;Species: Mus spretus (western wild mouse)
C;Date: 02-011-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 149421
R;Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, C;Mann, Genome 5, 349-355, 1994
A;Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A;Accession: 149421
A;Accession: 149421
A;Accession: 149421
A;Accession: 1496: DNA
A;Reference number: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross·references: EMBL:U05736; NID:g497073; PIDN:AAB60477.1; PID:g642829
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:X68994; NID:g396171; PIDN:CAA48780.1; PID:g579816
C;Genetics:
A;Gene: CREB
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Best Local Similarity 100.(
Matches 2; Conservative
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5 CL 6
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diuretic neuropeptide F1 - migratory locust
C; Species: Locusta migratoria (migratory locust)
C; Species: Locusta migratoria (migratory locust)
C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C; Accession: A29477
R; Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schoo Biochem Biophys. Res. Commun. 149, 180-186, 1987
A;Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta A; Reference number: A29477; MulD:88077077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Note: two neuropeptides, F1 and F2, were identified. F2 is an antiparallel dimer of C;Keywords: neuropeptide
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C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C;Accession: 173804
F;Scheneider-Maunoury, S.; Croissant, O.; Orth, G.
J. Virol. 61, 3295-3298, 1987
A;Title: Integration of human papillomavirus type 16 DNA sequences: a possible early A;Reference number: 156695; MUID:87311896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M31225; NID:9190254; PIDN:AAA65996.1; PID:9553617 C;Comment: This is the hypothetical translation of a viral sequence integrated into
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151434
H4 histone - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: IS1434
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                                                                                                                      Score 13; DB 2; Length 9;
pred. No. 1.8e+05;
! Mismatches 0; Indels
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A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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A; Residues: 1-9 <PRO>
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DE5>
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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4 IAGA 7
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R:Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A 14, 245-254, 1965
A;Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce
A;Reference number: A61364
A;Accession: A61364
A;Accession: A61364
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ACH>
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F;9/Modified site: amidated carboxyl end (Gly) #status experimental
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C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:9138452
A;Accession: C41170
A;Reference number: A41170; MUID:91388452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Cyprinus carpio (common carp)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
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                           Score 13; DB 2;
Pred. No. 1.8e+05;
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50.0%;
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Matches 2; Conserv
                           Query Match
Best Local Similarity
Matches 2; Conserv
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1 MAGA 4
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Unidentified 6.5/31K protein [imported] - rice (fragment)
C;Species: Oryza sativa (rice)
C;Species: A;Species: Oryza (rice)
C;Species: 
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C; Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 28-Feb-1997
C; Accession: 157018
R; Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D. Mamm. Genome 5, 465-472, 1994
A; Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse 1 A; Reference number: 157018; MUID:95037043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A21440
variant surface glycoprotein pSLcl - Trypanosoma brucei (fragment)
c;Species: Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
C;Accession: A21440
R;Parsons, M.; Nuslson, R.G.; Watkins, K.P.; Agabian, N.
Cell 38, 309-316, 1984
A;Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
A;Reference number: A90853; MUID:84282716
A;Reference number: A90853; MUID:84282716
A;Residues: 1-8 <ARN>
A;Residues: 1-8 <ARN>
A;Cross-references: GB:K02195; NID:g162150; PID:g162151
C;Reywords: glycoprotein
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Pred. No. 1.8e+05;
2; Mismatches 0
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A;Molecule type: DNA
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C;Genetics:
A;Gene: Cftr
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1 MSG 3
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J. Exp. Med. 176, 1209-1214, 1992
A;Title: Heavy chain variable (VH) region diversity generated by VH gene replacement in
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R;Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
Nucleic Acids Ros. 12, 4939-4938, 1984
A:Title: Are there major developmentally regulated H4 gene classes in Xenopus?.
A;Reference number: I51391; MUID:84247348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (clone micro m+ 46-6 PCR) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PH4407
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A;Residues: 1-8 <SHI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
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Pred. No. 1.8e+05;
0; Mismatches 2; Indels
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A;Molecule type: mRNA
A;Residues: 1-6 <WOO>
A;Cross-references: GB:K02304; NID:g214227; PID:g55517
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Pred. No. 1.8e+05;
1; Mismatches 0;
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A; Accession: PH1407
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RESULT 35
A44873
caldesmon - rabbit (fragment)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C; Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C; Accession: A44873
A; Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protein
A; Reference number: A44873
A; Accession: A44873
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-9 < IKE>
A; Residues: 1-9 < IKE>
A; Residues: 1-9 < IKE>
A; Experimental source: skeletal myosin
A; Note: sequence extracted from NCBI backbone (NCBIP:63199)
C; Superfamily: caldesmon
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25.0%; Score 12; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 1.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels
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Search completed: December 16, 2000, 03:35:13 Job time: 5646 sec

| | | immunogenic peptid Immunogenic peptid Fragment of the EG PW 1/85A peptide. | | | | | | LFA-1 alpha subuni Indernal tryptic p Immunomodulatory p Immunomodulatory p | | | | | | | | | | | | NCA analogue Bcr-Abl epitc | | Immunogenic | Amino acid sequenc BCR-ABL-derived li | | ALIGNMENTS | | | |
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| X82882 X49030 X39584 W70043 | X47153 X47480 | Y47563 Y47563 Y01944 R37279 | K3/280 R37281 R37282 R37283 | R37284 R37285 R37286 | R37287 W13449 | W//008 W40267 | W49470 Y47757 | R09414 R88476 W04985 W44992 | W12016 Y09418 R36235 | W30073 X16679 X16687 | R61804 R87430 R80907 | W04992 W44997 | Y48863 Y47313 | Y16690 Y09423 | W97825 W04984 W44991 | W13451 Y09417 | Y78206 R61827 | R79851 R77581 | R70563 W49644 | W000890 Y53336 | Y47152 Y47422 | Y47532 | X40150 X26674 | | ALIG | | : | AA |
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| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 4.5 Compugen Ltd. | | <pre>; Search time 107.12 Seconds (without alignments) 2.873 Million cell updates/sec</pre> | | | es | eters: 61695 | | | enesedD/AA1980 DAT:* | eneseqp/AA1981_DAT:* eneseqp/AA1982_DAT:* eneseqp/AA1983_DAT:* | eneseqp/AA1984.DAT:* eneseqp/AA1985.DAT:* eneseqp/AA1986.DAT:* | eneseqp/AA1987.DAT:* eneseqp/AA1988.DAT:* | geneseqp/AA1990.DAT:* geneseqp/AA1990.DAT:* | geneseqp/AA1992.DAT:* geneseqp/AA1993.DAT:* | geneseqp/AA1994.DAT:* geneseqp/AA1995.DAT:* geneseqpyAA1995.DAT:* | geneseqp/AA1997.DAT:* geneseqp/AA1998.DAT:* | geneseqp/AA1999 . DAT : * geneseqp/AA2000 . DAT : * | dicted by chance to have a re of the result being printed, | | | Description | 1 (| Carcinoempryonic a Human carcina-embr | CEA synthetic pept CEA derived HLA-A2 | Immunogenic peptid Carcinoembryonic a | Carcinoembryonic a | Calcinoembiyonic a Carcinoembiyonic a | HLA binding peptid Peptide comprising |
| GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. | protein search, using sw model | Search time 107.12 [without alignments 2.873 Million cell | US-09-529-121-5 score: 48 :: 1 YLSGACLNL 9 | e: BLOSUM62 Gapop 10.0 , Gapext 0.5 | 268485 seqs, 34193795 residues | 6169 | seq length: 0 seq length: 9 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries | A_Geneseq_36:* 1: /sTDS6/acadata/geneseg/denesegg/AA1980_DAT:* | 2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:* 3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:* 4: /SIDS6/gcgdata/geneseq/geneseqp/AA1983.DAT:* | 5: \forestable \fo | 8: /SIDS6/gcgdata/geneseq/geneseqp/AA1987.DAT:* 9: /SIDS6/gcgdata/geneseq/geneseqp/AA1988.DAT:* 10: /SIDS6/gcgdata/geneseq/geneseqp/AA1988.DAT:* | 12: /SIDS6/gcgdata/geneseq/geneseqg/AA1990.DAT:* 12: /SIDS6/gcgdata/geneseq/geneseqg/AA1990.DAT:* 12: /SIDS6/gcgdata/qeneseqsqeneseqy/AA1991.DAT:* | <pre>13: /SIDS6/gcgdata/geneseq/geneseqp/AA1992.DAT:* 14: /SIDS6/gcgdata/geneseq/geneseqp/AA1993.DAT:*</pre> | 15: /SIDS6/gcgdata/geneseq/geneseqp/AA1994.DAT:* 16: /SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT:* 17: /GTDS6/grafa-a-frenceseggeneseqs/AA1945.DAT:* | 18: /SIDS6/gcgdata/geneseq/geneseqp/AA1997.DAT:* 19: /SIDS6/gcgdata/geneseq/geneseqp/AA1997.DAT:* | /SIDS6/gcgdata/geneseq/geneseqp/AA1999 .DAT:* /SIDS6/gcgdata/geneseq/geneseqp/AA2000.DAT:* | number of results predicted by chance to have or equal to the score of the result being | inalysis of the total score di | SUMMARIES . | Query Score Match Length DB ID Description | | 100.0 9 18 W39723 | 75.0 9 19 W77134 75.0 9 19 W70045 | 36 75.0 9 20 X47655 Immunogenic peptid 36 75.0 9 20 X09525 Carcinoembryonic a | 75.0 9 20 109526 | 70.8 9 20 109528 | 68.8 9 21 Y541/3 60.4 9 17 W00680 |

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WO9741440-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                       or antigonists (Tb) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma calls that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                         immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                                               Peptide agonists and antagonists of carcinoembryonal antigen
\mathcal{F}_{\mathcal{F}}(A)
                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9;
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                                                                      Carcinoembryonic antigen peptide agonist SEQ ID NO:5.
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100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 53; 72pp; English.
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Best Local Similarity 100.،
است 9; Conservative
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                                              20-JUL-1999
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                                                                                                                                                                                                                     22-APR-1999
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                                                                                                                                                                       Synthetic.
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                                                                                                                                                           Homo
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immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                            selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                   Van Der Burg SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                Method of selecting T cell peptide epitope(s) - by measuring stability of HLA class I-peptide complexes on intact B cells
                                                                                                                                                                                                                                                                                                                                                                                                       Peptides W39430-W39734 are used in a novel method for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 36; DB 18; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                     SCI SEED CAPITAL INVESTMENTS BV
                                                                                                                                                                                                                 Offringa R,
                                                                                                                                                                                                                                                                                                                                                                Example 3; Page 85; 109pp; English.
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88.9%;
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96EP-0201145.
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Best Local Similarity 88.9
ممات: 8; Conservative
                                                                                                                                                 (UYLE-) RIJKSUNIV LEIDEN. (SCIS-) SCI SEED CAPITAL
                                                                                                                                                                                                                 Kast WM, Melief CJM,
                                                                                                                                                                                                                                                           WPI; 1997-549891/50
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26-APR-1996;
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                                         28-APR-1997;
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06-NOV-1997.
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leukocyte antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLS) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCS) pretreated with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing offs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLS which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLS can be used for treating canners, immune disorders, viral infections, contactions, malaria or contactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic peptide having a human leukocyte antigen binding motif #2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 19; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-US05039.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
E... 8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-551214/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YLSGACLNL
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| ylsganlnl
                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sednence
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                                                                                                                                                                                                 The peptide epitope W77119-W77138 were created for human tumour-specific cytocoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human leukocyte antigen; HLA; tumour associated antigen; cancer;
antigen presenting cell; APC; immunogenic peptide; immune disorder;
viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                                            Disease specific immunogen – comprises disease specific cytotoxic lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 19; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tsai V;
         Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Southwood S,
         Kittlesen D,
                                                                                                                                                              Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 6; Page 75; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W70045 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.0%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.0
Best Local Similarity 88.9
Matches 8; Conservative
         Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                presenting cells
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                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
         Engelhard VH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                     epitope
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HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans).

They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell are an immune response.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to Kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                     produce CTLS ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                  Score 36; DB 20; Lengtu >,
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoembryonic antigen peptide agonist CAP-1.
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                                                                                                                                                                                                                                                                                                                                                                                   75.0%;
88.9%;
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Best Local Similarity
'-hac 8; Conserv?
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Synthetic.
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immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                         Gaps
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                                                                                                                                                                      Length 9;
                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen peptide agonist SEQ ID NO:2.
                                                                                                                                                                    Score 36; DB 20;
Pred. No. 2.1e+05;
                                                                                                                                                                                                       Mismatches
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88.9%;
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                                                                                                                                                                                                      Conservative
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Best Local Similarity
'-has 8; Conserve
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                                                                                                                   9 AA;
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| ylsganlnl
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                                                                                                                     Sequence
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6

Length

DB 20;

Score 36;

75.08;

Query Match

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Carcinoembryonic antigen peptide agonist SEQ ID NO:4.
                                         20-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                         Barzaga E, Schlom J,
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1 ylsganinl 9
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                                                                                                                                     sapiens
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                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or antigonists (Tb) of human carcinoembryonal antigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use. In adoptive transfer therapy. (Ib) are used to inhibit CEA-specific. Immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generate a compart of the present sequence (I) and sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes peptides (A) that comprise agonists (Ia)
                     Gaps
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                                                                                                                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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Pred. No. 2.1e+05;
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                                                                                                                                                                            Carcinoembryonic antigen peptide agonist SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 2.1e+05;
1; Mismatches 1
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                                                                                                             Y09527 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.8%;
77.8%;
         88.98;
                                                                                                                                                                                                                                                                                                                            98WO-US19794
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                                                                                                                                                        (first entry)
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Matches 7; Conservative
        Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 53; 72pp;
                                                                                                                                                                                                                                                                                                                                                                                        Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-326544/27.
                                        1 YLSGACLNL 9
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                                                                                                                                                                                                                                                                                                                           22-SEP-1998;
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                                                                                                                                                        20-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                        Barzaga E,
                                                                                                                                                                                                                                                               Synthetic.
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                                                                                                                                   Y09527;
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Y09528
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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, ung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA binding peptide 1233.11 derived from source CEA.605v9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
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Pred. No. 2.1e+05;
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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13-FEB-1996;
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               29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W76240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allele specific binding motif for the major histocompatibility complex (MHC) molecule HLA, e.g. HLA-A2.1. The peptides have conserved residues at certain positions such as positions 2 and 9. Also, the peptides do not comprise negative binding residues at other positions, such as positions comprise negative binding residues at other positions, such as positions 1, 3, 4, 5, 7, 8 and/or 7 (peptides 9 amino acids long). The peptides are used to induce a cytocoxic T cell response to a preselected antigen. The method comprises contacting cytotoxic T cells from a patient (optionally expressing a specific MHC class I allele) with the present peptides.

The peptides are used to treat and prevent microbial infection, AIDS, viral hepatitis B and C, human papilomavirus (HPV) infection, AIDS, viral hepatitis B and C, human papilomavirus (HPV) infection, AIDS, viral hepatitis B and C, human papilomavirus (HPV) infection, AIDS, cytomegalovirus (CM), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Patients in the acute phase of infection can be treated with the peptides in conjunction with other treatments. The antigenic peptides may be used to elicit cytotoxic T lymphocytes (CTLS) ex vivo and in vivo. The resulting CTLS can be used to treat chronic infections (viral consecrial) or tumours in patients that do not respond to conventional corms of therapy. The peptides may also be used to produce monoclonal antibodies, which are useful as potential diagnostic or therapeutic agents. The peptides may also be used as diagnostic reagents.
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                                                                                                                                                                                                                               Novel HLA binding immunogenic peptides used to induce {\tt T} cell activation and to induce an immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                  Peptides Y54171-Y54236 represent immunogenic peptides comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide comprising residues 571-579 of Carcinoembryonic antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinoembryonic; antigen; human; cytotoxic T cell; pox virus; vector; epitope; determination; screening; tumour; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 21; Length 9; Pred. No. 2.1e+05; 1; Mismatches 1; Indels
                                                                                                                                                                              Southwood S;
                                                                                                                                                                                                                                                                        Claim 1; Page 32; 42pp; English.
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77.88;
                                                                                                                       98US-0098584
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                  (EPIM-) EPIMMUNE INC
                                                                                                                                                                            Sidney J,
                                                                                                                                                                                                      WPI; 2000-106018/09
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            Unidentified
                                       W09965522-A1
                                                                                            17-JUN-1999;
                                                                                                                       17-JUN-1998;
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                                                                  23-DEC-1999
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Protein-ligand binding pocket, PLBP, binding protein; ligand; modulator; bacterial periplasmic binding protein; interaction energies; ischaemia; basis set molecules; BSM; ionotropic glutamate receptors; treatment; neuroprotectant; stroke; epilepsy; neuropathic pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Producing carcinoembryonic antigen (CEA) specific human cytotoxic T cells (CTC), comprises introducing a 1st pox virus vector, having at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC production, and at least 1 periodic interval after that, contacting the host with an additional antigen. The CEA specific CTC can be used to determine the CTC eliciting epitope of CEA, and to screen for compounds which enhance the ability of the antigen to create a CTC response. A host with a CEA expressing tumour can be treated by introducing the CTC to the host, and at least 1 periodic interval after that introducing a CEA peptide, i.e. the present peptide.

The present peptide is positive for binding to HLA-A2, and scored so and 806 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HLA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HLA-A2 antibody (background 280 and 300).
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                                                                                                                                                                                                                                                                                                                                                                                                Generation of human cytotoxic T-cells specific for CEA - useful in
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                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy, epitope mapping and drug screening
                                                                                                                                            (THER-) THERION BIOLOGICS CORP. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                           Tsang KY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 57; 76pp; English.
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96WO-US02156.
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Best Local Similarity 87.55,
From 7; Conservative
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                                                                                                                                                                                                                                                    Panicali D, Schlom J,
                                                                                                                                                                                                                                                                                                                          WPI; 1996-402364/40
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981L-0125608.
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                                                                 Eisenbach L, Ca
Fitzer-attas C;
30-JUL-1998;
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Y49030
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                                                                                                                                                                                                                                                                                                                                              for lead compounds for developing such compounds). The ligands are potentially useful therapeutically, e.g. as neuroprotectants during ischemia and for treatment of stroke, head injuries, epilepsy, neuropathic pain etc. The method allows affinity of ligands to be estimated without having to prepare them and then test them, in vitro. Ligands with high selectivity for particular glutamate receptors should have fewer side effects than known receptor antagonists.
                                                                                                                                                                              W76226-W76250 are protein fragments used in the design of a model of a protein-ligand binding pocket (PLBP) of a binding protein. A model is constructed based on typographic similarity to the binding pocket of a bacterial periplasmic binding protein. The model is refined by energy minimisation, with a high affinity ligand in the binding pocket. Interaction energies of basis set molecules (BSM) are obtained by calculating energy of the models for the binding pocket BP and BSM individually (Er and Em) and total energy (Erm) of bound complexes formed. The model is used to predict the selectivity of a potential ligand for a set of related PLBP's, specifically innorropic glutamate receptors. Identified ligands are potentially useful for studying receptor binding and activity and as modulators of receptor activity
                                                                            Designing a model for a ligand-binding pocket in a protein and its use for assessing ligand affinity - without the need to prepare test ligand, for identifying selective antagonists for ionotropic glutamate receptors, potentially useful as neuroprotectants with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Teratocarcinoma-derived growth factor (CRIPTO-1) antigenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment; prevention; cure; anti-tumour vaccine; metastases; breast; bladder; prostate; pancreas; ovary; thyroid; colon; stomach; carcinoma; MHC class I; HLA-A2; human; Major Histocompatibility Complex; uroplakin; prostate specific antigen; prostate specific membrane antigen; prostate acid phosphatase; mucin; lactadherin; teratocarcinoma derived growth factor; PSA; PSNA; PAP; CRIPTO-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour associated antigen peptide; TAA; cancer; carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 26; DB 19; Length 7;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                                                                                                                                                        Disclosure; Page 216; 218pp; English.
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(BEAR-) BEARSDEN BIO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                 reduced side effects
                                                   WPI; 1998-495386/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA;
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Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast, bladder, prostate, pancreas, ovary, thyrold, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HLA-A2 molecules and are generally between 8 to 10 amino acids in length. The amino acids located at positions 2 and 9 of the tumour associated antigens are the anchor residues which participate in the binding to MHC class I molecules, more specifically HLA-A2. More tumour associated antigens are described in GENESEO records Y82306-Y82882.
                                                                                                                                                                                                                                                                                                                                           Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Those tumour associated antigens described in records 182806-18284 and 18285-1982869 are derived from Uroplakin, such as Uroplakin II, Uroplakin III, Those described in records 182825-182829 are derived from prostate specific antigen (PSA). Those described in records 182825 are derived from prostate specific antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prostate specific membrane antigen (PSMA). Those described in records YY82836-Y82839 are derived from prostate acid phosphotase (PAP). Those described in records Y82840-Y82846 are derived from Lactadherin (BA-46). Those described in records Y82841-Y82884 are derived from Mucin and those described in records Y82841-Y82884
                                                                                                                                 Fridkin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                      Paz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane dipeptidase-binding liver homing peptide #2.
                                                                                                                                 Bar-haim E,
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                                                                                                                                 Tirosh B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 19; Page 108; 113pp; English.
(YEDA ) YEDA RES & DEV CO LTD.
(BIOT-) BIO-TECHNOLOGY GEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTLA-4; cytotoxic T-lymphocyte associated antigen 4; binding agent; VLD;
variable-like domain; human; diagnosis; cancer; blood clot.
                                                                                                                                           The present invention describes peptides that selectively home to a tissue or organ. The peptides can be used for identifying an organ or tissue, for identifying a target molecule expressed by an organ or tissue or for treating an organ or tissue pathology, where the organ or tissue is selected from prostate, lung, skin, retina, pancreas, gut, ovary, adrenal gland, liver, and lymph node. The peptide bind to the membrane dipeptidase (MDP). Y48618 to Y49066 represent sequences which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is an insert in the CDR1 of the variable-like domain (VLD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New binding agent comprising monomeric V-like domain in which at least one complementarity determining region loop is modified, useful for
                                                                                                                                                                                                                                                                                   Gaps
                                                                                    New peptides which selectively home to organs or tissues, used for, e.g. identifying target ligands and for therapy of pathological
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                                                                                                                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                                              50.0%; Score 24; DB 20;
66.7%; Pred. No. 2.1e+05;
iive 1; Mismatches 1;
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                                               Ruoslahti EI;
                                                                                                                         Example 6; Page 156; 193pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hudson PJ,
                                                                                                                                                                                                                                                                                                                                                                      Y39584 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                CTLA-4 VLD CDR1 region insert.
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98US-0042107
99US-0042107
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                                               Rajotte D, Pasqualini R,
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Matches 4; Conservative
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                            (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coia G, Galanis M,
                                                                 WPI; 1999-571717/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis of cancer
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2 ltggcl 7
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13-MAR-1998;
26-FEB-1999;
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                                                                                                        conditions
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Y39584
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of the human cytotoxic T-lymphocyte associated antigen 4 (CTLA-4), used in the binding agent of the invention. The binding agent (I) comprises at least one monomeric VLD that is derived from a non-antibody ligand and has at least one CDR (complementarity determining region) loop sequence.

Or part of it, modified or replaced so that, compared to unmodified VLD, its solubility is increased and/or the size is altered and/or a clisulphide bond is created within, or between, one or more CDR loops. (I) are used for diagnosis, e.g. in vivo detection/localisation of cancer, blood clots etc., also in vitro when immobilised on solid supports or blood clots etc., also in vitro when immobilised on solid supports or bloosensors and therapeutically. Modified VLD may have binding affinity for drugs, steroids, pesticides, andigens, growth factors, tumour and alters binding specificity. Since VLD are derived from human proteins, the need for a humanizing step (to avoid adverse immune responses) is avoided, and modification also improves expression in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAGE 3 antigen derived HLA-A2.1 binding peptide 9 (residues 174-182)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal infection; tuberculosis; melanoma; MAGE antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
80.0%;
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vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCS) pretreated with pretreatment growth factors, and incubating the APCs with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen:specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytocoxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, the contactions, hepstilis, bacterial infection, fungal infection, malaria or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Immunogenic peptide having a human leukocyte antigen binding motif #1764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinome;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Pred. No. 2.1e+05;
1; Mismatches 4; Indels
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Best Local Similarity 44.4
Matches 4; Conservative
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                                                                                                                                                                                                                                                                                                         tuberculosis.
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concer, by contacting or otherwise at risk of viral infection or used to treat the condition of a peptide fragment bound to a HLA molecule, rather than the intext foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections and cancers in mammals (especially humans) concer, or prevent viral infections and cancers in mammals (especially humans). They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cyctoxic T cell response, by contacting a cyctoxic T cell with the peptide e.g. to produce CILE ax vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide having a human leukocyte antigen binding motif #2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
Cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are
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Pred. No. 2.1e+05;
1; Mismatches 4;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighthing viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, ALDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to polynucleotides encoding the immunogenic peptides are also useful
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Pred. No. 2.1e+05;
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44.48;
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide having a human leukocyte antigen binding motif #2174.
to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynuclectides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
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Pred. No. 2.1e+05;
1; Mismatches 4; Indels
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Best Local Similarity
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are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes antagonists which specifically prevent laminin interaction with nidogen which is essential in the supramolecular assembly of basement membranes. These antagonists can be used as therapeutic agents in diabetic patients where basement membrane thickening leads to chronic renal failure and blindness (retinopathy). Several other vascular injuries including vasculitis, scleroderma and systemic lupus can also be treated by the antagonists. Further, the antagonists can break down basement membrane formation around tumour cells to allow attack of the cells by antibodies and immune cells. The present sequence was used in the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antagonist; laminin interaction; nidogen; basement membrane assembly; therapeutic agent; diabetic patient; basement membrane thickening; chronic renal failure; blindness; retinopathy; vasculitis; scleroderma; systemic lupus; tumour cell.
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide antagonists for preventing laminin interaction with nidogen - useful for preventing basement membrane formation e.g. in patients
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Pred. No. 2.1e+05;
1; Mismatches 4; Indels
                                                                                                                                                      therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragment of the EGF-like repeat 4 of laminin.
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Best Local Similarity 44.4
احد 4; Conservative
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                                                     Gaps
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PM-1; bovine serum albumin; BSA; epitope.
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     Length 6;
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  Score 23; DB 17;
Pred. No. 2.1e+05;
1; Mismatches 1.
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  47.9%;
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Query Match
Best Local Similarity
Matches 4; Conserv
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RESULT

R37280;

4 GACL

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Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
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PM-1; bovine serum albumin; BSA; epitope.
Neuroendocrine; antigen; diabetes mellitis; pancrease; insulinoma;
PM-1; bovine serum albumin; BSA; epitope.
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92US-0901523.
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19-JUN-1992;
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100.0%; Pred. No. 2.1e+05;
Live 0; Mismatches 0;
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Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
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100.0%; Pred. No. 2.1e+05;
Live 0; Mismatches 0;
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19-JUN-1992;
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                                                           Neuro-endocrine protein antigen PM-1 - useful for treating auto:immune diseases \mathbf{e}.g. type I diabetes
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2.1e+05;
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Pietropaolo M;
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Eisenbarth GS,
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R37285 ID R3

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Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IGG anti-BSA antibodies. Thus, BSA may represent a leastet antigen for row milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                   Neuroendocrine; antigen; diabetes mellitis; pancrease; insulinoma; PM-1; bovine serum albumin; BSA; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuroendocrine; antigen; diabetes mellitis; pancrease; insulinoma; PM-1; bovine serum albumin; BSA; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neuro-endocrine protein antigen PM-1 - useful for treating auto:immune diseases e.g. type\ I diabetes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47.9%; Score 23; DB 14; Length 8; 100.0%; Pred. No. 2.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 38; 56pp; English.
           R37285 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R37286 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pietropaolo M;
                                                                                                                                                                                                                                                                                                                                                                                                    (JOSL-) JOSLIN DIABETES CENT.
                                                                                                                                                                                                                                                                                                             92WO-US09428
                                                                                                                                                                                                                                                                                                                                               91US-0788118.
92US-0901523.
                                                                                 (first entry)
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Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Eisenbarth GS,
                                                                                 06-SEP-1993
                                                                                                                                                                                                                                                                                                             29-OCT-1992;
                                                                                                                                                                                                                                         WO9309141-A.
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gacl 6
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                                                                                                                                                                                                      Synthetic.
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59

δ qq RESULT R37286 ID R37

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Gaps

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0; Indels

Gaps

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Score 23; DB 18; Length 8; Pred. No. 2.1e+05;); Mismatches 1; Indels

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Peptide mimetic; gamma-chain; cytokine receptor; signal transduction; autoimmune disease; graft vs. host disease; transplant rejection; graft rejection; interleukin; immunosuppressant; T cell; B cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide(s) mimicking a loop in the gamma chain of cytokine receptors - inhibit signal transduction through these receptors useful as immunosuppressants for treating or preventing e.g. leukaemia, autoimmune disease, graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                    Peptide mimetic of cytokine receptor gamma chain 31.
                                                                                                                                                                                                                                                                                      W77008 standard; peptide; 8 AA.
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                                                                        47.9%;
80.0%;
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                                                        Ouery Match
Best Local Similarity 80.۰۰
امر 4; Conservative
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                     8 AA;
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                                                                                                                                                       2 LSGAC
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                       Sequence
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                                   Sequence analysis of the PM-1 protein revealed two regions of similarity with bovine serum albumin (BSA). These regions of similarity may contain epitopes shared by the PM-1 molecule and BSA. It has been shown that many patients with Type I diabetes have elevated levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a target antigen for cow milk induced islet autoimmunity. Peptides comprising amino acids residues shared by the PM-1 protein and BSA may be useful in the form of a therapeutic composition to treat an autoimmune disease, such as Type I diabetes in an individual.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This synthetic peptide is an example of a kidney-homing peptide that was identified using a claimed method for obtaining that was identified using a claimed organ or tissue. This in vivo molecules that home to a selected organ or tissue. This in vivo panning method typically involves administering a phage display. I ibrary to a subject, and identifying expressed peptides which home to the desired organ or tissue, e.g. brain, kidney, angiogenic vascular tissue or tumour tissue. The isolated peptides (see M1312-52, W1181-86) can be used to target e.g. drugs, toxins or labels to the selected organ/tissue (claimed) or to identify and/or isolate target molecules (claimed). The peptides can be directly inductive in vivo, as compared to prior art in vitro screening specificity in vivo.
                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Obtaining compound that homes to selected organ or tissue - by vivo panning method, specifically to identify brain, kidney, angiogenic vasculature or tumour tissue homing peptide(s)
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Claim 20; Page 38; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W13449 standard; Peptide; 8 AA.
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95US-0526708.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1998 (first entry)
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kidney homing peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-202359/18.
                                                                                                                                                                                                                               8 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      drug delivery
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11-SEP-1995;
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|3 gac1 6
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                                                                                                                                                                                                                                 Sequence
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                                                              The peptide mimetics W61734-W61756 and W77001-W77014 mimic a loop on the gamma-chain of cytokine receptors, and interacts with a cytokine or a gamma-chain partner receptor chain of a heterodimenic cytokine receptor. They inhibit signal transduction mediated by cytokine:receptor binding (of cytokines that bind to receptors with a gamma-chain). They are used to inhibit or suppress cytokine-mediated immune responses, growth, proliferation, function and activity of cells. Particularly they are used for treatment or prevention of Lymphoma, leukaemia, allergy (e.g. asthma), autoimmune disease (e.g. rheumatoid arthritis, lupus, multiple sclerosis or myasthenia gravis), graft vs. host disease and transplant or graft rejection. They inhibit function of interleukin (IL)-2, -4, -7, -9, -13 and -15 (the receptors for which include a common gamma -chain), so function as immunosuppressants by reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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Claim 8; Page 29; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation of T and B cells.
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Best Local Similarity 100.vv
''haa 4; Conservative
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receptors,

Fridkin M;

Paz A,

Bar-haim E,

Tirosh B,

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Tumor associated antigen peptides, especially derived from uroplakin, useful as vaccines to prevent or cure cancers including breast, bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
                                                              teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1
breast; bladder; prostate; pancreas; ovary; thyroid; colon; stomach; carcinoma; MHC Class I; HLA-A2; human; adjor Histocompatibility Complex; uroplakin; prostate specific antigen; prostate specific antigen; prostate specific membrane antige prostate acid phosphatase; mucin; lactadherin;
                                                                                                                                                                                                                                                                                                                                                                Claim 19; Page 108; 113pp; English.
                                                                                                                                                                                                                 (YEDA ) YEDA RES & DEV CO LTD. (BIOT-) BIO-TECHNOLOGY GEN CORP.
                                                                                                                                                                                         981L-0125608.
                                                                                                                                                                 99WO-IL00417
                                                                                                                                                                                                                                                       Carmon L,
                                                                                                                                                                                                                                                                                         WPI; 2000-205463/18
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Fitzer-attas C;
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                                                                                        Homo sapiens
                                                                                                                                                                                      30-JUL-1998;
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                                                                                                                                         10-FEB-2000
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-1soforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tr1:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation
- by stereoselective hydrolysis of corresponding racemic amide using
microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Teratocarcinoma-derived growth factor (CRIPTO-1) antigenic peptide.
                                                                                                                                                                        R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
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treatment; prevention; cure, anti-tumour vaccine; metastases;
                                                                                                                                                                                                                                                                                                                                                                          Tinschert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 19; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 3; Indels
                                                                                                                                               K. oxytoca R-specific amidohydrolase peptide T5
                                                                                                                                                                                                                                                                                                                                                                          Shaw N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 10.2; Page 29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                          Robins K,
                                                                       W40267 standard; Protein; 9 AA.
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                                                                                                                                                                                                                                                                                                             97CH-0000500
96CH-0001723
                                                                                                                        (first entry)
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Naughton A,
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-101063/09
                                                                                                                                                                                                             Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                 (LONZ ) LONZA AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
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| ytvgamln
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                                                                                                                                                                                                                                      WO9801568-A2
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10-JUL-1996;
                                                                                                                        16-JUN-1998
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                                               RESULT
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Tumour associated antigen peptides (TAA) may be used for the treatment, prevention and cure of cancer or cancer metastases. The cancer may be breast, bladder, prostate, penciesa, ovary, thyroid, colon, stomach, head or neck cancer or a carcinoma. The tumour associated antigens are presentable to the immune system by HiA-A2 molecules and are generally between 8 to 10 amino acids in length.

The amino acids located at positions 2 and 9 of the tumour associated antigens are described in garticipate in the binding to migens are the anchor residues which participate in the binding to MMC class I molecules, more specifically HiA-A2. More tumour associated antigens described in GRNESE records Y82806-Y8282 and Y82825-Y82869 are derived from Uroplakin, such as Uroplakin III and Uroplakin ib. Those described in records Y82835 are derived from CC Groods Y82825-Y82839 are derived from prostate specific antigen (PSA). Those described in records Y82835-Y82839 are derived from prostate acid phosphotase (PRA). Those described in records Y82846-Y82856 are derived from CC Front Lactadherin (BA-46). Those described in records Y82846 are derived are derived from Mucin and those described in records Y82847-Y82856.

Those described in records Y82846-Y82846 are derived from Lactadherin (BA-46). Those described in records Y82847-Y82859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                               HLA-binding oligopeptide and an immuno:regulator contg it - used in the treatment of auto:immune disease
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                             Human leucocyte antigen; HLA-DQ4; combinatorial library; autoimmune disease; chronic articular rheumatism.
Human leucocyte antigen DQ4 binding peptide #361.
                                                                                                                                                                                                                                                                                                                           Claim 4; Page 42; 61pp; Japanese.
                                                                                                                                                             94JP-0292657.
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                                                                                                                                                                                                                                                     WPI; 1996-329479/33.
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O9xvm8 caenorhabdi
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Q65125 african swl
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Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 AA; 14405 MW; 903318CDAD6E4C0D CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
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NADH DENYDROGENASE SUBUNIT 5 (ND5) (FRAGMENT).
Strongylocentrotus pallidus.
Mitochondrion.
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09109 anas platyr
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094446 alcaligenes
026339 methanobact
02641 caenorhabdi
020421 caenorhabdi
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7.424 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
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Matches 6; Conservative
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Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Edjameier K., Gas S., Barry C.E. III, Trakaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers M., Seeger K., Skelton S., Squres S., Sqares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";

Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 98183404. Weissbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.; "Detection of an interleukin-1 intracellular receptor antagonist mRNA
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                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2000 (TrEMBLrel. 14, Last annotation update)
INTERLEUKIN-1 INTRACELLULAR RECEPTOR ANTAGONIST VARIANT (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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143 Aa; 16142 MW; 4CAD6784B890906B CRC64;
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Biochem. Biophys. Res. Commun. 244:91-95(1998).
EMBL; AF043143; AAC39672.1; -
INTERPRO; IPRO00975; --
PRINTS; PR00340; interleukin-1; 1.
PRINTS; PR00264; INTERLEUKINI.
PROSITE; PS00253; INTERLEUKIN_1; 1.
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87.5%; Pred. No. 31;
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PROBABLE FATTY-ACID COA LIGASE
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Best Local Similarity 87.5
Matches 7; Conservative
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RESULT Q9UPC0

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Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L., Arend W.P., Smith M.F. Jr., "Intracellular IL-1 receptor antagonist promoter: cell type-specific and inducible regulatory regions.";

J. Immunol. 158:748-755(1997).
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE, 95355865.
Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
Introna M., Mantovani A., Colotta F.;
"Cloning and characterization of a new isoform of the interleukin 1
receptor and anagonist:";
J. Exp. Med. 182:623-628(1995).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X84348; CAA59087.1; -
EMBL; X84348; CAA59087.1; -
HSSP; P18510; ABB2269.1; -
HSSP; P18510; IRPP.
HNTERPRO; IPRO00975; -
PFAM: PF00340; interleukin.1; 1.
PRINTS; PR00264; INTERLEUKINI.
PROSITE; PS00253; INTERLEUKINI.
SEQUENCE 180 AA: 19897 MW; 624A1574C2334229 CRC64;
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STRAIN=84-I-1-13;
Dunn M.G., Ellar D.J.;
Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAX-2000 (TEMBLrel. 13, Last annotation update)
INTRACELLULAR IL-1 RECEPTOR ANTAGONIST TYPE II.
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Bacillus/Staphylococcus group; Bacillus.
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180 AA
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Pred. No. 14;
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SEQUENCE FROM N.A.
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MEDLINE; 20036896.
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240 LAGANVNL 247
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DNA RES. 6:63.70(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-BERKELEY;
MEDLINE: 20196006.
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                            MEDLINE; 99246063.
Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosawa M.,
Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 790;
                                           Length 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
            6013163292D0329E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                    790 AA; 87995 MW; 24F70D670D70F946 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CG6718 PROTEIN.
                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
KIAA0922 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00340; RECEPTOR_CYTOKINES_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%; Score 34; DB 4; Le 66.7%; Pred. No. 1.2e+02; tive 1; Mismatches 2;
                                            5;
                                                                                                                                                                 790 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877 AA.
                                           ; DB
                                                                 1; Mismatches
                                           75.6%; Score 34;
75.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
EMBL; Y10168; CAA71249.1; -. SEQUENCE 385 AA; 43949 MW;
                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB023139; BAA76766.1; INTERPRO; IPR002465; -.
                                                     Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
کمح 6; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                           278 YLSGPNLN 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YLSGANINL 9
                                                                                        1 YLSGANIN 8
                                                                                                                                                                                                                                                                                                    TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                            Query Match
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                                                                                                                                                                 09Y2D7
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Q9VT60
                                                                                                                                             RESULT
09Y2D7
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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Rabilar J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basua A., Baxendale J. Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., Raborkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Candra J., Cherter A., Chandra I., Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I., Roberty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Rabotson K., Doup L.E., Downes M., Durbin K.J., Evangelista C.C., Ferraz C., Ferraz S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferras S., Pleischman W., Rabush K.J., Gorrell J.H., Gu Z., Ganp W.M., Glasser K., Golock A., Gong F., Gorrell J.H., Gu Z., Ganp N., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Wei M., In Degwam C., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.E., In X., Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.B., Lasko P., Lei Y., Levitz S., Kulp D., Lai Z., R. Alasko P., Lei Y., Levitz S., Kulp D., Lai Z., R. Alasko P., Lei Y., Levitz S., Kulp D., Lai Z., R. Alasko P., Lei Y., Levitz S., Kulp D., Nelson D., R. Melson M., Murphy L., Murzhy D.M., Nelson D.M., Nelson M., Stupski M.P., Santh T., Raben H., Spier E., Shen H., Spier E., Spradling A.C., Stepleton M., Stupski M.P., Santh T., Rabon E., Sarenington K., Sunpson M., Stupski M.P., Santh T., Shon Q., Zhen G., Shen B.C., Siden-Klamos I., Simpson M., Stupski M.P., Santh H.O., R. Mang Z.-Y., Wassarman D.A., Wellston M., Welssenbach J., R. Menson E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhen G., Zheng S., Yao Q.A., R. Mang Z.-Y., Wassarman D.A., Wellston M., Welssenbach J., R. Aleng K.H., Zhong F.N., Zhong W., Zhou X., Zhang G., Zhao Q., Zhen G., Schence 287:12882 R., Redolston D. Santh M., Schone S., Calander E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang S., Calander P., Zhang S., Zhao G., Zhao G., Zhao G., Zhao G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB 5; Length 877;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C9DC2CD6C282869B CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2000 (TrEMBLrel. 14, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCINE CLEAVAGE SYSTEM P PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00023; ank; 5.
SEQUENCE 877 AA; 96862 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLYBASE; FBgn0036053; CG6718.
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deinococcus radiodurans
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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Q9PUU9
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WHISON R., Albacough R., Anderson K., Baynes C., Berks M.,
Wilson R., Albacough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulschon J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston J.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
P. A. Mo of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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Pred. No. 1.5e+02;
1; Mismatches 1; Indels
                                                                                                                           Score 34; DB 2; Length 949;
Pred. No. 1.4e+02;
                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Favello T.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
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                                                             949 AA; 102122 MW; FDCBA42D4E088BD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) SIMILAR TO GLYCINE DEHYDROGENASE.
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,01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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                                                                                                                                                                       1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                              PRT;
Science 286:1571-1577(1999).
EMBL; AE002021; AAF11360.1; -.
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75.0%;
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Best Local Similarity 75.v.
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Best Local Similarity 75.0
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U23510; AAC46780
NCE 979 AA; 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                         || |||:|
668 YLDGANMN 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A
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                                            TIGR; DR1809;
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                                                                  SEQUENCE
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Q9VH09
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RA MEDINE; 20196006.

RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Gutch G.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Randon R.C., Rogers Y.H.C., Blazej R.G., Change M., Miklos G.L.G., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.W., Bsuu A., Baren B.D., Man K.H., Doyle C., Barter E.G., Helt G., Nahdrews-Pfannkoch C., Baldwin D., Ballew R.W., Basu A., Barenna B.P., Bhandari D., Bolshakov S., Bortchan M.R., Bouck J., Bortchan M.R., Doyle C., Perraz C., Perriar C., Center A., Chadra I., Ra Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Man Ballier R., Doyle C., Perraz C., Perriar S., Dunkov B.C., Dunn P., Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P., Man Ballista C.C., Perraz C., Perriar S., Dunkov B.C., Dunn P., Goder C., Gabrielista C.C., Perraz C., Perriar S., Dunkov B.C., Dunn P., R.A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Harris M., Alalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalali M., Malush F., Karpen G.H., Ke Z., Kennison J.A., Merluson D.L., Morntosh T.C., McLeed M.P., Tour Y., Bresse M.G., Reinert K., Nelson M., Pittuna G.S., Pan S., Pollard J., Pully V., Reese M.G., Reinert K., Wong K.A., Nobarry C., Morris J., Woshrefi A., Shien H., Shien K., Shien H., Shien K., Shien H., Shien K., Shien E., Spradling A.C., Stapleton M., Stuong K., Shang G., Shao Q., Zheng L., Shang K.H., Shoo Q., Zheng C., Shang K.H., Shoo Q., Zheng C., Shang K.H., Shoo Q., Zhang G., Shoo Q., Zheng C., Shen
Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.5e+02;
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SEQUENCE 985 AA; 109713 MW; F8FBF5CFD251EDE7 CRC64;
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U-MAY-2000 (TIEMBLrel. 13, Last sequence update)
01-MAX-2000 (TIEMBLrel. 13, Last annotation update)
GLYCINE DECARBOXYLASE P PROTEIN
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75.0%;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                              SEQUENCE FROM N.A.
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MEDLINE; 20196006.
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STRAIN=D/UW-3/CX:
MEDLINE; 99000809.
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans:
Chlamydia trachomatis.";
Science 282:754-759(198).
EMBL; AE001288; AAC67739.1; -.
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Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
Methanobacterium.
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Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                    Length 507;
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Pred. No. 1.1e+02;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                   507 AA; 57864 MW; 2361E01C40A00D13 CRC64;
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03, Last sequence update)
14, Last annotation update)
DEPOLYMERASE.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
10-JAUG-1998 (TrEMBLrel. 07, Last annotation update)
MAGNESIUM CHELATASE SUBUNIT.
               Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 6; Conservative
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290 YLSGVNSNI 298
                                                                SEQUENCE FROM N.A.
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287 YVSGASIN 294
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SEQUENCE 507
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P94146
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"The coat protein gene of Turnip Mosaic Virus isolated from Radish in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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STRAIN-PERKIN DUCK; TISSUE-LIVER;
Li J., Tong S., Wands J.R.;
Tidentlication and Expression of Glycine Decarboxylase (p120) as in the properties B Virus Pre-S Envelope-binding Protein.";
J. Blol. Chem. 274:27658-27665(1999).
EMBL; AF137264; AAAD56281.1; -.
SEQUENCE 1024 AA; 113473 MW; 657EFC89374DFEC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                             SEQUENCE FROM N.A.
STRAIN-PEKIN DUCK, TISSUE-LIVER;
MEDLINE; 96323119.
Li J.S., Tong S.P., Wands J.R.;
"Characterization of a 120 Kilodalton pre-S-binding protein as candidate duck hepatitis B virus receptor.";
J. Virol. 70:6029-6035(1996).
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Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
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62;
                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF103785; AAD20296.1; -. INTERPRO; IFR01592; -. PFAM; PF00767; POLY_coat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COAT PROTEIN.
44AADIDEC41498F8 CRC64;
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Last annotation update)
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Last annotation update)
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34124 MW;
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084150;
01-00v-1998 (TrEMBLrel. 08, Ci
01-NOv-1998 (TrEMBLrel. 08, La
01-NOV-1998 (TrEMBLrel. 13, La
MONOOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13, POLYPROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                Query Match 75.6' Best Local Similarity 75.0' Matches 6; Conservative
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Best Local Similarity
Matches 7; Conserv
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NON_TER
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O84150
ID O84150
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Q9WA61
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RX MEDLINE; 98037514.

RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., DuBois J., RA Aldredge T., Bashizadeh R., Blakely D., Cook R., Gilbert K., RA Harrison D., Heang L., Keagle P., Lumm W., Pothier B., Qiu D., RA Harrison D., Heang Y., Wierzbowski J., Gibson R., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.; RT "Complete genome sequence of Methanobacterium thermoautotrophicum RT deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).

R. Babl. AE00810; AAB84743.1; -. S. Score 33; DB 1; Length 1321; Best Local Similarity 75.0%; Pred. No. 3.38+02; Matches 6; Conservative I; Mismatches 1; Indels 0; Gaps 0; Matches 6; Conservative I; Mismatches 1; Indels 0; Gaps 11:1 | II | II | Db 1081 YLTGRNIN 1088
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Search completed: December 16, 2000, 02:00:58 Job time: 5932 sec

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schrewe H., Thompson J., Bona M., Hefta L.J.F., Maruya A., Hassauer M., Shively J.E., von Kleist S., Zimmermann W.; "Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 89122014.
Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
"Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 87128144.
Oikawa S., Nakazato H., Kosaki G.;
"Primary structure of human carcinoembryonic antigen (CEA) deduced from CDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 84:2960-2964(1987).
--- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
--- TISSUE SPECIFICITY: FOUND IN ADENOCARCINOWAS OF ENDODERMALLY
DERIVED DIGESTIVE SYSTEM BPITHELLUM AND FETAL COLON.
--- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immermann W., Ortileb B., Friedrich R., von Kleist S.; "Isolation and characterization of cDNA clones encoding the human carcinoembryonic antigen reveal a highly conserved repeating
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  01-JAN-1988 (Rel. 06, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100)
                                              022523
P09880
P07015 e
P47652 n
P52695 v
P25085 n
P249173 r
                  P47260
005921
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                                                                                                                                                                                                                             ALIGNMENTS
                Y014_MYCGE
RN5A_MOUSE
TRNL_YEAST
ODO1_ECOLI
Y412_MYCGE
HLYU_VIBCH
ILLX_MOUSE
Y121_BURCE
PMIP_NICAL
                                                                                                                                                                              PRIM_METJA
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 576
623
679
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769
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108
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseétsb-sib.ch).
COMPRISING 60% CARBOHYDRATE. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 7 IG-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC ANTIGEN
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MIM; 114890; -

MIN; 114800; -

PFAM; PF00047; 19; 7.

Immunoglobulin domain; Glycoprotein; GPI-anchor; Membrane; Signal.
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M29540; AAA51967.1; -.

X16455; CAA34474.1; -.

M15042; AAA51963.1; -.

M16234; AAA51963.1; -.
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EMBL;
EMBL;
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Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L., Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N., Hartis P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Sieu L.C., Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L., Truesdell S.E., Shelly J.A., Eessalu T.E., Taylor B.M., Tracey D.E.; "Purification, cloning, expression and biological characterization of an interleukin-1 receptor antagonist protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Jenkins J.K., Drong R.F., Shuck M.E., Blenkowski M.J., Slightom J.L., Arend W.P., Smith M.F. Jr., "Intracellular IL-1 receptor antagonist promoter: cell type-specific and inducible regulatory regions."; J. Immunol. 158:748-755(1997).
                                                                                                 Gaps
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                                                                                                                                                                                                                                                                   01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUSHY-I RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-ILAN) (IRAP) (IL-1RA).
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Nature 343:341-346(1990).
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE; 90136920.
Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
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                                                               Length 702;
                                                                                                Indels
 MISSING (IN REF. 4).
6299AE26CDDBDB5C CRC64;
                                                                                              ;
                                                              Score 43; DB 1;
Pred. No. 0.33;
1; Mismatches
                                                                                                                                                                                                                                       177 AA
                                                                                                                                                                                                                                         PRT;
 320 M
76795 MW;
                                                               95.6%;
                                             Query Match
Best Local Similarity 88.5
hac 8; Conservative
                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antagonist gene.";
Cytokine 4:83-89(1992).
                702 AA;
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P18510;
CONFLICT
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Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F., Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P., "coNn cloning of an intracellular form of the human interleukin 1 receptor antagonist associated with epithelium."; Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
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"Refined crystal structure of the interleukin.1 receptor antagonist.
Presence of a disulfide link and a cis-proline.";
Eur. J. Biochem. 227:838-847(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92297633.
Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
Brunner D.P., Yem A.W., Deibel M.R. Jr.;
"Secondary structure and topology of interleukin-1 receptor
antagonist protein determined by heteronuclear three-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 386:194-200(1997).
-!- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
-!- SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.; "Interleukin-1 receptor antagonist activity of a human interleukin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94230368.
Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Elsenberg S.P.,
Brandhuber B.J.;
                                                                                                                             Blenkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
Heinrikson R.L., Chosay J.G., Tracey D.E.;
"Purification and characterization of interleukin 1 receptor level
antagonist proteins from THP-1 cells.";
J. Biol. Chem. 265:14505-14511(1990).
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Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
Yem A.W., Deibel M.R. Jr.;
"Solution structure of human interleukin-1 receptor antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
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                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (INTRACELLULAR FORM). MEDLINE; 91219436.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
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                                                       Nature 343:336-340(1990)
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                                       inhibitor.
                                                                                                                                                                                                                                                                                    MEDLINE;
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TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
SIMILARITY: BELONGS TO THE IL-1 FMAILY.
DATABASE: NAME-RED SYSTEMS, COM/CXT_CAT/ILIRA.HTML".

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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
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MEICRCLENHITLLELEHS -> MAL (IN
INTRACELLULAR ISOFORM).
DIG90776A794057 CRC64;
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PRIME: PR00264; INTERLEUKIN1.
PROSITE: PS00253; INTERLEUKIN1; 1.
Glycoprotein; Signal; Alternative splicing; 3D-structure.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
HYPOTHETICAL PROTEIN PH1989.
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1; Mismatchës
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AARHUS/GHENT-2DPAGE; 7105; IEF
MIM; 147679; -
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PDB; 11LR; 07-FEB-95
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11RA; 17-JUN-98
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Best Local Similarity
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59 YLQGPNVNL 67
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057713;
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Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
       Gregor J.,
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BINDING
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GCSP_CHICK
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Gaps
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SYRIN-KI2 / MG1655;
MEDLINE; 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Okamura-Ikeda K., Ohmura Y., Fujiwara K., Motokawa Y.;

Okamura-Ikeda nucleotide sequence of the gcv operon encoding the Escherichia coli glycine-cleavage system.";

Eur. J. Biochem. 216:539-548(1993).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
6LYCINE DEHYDROGENASE [DECARBOXYLATING] (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN).
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Stauffer L.T., Fogarty S.J., Stauffer G.V.;
"Characterization of the Escherichia coli gcv operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
95745BC337B7B494 CRC64;
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STRAIN-K12 / W3110;
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Pred. No.
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66.78;
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Best Local Similarity
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59 FLKGANINV 67
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P33195;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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The complete genome sequence of Escherichia coli K-12.";

Science 277:1453-1474(1997).

C-1-EVINCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE. THE PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE.

THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COPACTOR OF THE H PROTEIN.

C-1-CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-DIHYDROLIPOYLPROTEIN + CO(2).

C-1-CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-DIHYDROLIPOYLPROTEIN + CO(2).

C-1-CATALYTIC ACTIVITY: GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:

C-1-SIBUNIT: THE GLYCINE.

C-1-INDUCTION: BY GLYCINE.

C-1-SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licensedisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kume A., Koyata H., Sakakibara T., Ishiguro Y., Kure S., Hiraga K.; "The glycine cleavage system. Molecular cloning of the chicken and human glycine decarboxylase CDNAs and some characteristics involved in the deduced protein structures."; ". Biol. Chem. 266:3323-3329(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              707 707 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
956 AA; 104245 MW; 28B7A78D1D0DB6F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCINE DEHYDROGENASE [DECARBOXYLATING], MITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLATING), MITOCHONDRIAL PRECURSOR PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1;
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MEDLINE; 88106483.
Fujiwara K., Okamura-Ikeda K., Motokawa Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S36834; S36834.
ECOGENE; EG1810; GCVP.
Oxidoreductase; Pyridoxal phosphate.
INIT_MET 0
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P15505;
01-APR-1990 (Rel. 14, Created)
01-APR-1992 (Rel. 22, Last seque
15-JUL-1999 (Rel. 38, Last annot
GLYCINE DEHYDROGENASE [DECARBOXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000373; AAC75941.1; -.
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75.0%;
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Best Local Similarity
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Amino acid sequence of the phosphopyridoxyl peptide from P-protein of the chicken liver glycine cleavage system.";
Blochem. Blophys. Res. Commun. 149:621-627(1987).

- I- BUCKLINE. THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE. THE REVAINING METHYLAMINE MOIFTY IS THE THEN TRANSFERRED TO THE THE REMAINING METHYLAMINE MOIFTY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COPACTOR, CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIFTY. IS THE THEN TRANSFERRED TO THE LIPOAMIDE COPACTOR OF THE H PROTEIN.

- CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-
DIHYDROLIPOYLPROTEIN + CO(2).

- COFACTOR: PYRIDOXAL PHOSPHATE.

- SUBUNIT: HOMODIMER: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF THE FOUR PROTEINS: P, T, L, AND H.

- SUBCELLULAR LOCATION: MITOCHONDRIAL.
                                                                                   OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide. TRANSIT 1 ? MITOCHONDRION (POTENTIAL). CHAIN ? 1004 GLYCINE DEHYDROGENASE [DECARBOXYLATING].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human glycine decarboxylase cDNAs and some characteristics involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 91144593.

Kure S., Narisawa K., Tada K.;

Kure S., Narisawa K., Tada K.;

"Structural and expression analyses of normal and mutant mRNA encoding 91/cine decarboxylase: three-base deletion in mRNA causes nonketchic hyperglycinemia.";

Biochem. Biophys. Res. Commun. 174:1176-1182(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
6CYCINE DEHYDROGENNSE [DECARBOXYLATING], MITOCHONDRIAL PRECURSOR (EC 1.4 4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 738 PYRIDOXAL PHOSPHATE.
1004 AA; 111852 MW; 4446D7C66E0DC4BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M64402; AAA49029.1; -.
EMBL; D90266; BAA14313.1; -.
EMBL; D90240; BAA14287.1; -.
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75.0%;
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Best Local Similarity 75.0°
5. Conservative
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PIR; A39521; A39521.
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P23378:
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                                                                                                                                                         DISEASE: DEFECTS IN GCSP ARE THE CAUSE OF TYPE I NONKETOTIC HYPERGLYCINEMIA (RKH1). NKH IS AN AUTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY ACCUMULATION OF A LARGE AMOUNT OF GLYCINE IN BODY FLUID AND BY SEVERE NEUROLOGICAL SYMPTOMES. SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLYCINE DEHYDROGENASE [DECARBOXYLATING].
PYRIDOXAL PHOSPHATE (BY SIMILARITY).

S -> I (IN NKH1).

FTId-VAR_004979.

A -> R (IN REF. 2).

H -> Y (IN REF. 2).

V -> M (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Lost annotation update)
62 CLYCINE DEHYDROGENNSE [DECARBOXYLATING], MITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM PROTEIN).
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                                                                                                                  Kure S., Takayanagi M., Narisawa K., Tada K., Leisti J.;
"Identification of a common mutation in Finnish patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 1020;
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in the deduced protein structures.";
J. Biol. Chem. 266:3323-3329(1991).
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75.0%;
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                                                                                                                Takayanagi M.,
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                                                                    VARIANT NKH1 ILE-564.
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Best Local Similarity
Matches 6; Conserv
                                                                                            92340654.
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FRANSIT 1
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564
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P49095;
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Gene 56:185-198(1987).
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                                                                                                                                                            STRAIN=K12
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      RRARRER RRARRE
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                                                                                                                                                                                                                                                                               Pearson D., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF
GLYCINE. THE PERCEIN BINDS THE ALPHA-AMING GROUP OF GLYCINE
THROUGH ITS PRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND
THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE
LIPOAMIDE COFACTOR OF THE P PROTEIN.
-!- CATALYTIC ACTIVITY: GIXCINE + LIPOYLPROTEIN = S-AMINOMETHYL-
DIHYDROLIPOYLPROTEIN + CO(2).
-!- CORCTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITCOGHONDRIAL (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: MITCOGHONDRIAL (BY SIMILARITY).
                                                                                                                                 Sinclair D.A., Dawes I.W.; "Genetics of the synthesis of serine from glycine and the utilization of glycine as sole nitrogen source by Saccharomyces cerevisiae."; Genetics 140:1213-1222(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Mitchondrion; Pyridoxal phosphate; Transit peptide.
TRANSIT
CHAIN
7 1034 GLICINE DEHVDROCBNASE [DECARBOXYLATING].
BINDING 773 773 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 1034 Aa; 114451 MW; F4D52642B0BDA041 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1987 (Rel. 05, Created)
10-NOV-1986 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16) (THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 1034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 35;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U20641; AAB18933.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; 247815; CAA87810.1; -. SGD; S0004801; GCV2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12;
MEDLINE; 88056322.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                 96120340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YLSGANIN 8
                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Pro
Escherichia.
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                                                                                                                 MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92358234.
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: L-THREONINE + H(2)O = 2-OXOBUTANOATE + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structure 6:465-475(1998).
-!- FUNCTION: DEAMINATES L-THREONINE, BUT ALSO L-SERINE TO A LESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallagher D.T., Gilliland G.L., Xiao G., Zondlo J., Fisher K.E., Chinchilla D., Eisenstein E.; "Structure and control of pyridoxal phosphate dependent allosteric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 86111952.
Wek R.C., Hatfield G.W.;
"Nucleotide sequence and in vivo expression of the ilvY and ilvC genes in Escherichia coli K12. Transcription from divergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lopes J.M., Lawther R.P.; "Physical identification of an internal promoter, ilvAp, in the distal portion of the ilvGMEDA operon.";
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-!- PATHWAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOTETRAMER.
-!- SIBMILARITY: TO THREONINE DEHYDRATASE CATABOLIC AND SERINE DEHYDRATASE.
                                                                                                                                                                                                         MEDLINE; 87174741.
Lawther R.P., Wek R.C., Lopes J.M., Pereira R., Taillon B.E.,
Hatfield G.W.;
                                                                                                                                                                                                                                                                                                               "The complete nucleotide sequence of the ilvGMEDA operon of Escherichia coli K-12."; Nucleic Acids Res. 15:2137-2155(1987).
                                    Garrison E., Harms E., Umbarger H.E.;
Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         overlapping promoters.";
J. Biol. Chem. 261:2441-2450(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -! - COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 439-514 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X04890; CAA28577.1; -. EMBL; K03503; AAA24014.1; -.
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EMBL; M11689; AAA24027.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 257:771-778(1992).
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M87049; AAA67575.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          threonine deaminase.
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SEQUENCE FROM N.A.
                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (RNASE L) (RIBONUCLEASE 4).
RNS4 OR RNASEL.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNAASE)
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Dong B., Xu L., Zhou A., Hassel B.A., Lee X., Torrence P.F., Silverman R.H.;
"Intrinsic molecular activities of the interferon-induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 514;
Pred. No. 27;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03B881F542E363AF CRC64;
                                                                                                                                                                                                                                                                                                                               INTERPRO, IPR000634, -.
INTERPRO, IPR001721, -.
INTERPRO, IPR001721, -.
INTERPRO, IPR001926, -.
PFAM, PF00291, S.T.dehydratase, 1.
PFAM, PF00585, Thr.dehydrat.C; 2.
PROSITE, PS00165, DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis, Lyase, Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                741 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56276 MW;
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85.7%;
                                                                                                                                                                                                                                                           EMBL; M25498; AAA27151.1; -. PIR; JT0278; DWEBTT. STYGENE; SG10179; ILVA.
                                                                                                                                                                                                                                   EMBL; M26670; AAA27150.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Allosteric enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=KIDNEY;
MEDLINE; 93201598.
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Q05823;
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       SPERM NO DE LA MARIA MAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lopes J.M., Lawther R.P.; "Physical identification of an internal promoter, ilvAp, in the distal portion of the ilvGMEDA operon."; Gene 76:255-269(1989).
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-i- PATHWAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
-i- SUBUNT: HOMOTETRAMER.
-i- SIMILARITY: TO THREONINE DEHYDRATASE CATABOLIC AND SERINE DEHYDRATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SECUENCE FROM N.A.
MEDLING; 88258870.
Taillon B.E. Little R., Lawther R.P.;
"Analysis of the functional domains of biosynthetic threonine deaminase by comparison of the amino acid sequences of three wild-type alleles to the amino acid sequence of blodegradative threonine deaminase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16) (THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 514;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A -> R (IN REF. 2).

A -> R (IN REF. 2).

G -> C (IN REF. 2).

A -> G (IN REF. 3).

G -> V (IN REF. 2).

H; 9D389A0EDD8DE692 CRC64;
                                                                                                                                                                                                                                                                           PFAM: PF00231; S__dehydratase; 1.
PFAM: PF00281; S__dehydrat_C; 2.
PR05TFE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynchesis; Lyase; Pyridoxal phosphate;
Allosteric enzyme; 3D_structure.
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                                                                                                                                                                                                                                                                                                                                                                                                               PYRIDOXAL PHOSPHATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB :
Pred. No. 27;
1; Mismatches
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                                                                                                                         PDB; 1TDJ; 18-NOV-98.
ECO2DBASE; F050.1; 6TH EDITION.
ECOGENE; EG10493; ILVA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56195 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
EMBL; AE000453; AAC77492.1;
EMBL; M25497; AAA24015.1; -.
PIR; B27310; DWECTS.
PIR; S30670; S30670.
PIR; S48895; S48895.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                              INTERPRO; IPR001721; -. INTERPRO; IPR001926; -.
                                                                                                                                                                                                                                                                                                                                                                                                               62
120
140
195
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                                                                                                                                                                                                           INTERPRO; IPR000634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334
514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 89326124.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11111:1
314 LSGANVN 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSGANIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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P20506;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LT2
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Best Local S
Matches 6
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CONFLICT
CONFLICT
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CONFLICT
SEQUENCE
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PIR; S28634; S28634.
Cell adhesion; Signal; Outer membrane; Plasmid.
SIGNAL 49 ADHESIN AIDA-I.
                                                                                                                                                                                          507 SGANVNL 513
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                                                                                                                                                                  3 SCANINL 9
                                                                                                                                                                                                                                                             NTPA_PEA
P52914;
                                                                     SEQUENCE
                                          CHAIN
PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YDYD_SCHPO
ID YDYD_SC
AC 013692;
DT 15-JUL-
                                                                                                                                                                                                                                     RESULT 12
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                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Benz I., Schmidt M.A.;
"ALDA-I, the adhesin involved in diffuse adherence of the
diarrhoeagenic Escherichia coli strain 2787 (0126:H27), is
synthesized via a precursor molecule.";
Mol. Microbiol. 6:1539-1546(1992).
-i- FUNCTION: THIS IS AN ADHESION PROTEIN NECESSARY FOR THE DIFFUSE
ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                               PROSITE; PS50297; ANK_REP_REGION; 1.
PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
Hydrolase; Nuclease; RNA-binding; Endonuclease; Zinc-finger.
DOMAIN 229 24 2-5A BINDING (P-LOOP).
DOMAIN 253 275 2-5A BINDING (P-LOOP).
                                                                                                                                                                                                                                                                                                                                                                                  73.3%; Score 33; DB 1; Length 741; 66.7%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE LIKE.
C6-TYPE (POTENTIAL).
91385EA307E3CEID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND SEQUENCE OF 50-56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: OUTER MEMBRANE
                                                                                                                                                               MIM; 180435; -
INTERPRO; IPRO00719; -.
INTERPRO; IPRO12110; -.
PFAM; PF00023; ank; 8.
PFAM; PF00069; pkinase; 1.
PROSITE; PS50088; ANK_REPEAT; 6.
                                                                                                                                                                                                                                                                                                                                              83532 MW;
    -! - INDUCTION: BY INTERFERON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X65022; CAA46156.1; -
                                                                                                                                      EMBL; L10381; AAA18032.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADHESIN AIDA-I PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND STRAIN=2787 (0126:H27); MEDLINE; 92326638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TO EPITHELIAL CELLS
                                                                                                                                                      HSSP; Q00420; 1AWC.
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | |||:||
145 YKRGANVNL 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YLSGANINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmid pIB6.
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Q03155;
                                                                                                                                                                                                                                                                                                                               ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                    DOMAIN
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AIDA_ECOLI
    g
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                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0VT-197 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 34, Last sequence update)
NOV-1997 (Rel. 34, Last annotation update)
PHOSPHOHYDROLASE) (NTPASE).
PHOSPHOHYDROLASE) (NTPASE).
PLISH Sativum (Garden pea).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Pisum.
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0
                                                                                 Score 33; DB 1; Length 1286; Pred. No. 71; 0; Indels
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Pred. No. 38;
0; Mismatches 2; Indels
                  1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000407; -...
PFAM; PF01150; GDA1_CD39; 1.
PROSTE; PS01238; GDA1_CD39_NTPASE; 1.
Hydrolase; Nuclear protein:
SEQUENCE 455 AA; 50072 MW; 50FDF0023ABC4299 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 AA.
                                                                                                                                                                                                                                                                                                                           455 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z32743; CAA83655.1; -.
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75.0%;
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                             STANDARD;
1286
                                                                 Query Match
Best Local Similarity
6; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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IDENTIFICATION.
Koonin E.V., Rudd K.E.;
Submitted (SEP-1995) to the SWISS-PROT data bank.
                                      Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPR001926;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Allosteric enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEHYDRATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 315 LSGANLN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 LSGANIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HI0738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLYP_CHICK
ID GLYP_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P50593;
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         NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
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                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 53.7 KDA PROTEIN C11E3.13C IN CHROMOSOME I PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                      Murphy L., Harris D., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE GASI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16) (THREONINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL PROTEIN C11E3.13C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.1%; Score 32; DB 1; Length 510; 75.0%; Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3D515CCDB5651087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..............................
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SER-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53692 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; Z98595; CAB11192.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        491
510 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 YLQGLNIN 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YLSGANIN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THD1_HAEIN P46493;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shi N., Antin P., Filnk I.L., Morkin E.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELL SURFACE PROTEOGLYCAN THAT BEARS HEPARAN SULFATE.
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostoml;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                              EXTENT (BY SIMILARITY).

CATALYTIC ACTIVITY: L-THREONINE + H(2)O = 2-OXOBUTANOATE + NH(3)
-!- FUNCTION: DEAMINATES L-THREONINE, BUT ALSO L-SERINE TO A LESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
GLYPICAN-1 PRECURSOR (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN).
Gallus gallus (Chicken)
                                                                                                                                                                        -i- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHILE VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME (BY SIMILARITY).
-i- PATHWAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.1%; Score 32; DB 1; Length 513; 85.7%; Pred. No. 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRIDOXAL PHOSPHATE.
DF42CA8B6FDE4CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM; PF00291; S_T_dehydratase; 1.
PFAM; PF00585; Thr_dehydrat_C; 2.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                     + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
-!- SIMILARITY: BELONGS TO THE GLYPICAN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U32757; AAC22398.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPR000634; ... INTERPRO; IPR001721; ...
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                 POTENTIAL.

GLYPICAN-1.

REMOVED IN MATURE FORM (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).
                                                                                                      EMBL, L29089; AAA65199.1; ALT_INIT.

INTERPRO; IPR001863; -
PROSITE; PS01207; GLYPICAN; 1.

Proteoglycan; Heparan sulfate; Glycoprotein; Signal; GPI-anchor; Signal matrix.

SIGNAL 21 7 GLYPICAN-1.

POPERTIAL.

CHAIN 21 7 GLYPICAN-1.

PROPEP 7 FS0 REMOVED IN MATURE FORM (POTENTIAL).

CARBOHYD 76 76 N-LINKED (GLCNAC...) (POTENTIAL).

CARBOHYD 113 113 N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                    61084 MW;
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76
1113
382
52
483
485
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485
487
487
550 AA;
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CARBOHYD
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Gaps

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Query Match 71.1%; Score 32; DB 1; Length 550; Best Local Similarity 66.7%; Pred. No. 47; Matches 6; Conservative 1; Mismatches 2; Indels

Search completed: December 16, 2000, 03:05:20 Job time: 8040 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2000, 01:51:15; Search time 91.14 Seconds

(without alignments)
6.267 Million cell updates/sec

Title: US-09-529-121-4
5 Sequence: 1 YLSGANINL 9
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 182106 seqs, 63460219 residues
```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Dost-processing: Minimum Match OB

182106

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | carcinoembryonica | \neg | probable acidCoA | interleukin-1 rece | | hypothetical prote | ical | > | glycine dehydrogen | | dehyd | glycine dehydrogen | | aminomethyltransfe | probable monooxyge | threonine dehydrat | threonine dehydrat | 2-5A-dependent RNA | glycine dehydrogen | adhesin AIDA-I pre | protoporphyrin IX | hypothetical prote | | hypothetical prote | | þ | hypothetical prote | hypothetical prote | Q, |
|-----------|-----------------------|-------------------|--------|------------------|--------------------|----------|--------------------|--------|--------|--------------------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------|--------------------|--------|--------|--------------------|--------------------|--------|
| SUMMARIES | DI DI | 363 | C81704 | A70904 | A30368 | A39386 · | I64001 | E71215 | E75352 | 536834 | T16734 | A39521 | JN0124 | B39521 | S50917 | E71551 | DWECTS | DWEBTT | A45771 | D81821 | S28634 | E69129 | T16416 | T22220 | T26461 | 876576 | C81384 | T22562 | T15192 | G72386 |
| | DB | ~ | ~ | 7 | 7 | 7 | ~ | ~ | 7 | 7 | 7 | ~ | 7 | ~ | ~ | 7 | - | | ~ | ~ | ~ | 7 | ~ | ~ | 7 | 7 | | | | |
| | Query Match Length | 702 | 506 | 554 | 177 | 180 | 83 | 335 | 949 | 957 | 979 | 1003 | 1020 | 1020 | 1034 | 202 | 514 | 514 | 741 | 950 | 1286 | 1321 | 1956 | 236 | 248 | 259 | 262 | 272 | 343 | 356 |
| d | Query Match | 95.6 | | 80.0 | | 77.8 | | ď. | 5. | ď. | ď. | 75.6 | ď. | ς. | S. | Э. | ä | ω. | 73.3 | ω. | | | 73.3 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 |
| | Score | 43 | 37 | 36 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | | 32 | 32 | 32 | 32 | 32 | 32 |
| | Result No. | | 7 | 3 | 4 | 5 | 9 | 7 | 89 | σ | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | . 29 |

| nucleoside triphos | probable membrane | hypothetical prote | probable glycolipi | hypothetical prote | probable qcvB prot | probable glycine d | hypothetical prote | qlycine dehydrogen | aminomethyltransfe | aminomethyltransfe | probable glycine d | aminomethyltransfe | P protein - Flaver | probable glycine d | glycine dehydrogen |
|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S48859 | B81919 | E81182 | T37541 | T24745 | A70722 | T44754 | S76257 | T46636 | S63536 | T07826 | T05309 | S63535 | S40216 | T02615 | A42109 |
| 7 | 7 | ~ | ~ | ~ | ~ | 7 | 7 | ~ | 7 | ~ | 7 | 7 | 7 | 7 | 7 |
| 455 | 473 | 473 | 510 | 753 | 941 | 952 | 983 | 1031 | 1034 | 1035 | 1037 | 1037 | 1037 | 1044 | 1057 |
| 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 |
| 32 | 3.5 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 35 | 32 | 32 | 32 | 32 |
| 30 | 3.1 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| RESULT 1 A36319 Carcinoembryonic antigen precursor - human Natternate names: CRA; meconium antigen 100 C; Species: Homo saplens (man) C; Species: Homo saplens (man) C; Species: Homo saplens (man) C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000 C; Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; R; Schrewe, H; Thompson, J; Bonda, M; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shive MO. Cell. Biol. 10, 2738-2748, 1990 A.71tle: Cloning of the complete gene for carcinoembryonic antigen: analysis of its p A; Reference number: A36319; MUD: 90258861 A; Rocession: A36319 A; Residues: 1-702 A; Molecule type: DNA A; Residues: 1-702 A; Molecule the authors show the codons T74 for residue 641-Phe and CAG for residue 646-T R; Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P. Mol. Cell. Biol. 7, 3221-3320, 1987 A; Title: Isolation and characterization of full-length functional cDNA clones for hum A; Reference number: A37773; MUD: 88038876 A; Coll. Biol. 7, 3221-3320, 1987 A; Molecule type: mRNA A; Residues: 1-702 <bba; 130="" 3221-3320,="" 7,="" 900222;="" 9180223="" 98038876="" 990222;="" 99122014="" a31037="" a31037;="" a;="" aa51967.1;="" as="" authors="" barnett,="" biol.="" codon="" coll.="" cross-references:="" elting,="" for="" franslated="" gb:m29540;="" geboodic="" gobel,="" goebel,="" gyg="" j.j.="" j;="" leu<="" m.a.;="" molecule="" mrna="" mud:="" note:="" nothdufft,="" number:="" pid:="" pidn:="" r;="" reference="" residue="" rolecule="" s.j.;="" s;="" t.;="" th="" the="" type:=""><th>Riokawa, S.; Nakazato, H.; Kosaki, G. Biochem. Biophys. Res. Commun. 142, 511-518, 1987 A; Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from CDNA A; Reference number: A25845; MUID:87128144 A; Recession: A25845 A; Molecule type: mRNA A; Residues: 5-702 < COIKA A; Residues: 5-702 < COIKA A; Residues: 5-702 < COIKA A; Residues: S-702 < COIKA A; Residues: S-703 < COIKA A; Reference number: S08106 A; Rocession: S08106 A; Molecule type: mRNA A; Residues: S-319, 321-702 < COIZ> A; Cross-references: EMBL: X16455; NID:929854; PIDN:CAA34474.1; PID:9825638 B; Barnett, T. Submitted to the EMBL Data Library, September 1991 A; Description: Genomic DNA sequence upstream of the translational start of the carcin</th></bba;> | Riokawa, S.; Nakazato, H.; Kosaki, G. Biochem. Biophys. Res. Commun. 142, 511-518, 1987 A; Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from CDNA A; Reference number: A25845; MUID:87128144 A; Recession: A25845 A; Molecule type: mRNA A; Residues: 5-702 < COIKA A; Residues: 5-702 < COIKA A; Residues: 5-702 < COIKA A; Residues: S-702 < COIKA A; Residues: S-703 < COIKA A; Reference number: S08106 A; Rocession: S08106 A; Molecule type: mRNA A; Residues: S-319, 321-702 < COIZ> A; Cross-references: EMBL: X16455; NID:929854; PIDN:CAA34474.1; PID:9825638 B; Barnett, T. Submitted to the EMBL Data Library, September 1991 A; Description: Genomic DNA sequence upstream of the translational start of the carcin |
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R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Malture 393, 537-544, 1998
A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A.Reference number: A70500; MUID:98295987
A.Reference number: A70504
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                           R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MUID:20150255
A;Scession: C81704
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:297050; GB:AL123456; NID:93256008; PIDN:CAB09749.1; PID:922135
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule, type: DNA*
A; Residues: 1-566 <-Pre>
A; Resperimental source: strain Nigg (MOPn)
                                                                                                                                                                                         monooxygenase-related protein TC0425 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Actes 31.Mar-2000 #sequence_revision 31.Mar-2000 #text_change 11-May-2000 C;Accession: C81704 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable acid--CoA ligase (EC 6.2.1.-) - Mycobacterium tuberculosis (strain H37RV) C,Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: fadD5
C;Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
C;Reywords: acid-thiol ligase
F;72-525/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 2;
Pred. No. 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 36; DB
Pred. No. 12;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82.2%;
66.7%;
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 87.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-554 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||| |:|:
290 YLSGVNLNI 298
605 YLSGANLNL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217 YTSGANIN 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: A70904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: TC0425
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A; Actavas: prelluminary; not compared with conceptual translation
A; Retautus: prelluminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 35-141 < CKHA>
R; Willocoks, T.C.; Craig, 1.W.
Genomics 8, 492-500, 1990
A; Title: Characterization of the genomic organization of human carcinoembryonic antigen
A; Accession: 154224
A; Accession: 154224
A; Molecule type: DNA
A; Residues: 1-37 < CKHS>
A; Cross-references: GB: M60964; NID: 91199118
A; Molecule type: DNA
A; Residues: 1-37 < CKHS>
A; Cross-references: GB: M60964; NID: 9180215; PIDN: AAA51964.1; PID: 9180217
A; Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon
A; Reference number: 159098; MUID: 87204247
A; Residues: 331-702 < CKES>
A; Cross-references: GB: MG-6234; NID: 9180240; PIDN: AAA51972.1; PID: 9180241
A; Molecule type: mRNA
A; Residues: 331-702 < CKES>
A; Cross-references: GB: MG-6234; NID: 9180240; PIDN: AAA51972.1; PID: 9180241
B; Siepen, D: Paxton, R.J; Neumaler, M.; Shively, J.E.; Wagener, C.
Biochem: Biophys. Res. Commun. 147, 212-218, 1987
A; Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and 105
A; Reference number: A26831; MUID: 87326349
A; Molecule type: number: A26831; MUID: 87326349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 35-64 <SIE>
R; Thomas, P.; Toth, C.A.
Blochem. Blophys. Res. Commun. 170, 391-396, 1990
A; Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at the A; Reference number: A35490
A; Molecule type: protein
A; Rocesidues: 'X', 140-151, 'X', 153, 'X', 155-156 <THO>
A; Note: this is the amino terminal end of a fragment shown to mediate uptake by Kupffer C; Comment: This heavily glycosylated membane protein of unknown function is a widely use C; Comment: This protein may be processed at its C-terminus. It is anchored to the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Cross-references: GDB:119054; OMIM:114890
A.Map position: 19q13.2-19q13.2
A.Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
A.Introns: 22/1; 142/1; 235/1; 320/1; 413/1; 498/1; 591/1; 676/1
C.Superfamily: carcinoembryonic antigen: carcinoembryonic antigen precursor amino-termin C.Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatiff:1-138/Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>F:1-34/Domain: signal sequence #status predicted <SIG>F:35-678/Product: carcinoembryonic antigen #status predicted <MAT>F:100-117/Domain: immunoglobulin homology <IMM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
                                                                                                                                                                                                                                                                                       and estimation of the size of the carcinoembi
                                                                                                                                                                                                          s.
                     A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-141 < BA2>
A.Residues: 1-141 < BA2>
A.Cross-references: Baze: X62151
R.Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, Senomics 14, 384-390, 1992
A.Title: Identification of three new genes and estimation of the size of the carcinoer A.Reference number: A44476; MuID:93052339
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Pred. No. 0.55;
1; Mismatches
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F;253-301/Domain: immunoglobulin homology <IRM2>
F;338-395/Domain: immunoglobulin homology <IRM3>
F;516-573/Domain: immunoglobulin homology <IRM3>
F;516-573/Domain: immunoglobulin homology <IRM4>
F;608-657/Domain: immunoglobulin homology <IRM4>
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Best Local Similarity
Matches 8; Conserv
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Indels

Length 506;

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Gaps

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Length 554;

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C;Species: Homo sapiens (man) C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000

interleukin-1 receptor antagonist secreted form precursor - human

RESULT A30368

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Gaps ;

Indels

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Conservative

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A)Cross-references: GDB:125897; OMIM:147679
A;Map position: 2q14.2-2q14.2
C;Superfamily: interleukin-1
C;Superfamily: interleukin-1
C;Superfamily: seppicing: cytokine receptor
C;Superfamily: interleukin-1 receptor antagonist, long intracellular splice form #s
F;1-180/Product: interleukin-1 receptor antagonist, short intracellular splice f
F;1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dottolin H10117 - Haemophilus influenzae (strain Rd KW20) C.Species: Haemophilus influenzae (species: Haemophilus influenzae (species: Haemophilus influenzae (c.Species: Haemophilus influenzae (c.Species: Haemophilus influenzae (c.Species: Haemophilus influenzae (c.Species: Haemophilus influenzae) H. Species: Hammann, S.D.; Addams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage (c.Cayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.D.; Scott, J.95; M. McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A. Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente A. Freference number: A64000; MUID:95350630
A. Accession: 164001
A. Stetus: nucleic acid sequence not shown; translation not shown A. McHoecule type: DNA A. McHoecule type: DNA A. McHoecule type: DNA A. McHoecule type: H3 XTIGR> A. Cross-references: GB:U32697; GB:L42023; NID:91573067; PID:91573069; TIGR:H10117
                                                                                                          interleukin-1 receptor antagonist, long intracellular splice form - human N;Contains: interleukin-1 receptor antagonist, short intracellular splice form C;Specias: Homo sapiens (man) (c;Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000 C;Accession: 137893; A39386 K;Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Giola, L.; Introna, M.; Manto J. Exp. Med. 182, 623-628, 1995 A;Title: Cloning and characterization of a new isoform of the interleukin 1 receptor A;Reference number: 137893; MUID:95355865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-fr: William (RES)
A;Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
B;Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A;Title: CDNA cloning of an intracellular form of the human interleukin 1 receptor A;Reference number: A39386; MUID:91213436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: mRNA
A;Residues: 1-3,25-180 < HAS>
A;Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C;Comment: For an alternative splice form, see PIR:A30368
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Pred. No. 6;
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66.78;
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Best Local Similarity 66.77
Local 6; Conservative
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Best Local Similarity
Matches 7; Conserv
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62 YLQGPNVNE 70
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A; References: GB: X52015; NID: 932576; PIDN: CAA36262.1; PID: 932577
B; Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Ar Nature 343, 336-340, 1990
A; Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor. A; Reference number: S08159; MUID: 90136920
A; Accession: S08159
A; Molecule type: protein
A; Residues: 26-75; 97-108, 110-116; 120-131; 163-176 (HAN)
A; Reference number: A37822; MUID: 90354444
A; Reference number: A37822
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A;Introns: 39/2; 69/1: 106/3
C;Superfamily: interleukin-1
C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>
F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental
C;Accession: A40956; I37894; A30368; S08160; S08159; A37822
R;Elsenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A;Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family: A;Reference number: A40956; MUID:91271363
A;Accession: A40956
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A;Residues: 26-25;70-77;122-127;170-175 <BIE>
A;Experimental source: culture medium, PMA-stimulated THP-1 cells
C;Comment: For an alternative splice form, see PIR:A39386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: S08160
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
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A;Cross-references: GDB:125897; OMIM:147679
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Best Local Similarity 66.7%
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59 YLQGPNVNL 67
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A; Kesludes: 1-97, COMA,
A; Kesludes: 1-97, COMA,
A; Kesludes: 1-97, COMA,
A; Title: Characterization of the Escherichia coli gcv operon.
A; Reference number: 141231; MUID:94237484
A; Title: Characterization of the Escherichia coli gcv operon.
A; Reference number: 141231; MUID:94237484
A; Reseidues: 1957 cRES.
A; Scausis preliminary
A; Molecule type: DNA
A; Residues: 1-957 cRES.
A; Rossi- 1-957 cRES.
A; Rossi- 1-957 cRES.
A; Rossi- 1-957 cRES.
A; Rossi- 1-957 cRES.
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Rosci- 277, 1453-1462, 1997
A; Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617
A; Residues: 1-957 cBLAT>
A; Rossi- 1-957 cBLAT>
A; Rossi- 1-957 cBLAT>
A; Rossi- 1-957 cBLAT>
A; Residues: 1-957 cBLAT>
A; R
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A; Cross-references: EMBL:U23510; NID:9746453; PID:9746454; PIDN:AAC46780.1; CESP:R12C
A; Experimental source: strain Bristol N2
A;Title: Cloning and nucleotide sequence of the gcv operon encoding the Escherichia A;Reference number: S36832; MUID:93387305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:R12C12.1
A;Introns: 52/3; 149/3; 325/2; 393/1; 470/3; 546/3; 619/3; 749/2; 827/1; 883/1
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hypothetical protein R12C12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T16734
R;Favello, T
R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;708/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keywords: oxidoreductase; phosphoprotein; pyridoxal phosphate
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Pred. No. 59;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 979;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 60;
1; Mismatches
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 75.09
Matches 6; Conservative
                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-957 < OKA>
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A39521
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E75352
glycine cleavage system P protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Satersion: P5352
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.; Snith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Tille: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
A;Accession: E75352
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-494 cMHI>
A;Cross-references: GB:AE002021; GB:AE000513; NID:g6459573; PIDN:AAF11360.1; PID:g645958
A;Gene: DR1809
A;Map position: 1
                      RESULT 7
E7125
hypothetical protein PH1989 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: E71215
R;Kawarabayasi, Y: Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin M.; Obfuku, Y: Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Accession: E71215
A;Status: prellminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-335 < KAW>
A;Residues: 1-355 
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836834
glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) - Escherichia coli
Glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) - Escherichia coli
Clypecies: Escherichia coli
Clypecies: Escherichia coli
Clypecies: Sacana, 141232; G65074
R.Okanura - Ikada, K.; Ohnura, Y.; Motokawa, Y.
Eur. J. Biochem. 216, 539-548, 1993
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Pred. No. 19;
2; Mismatches 1; Indels
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66.78;
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Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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59 FLKGANINV 67
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NATIENTAL MATERIAL NAMES: 19 A CONTROLL NAMES: Note of the Chief of th
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N;Alternate names: glycin cleavage system protein P; protein YM9646.01; protein YMR18
C;Species: Saccharomyces cerevisiae
C;Date: 10-Feb-1095 #sequence_revision 12-May-1995 #text_change 29-Oct-1999
C;Accession: S50917; S59810; S70896
R;Pearson, D: Bowman, S.
submitted to the EMBL Data Library, January 1995
A;Reference number: S50917
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A;MoLecule type: DNA
Residuca: 1-1034 <PEA>
A;Cross-references: EMBL:247815; NID:g642280; PIDN:CAA87810.1; PID:g642281; MIPS:YMR1
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A; Description: Cloning and expression of glycine decarboxylase from Saccharomyces cer A; Reference number: $59809
A; Accession: $59810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1020 <KUM>
A;Cross-references: GB:M64590; GB:J05742; NID:g190208; PIDN:AAA36463.1; PID:g190209
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A;Cross-references: EMBL:U20641
C;Genetics:
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F;754/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A;Residues: 1-1034 <SIN>
A;Cross-references: EMBL:U20641; NID:g676869; PIDN:AAB18933.1; PID:g676871
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C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;773/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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                                                               glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) precursor - human
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Pred. No. 63;
1; Mismatches
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A;Title: Specific induction by glycine of A;Reference number: S70896; MuID:96228709
A;Accession: S70896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown A;Molecule type: DNA A;Residues: 1-77,'V',79-121,'VS',124-247,
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Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) precursor - chicken N.Alternate names: glycine decarboxylase; P-protein C; Species: Gallus gallus (chicken) (chic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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C;Keywords: mitochondarion; oxidoreductase; phosphoprotein; pyridoxal phosphate
F;761-768/Region: 9lycine-rich
F;754/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A; Residues: 1-1020 - KURD;
A; Cross-references: GB: M63635; NID: 9190286; PIDN: AAA36478.1; PID: 9190287
A; Note: deletion of 756-Phe causes nonketotic hyperglycinemia
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Pred. No. 62;
1; Mismatches
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75.0%; Pred. No. 63;
tive 1; Mismatches
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708 YLDGANMN 715
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C) Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999

C) Accession: E71551

R) Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Solence 282, 754-759, 1998

A) Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia track A) Accession: E71551

A) Accession: E71551

A) Accession: E71551

A) Molecule type: DNA

A) Residues: 1-507 ARN>

A) Conserreferences: GB:AE001288; GB:AE001273; NID:g3328545; PIDN:AAC67739.1; PID:g332854

A) Genetics: A) Genetics: A) Genetics: A) Genetics: A) Genetics: A) Genetics: A) CX
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73.3%; Score 33; DB 2; Length 507;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 2; Indels
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                               Carcinoembryonic a
                                                            Carcinoembryonic a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide agonists and antagonists of carcinoembryonal antigen
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R65168
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W00182
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                                                                                                                                                                                                                                                                                                                                                                                                     Y09528 standard; peptide; 9 AA
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Homo sapiens.
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Y09528;
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BGP (1-314)/CEA (4
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Immunogenic peptid
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                                                                  Search time 108.84 Seconds (without alignments)
2.827 Million cell updates/sec
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| S1DS6/gcgdata/geneseqcgpAA1983.DaT:*
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         GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                 hits satisfying chosen parameters:
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Listing first 45 summaries

    protein search, using sw model

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W77134
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Gapop 10.0 , Gapext 0.5
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WO9833810-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated
                   or antegonists (Tb) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunchlerapy (i.e. to prevent attack on normal but generated a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
           present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatability complex; MHC; B cell; disease; anti-tumour; anti-viral.
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                                                                                                                                                                                                                                                           Gaps
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Pred. No. 2.1e+05;
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(SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-1998 (first entry)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melief CJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-549891/50.
                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                  1 YLSGANINL 9
                                                                                                                                                                                                                                                                                               1 ylsganinl 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1997;
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                                                                                                                                                                                           Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                 W39723
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with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC Class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide epitope W77119-W77138 were created for human tumour-specific cytotoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disease specific immunogen - comprises disease specific cytotoxic lymphocyte epitope used to elicit melanoma specific CTL response
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                                                                                                                                                                                                                  Score 43; DB 18; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tyrosinase; tyrosinase cytotoxic lymphocyte response; cytotoxic T lymphocyte; cysteine-depleted; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hunt DF, Kittlesen D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEA synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W77134 standard; peptide; 9 AA.
                                                                                                                                                                                                                  95.6%;
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                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                          Ouery Match
Best Local Similarity
8, Conserve
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                                                                                                                                                9 AA;
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| ylsqanlnl
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(first entry)

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Immunogenic peptide having a human leukocyte antigen binding motif #2266
                                                                                                                                                                                                     Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytocoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                         Y47655 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIM-) EPIMMUNE INC.
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                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
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                                                                                                                           01-DEC-1999
                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sette A,
                                                                                   X47655;
RESULT
Y47655
                                                                                   Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human leukocyte antigen (HEA), HLA-A2.1 and are used to examplify the method of invention of producing antigen-specific cytotoxic T cells (CTLS) in vitro. The method comprises contexting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) antigen presenting cells (APCS) pretreated with corrections with antigen presenting cells (APCS) pretreated with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLS. A method for specifically killing crarget cells in a human patient is also provided which comprises charget cells in a human patient is also provided which comprises charget cells with APCS pretreated with pre-treatment growth factors, where the APCS comprise class I MHC molecules. The pretreated APCS are incubated with the cytotoxic growth factors, thereby producing activated cCC composition can then be administered to the patient. The activated cCC can be used for treating cancers, immune disorders, viral infections, ALDS, hepatitis, bacterial infection, fungal infection, malaria or
                                                                                                                                                                                                                                human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                            major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
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Pred. No. 2.1e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood S,
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                                       W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.6%;
88.9%;
                                                                                                                                                                                                            Cytotoxic T lymphocyte; CTL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US01959.
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                                                                                                                        22-OCT-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presenting cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis.
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                       Synthetic.
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                                                                               W70045;
RESULT
                        W70045
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Southwood

Grey HM,

Celis E,

Kubo RT, Sidney J,

98WO-US05039. 98WO-US05039

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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CE HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cesponse against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) crop prevent viral infections and cancers in mammals (especially humans) crop prevent viral infections as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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Pred. No. 2.1e+05;
.; Mismatches 0; Indels
Claim 1; Page 118; 150pp; English.
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Best Local Similarity
Matches 8; Conserv
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Gaps

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8; Conservative

Matches

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1 YLSGANINL 9

Southwood

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RESULT

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immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                         New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases {\color{black} -}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunoglobulin; therapeutic; streptokinase; vaccine; 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 20; Length 10;
Pred. No. 0.0079;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                             Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein sequence of vaccine 2 708 VI.
                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 76; 150pp; English.
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                                                                                                                                                                                                                                                                                            Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%;
88.9%;
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Matches 8; Conservative
                                                                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC.
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                                                                                                     Homo sapiens
                                                                                                                                 W09945954-A1
                                                                                                                                                                                               13-MAR-1998;
                                                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                 16-SEP-1999
                                                                                    Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or artagonists (1b) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating asstrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use im adoptive transfer therapy. (Ib) are used to inhibit CEA specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide having a human leukocyte antigen binding motif #1166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
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                                                                                                                                                                           immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                        Carcinoembryonic antigen; CEA; human; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.6%; Score 43; DB 20; Le
88.9%; Pred. No. 2.1e+05;
ive 1; Mismatches 0;
                                                                                                                            Carcinoembryonic antigen peptide agonist CAP-1.
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                            Y09525 standard; peptide; 9 AA.
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                                                                                             (first entry)
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-326544/27.
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                                                                                                                                                                                                                                                                                                                                                 22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                10-0CT-1997;
                                                                                             20-JUL-1999
                                                                                                                                                                                                                                                                                                                 22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                              Barzaga E,
                                                                                                                                                                                                                                                       Synthetic.
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Gaps

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Y46555;

XX DE XX

RESULT Y46555

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Carcinoembryonic antigen fragments – used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens.
                                                                                                                                                                                                                                                                                       CEA fragments can be used in assays to determine the presence and amt. CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128 kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer; amplify; polymerse chain reaction; PCR; human; blilary giycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimmeric protein; PRLA3 epitope; anti-PRLA3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New molecules which bind carcinoembryonic antigen - used for the
                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length 178
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stewart LMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BGP (1-314)/CEA (490-643) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                    Score 43; DB ]
Pred. No. 0.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Snary D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "BGP (1-314)"
315..468
/note= "CEA (490-643)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                         Disclosure; page 4; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R77436 standard; Protein; 468 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Durbin H,
                                                                                                                                                                                                                                                                                                                                                                                                     95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB01816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93GB-0017423
                               89EP-0305232
                                                               88US-0198289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bodmer WF,
                                                                                             (CITY ) CITY OF HOPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1995-106813/14.
                                                                                                                                                           WPI; 1989-349991/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 ylsganlnl 115
                                                                                                                                                                                                                                                                                                                                                      178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YLSGANINL 9
                                                                                                                                                                            N-PSDB; N92449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9506067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1993;
                               24-MAY-1989;
                                                               25-MAY-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-1995
29-NOV-1989
                                                                                                                             Shively JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bates PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            roung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R77436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins. The method comprises determining at least part of the amino acid sequence of the protein: (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The immunoglobulins on theraputic proteins. •9. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the protein sequence of vaccine 2 708 VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for the production of non-immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                      Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43; DB 20; Length 107;
Pred. No. 0.11;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinoembryonic antigen; domain III; domain A; domain B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of carcinoembryonic antigen domain III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="domain A"
90..178
/note="domain B"
                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 19; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P93499 standard; protein; 178 AA.
                                                                                                                                         98GB-0007751.
97GB-0010480.
97GB-0016197.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.6%;
                                                                                                                                                                                       97GB-0025270.
97US-0067235.
                                                                                                            98WO-GB01473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                          (BIOV-) BIOVATION LTD
                                                                                                                                                                                                                                                                                                      WPI; 1999-045301/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YLSGANINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107
                Homo sapiens
                                             W09852976-A1
                                                                                                                                                                                       28-NOV-1997;
02-DEC-1997;
                                                                                                           21-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1990
                                                                                                                                          14-APR-1998;
21-MAY-1997;
                                                                                                                                                                          31-JUL-1997
                                                                            26-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP343946-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P93499;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doma.i.n
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Claim 15; ; 67pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09506067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bates PA,
Young S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R77437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R77437
       \mathbf{x} \otimes 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
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0
                                                                                                                                                                                                             portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCR; human; carcinoembryonic antigen;
                                                                                                                                                                                  sequences given in R77435-38 are chimaeric proteins comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation and purifications.
diagnosis and treatment of colorectal carcinoma and for isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer; amplify; polymerse chain reaction; PCR; human; blidary dlycoprotein; BGP; membrane-bound; carcinoembryonic CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stewart LMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BGP (1-314)/CEA (490-C-terminal) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "CEA (490-C-terminal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 1
Pred. No. 0.58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snary D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "BGP (1-314)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Durbin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R77435 standard; Protein; 493 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94WO-GB01816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93GB-0017423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JAN-1996 (first entry)
                                                                                                              Claim 16; ; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315..493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bodmer WF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-106813/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            468 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YLSGANINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9506067-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-AUG-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bates PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      molecules
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R77435
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The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they append and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Primer; amplify; polymerse chain reaction; PCR; human; blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimmeric protein; PRLA3 epitope; anti-PRLA3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation and purifications.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 43; DB 16; Length 493;
Pred. No. 0.62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BGP (1-314)/CEA (490-644)/BGP (391-430) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "BGP (1-314)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R77437 standard; Protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.6%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..469
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Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 ylsganlnl 404
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The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they append to the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R00619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine. R60619 can be used in a reagent composition for detecting neoplastic diseases in blological samples, or in an immunoasay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%; Score 43; DB 16; Length 511;
88.9%; Pred. No. 0.64;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinoembryonic antigen; CEA; neoplastic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinoembryonic antigen glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mach J, Pelegrin A, Terskikh A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R60619 standard; Protein; 642 AA.
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                   Claim 18; ; 67pp; English.
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Best Local Similarity
8; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                               511 AA;
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                                                                                                                                                                                  indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                      The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biliary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation and purifications.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 43; DB 16; Length 509;
Pred. No. 0.64;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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t.e= "CEA (490-642)"
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/note= "BGP (387-430)"
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/note= "BGP (1-314)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bates PA, Bodmer WF, Durbin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R77438 standard; Protein; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       95.6%;
88.9%;
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                 Claim 17; ; 67pp; English
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468..51
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Best Local Similarity
Matches 8; Conserv
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396 ylsganini 404
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Mismatches

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Matches
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                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen; immunogen; breast cancer; lung cancer; colon cancer; therapy; immunotherapy; vaccine; baculovirus; vector; Spodoptera frugiperda; insect; pA9080 AcNPV-CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A recombinant, soluble, immunogenic carcinoembryonic antigen (rCEA) (R98519) is encoded by vector pA9080 AcMPV-CEA (see also 196455) in which a modified human CEA gene is joined to a baculovirus signal sequence under control of a polyhedrin promoter. The baculovirus signal peptide directs translation of rCEA into the insect cell glycosylation pathway. rCEA can be produced at high levels in Sf900+ insect cells grown in serum-free media, and isolated to a purity of over 95%. It is used as an immunogen in humans to protect against cancer, partic. breast,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note- ....
18.663
/label= Mat_protein
/note= "amino acids 1-3 of the mature protein
are derived from the baculovirus vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic carcinoembryonic antigen produced using insect cell baculovirus expression system - useful in cancer therapy
                                                        ;
                         Query Match 95.6%; Score 43; DB 15; Length 642; Best Local Similarity 88.9%; Pred. No. 0.83; Matches 8; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Chimeric Autographa californica nuclear polyhedrosis virus;
Chimeric Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  1..18
/label= Sig_peptide
/note= "AcNPV 61k protein signal peptide"
                                                                                                                                                                                                                                                                        Immunogenic carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volvovitz F;
                                                                                                                                                                                      R98519 standard; Protein; 663 AA.
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                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-020581/02
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571 ylsganini 579
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                                                                                    1 YLSGANINL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                   R98519;
                                                                                                                                                         RESULT 15
R98519
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Score 43; DB 17; Length 663; Pred. No. 0.86;

95.6%;

Query Match Best Local Similarity

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01-JUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLRT).
GIN11 PROTEIN (FRAGMENT).
GIN11.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetaceae; Saccharomyces
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
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TISSUE-TIBIAL GLAND;
Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT).
                     Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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"Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and Limnodynastes terraeroginae"; Aust. J. Chem. 46:833-842(1993).

-I MASS SPECTROMETRY: MW=729; METHOD=FAB.
Amphibian skin.
SEQUENCE 8 AA; 729 MW; 7C28772865B72728 CRC64;
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070193; AAD23233.1; -.
NON_TER
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MEDLINE; 95053898.
al-Kaff N., Covey S.N.;
"Variation in biological properties of cauliflower mosaic virus
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
                                                                                                                                                                                                                                       33.3%; Score 15; DB 13; Length 8; 50.0%; Pred. No. 3e+05;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
01-NOV-1998 (TREMBLrel. 08, Last annotation update)
GENE III.
Cauliflower mosaic virus.
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J. Gen. Virol. 75:3137-3145(1994).
EMBL; S75948; CAB33416.1; ..
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALCYCLIN-ASSOCIATED PROTEIN, CAPSO-CA2+/PHOSPHOLIPID-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
"A calcyclin-associated protein is a newly identified member of the ca2+phospholipid-binding proteins, annexin family.";
J. Biol. Chem. 267:8919-8924(1992).
SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;
                                                                                                                                                                                                                               MEDLINE; 95180691.

Rosenow C., Roberts I.S., Jann K.;

Rosenow C., Roberts I.S., Jann K.;

Isolation from recombinant Escherichia coli and characterization
CMP-Kdo synthetase, involved in the expression of the capsular K5
polysaccharide (K-CKS).";

FEMS Microbiol. Lett. 125:159-164(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-7 FRAGMENT.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                 Plasmid pCR3.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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100.0%; Pred. No. 3e+05;
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50.0%;
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031415;
01-NOV-1996 (TrEMBLrel. 01,
01-JAN-1999 (TrEMBLrel. 09,
01-JAN-1999 (TrEMBLrel. 09,
                                              01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, KPSD PROTEIN (FRAGMENT).
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Plasmid.
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Best Local Similarity
Matches 3; Conserva
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Matches 3; Conserv
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GAKVIL 7
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3 LSG 5
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SEQUENCE.
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SEQUENCE
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Q9R7E8;
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MEDLINE; 92011685.
Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J., Schneider W.J.;
                                                                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)
COM DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Aarchosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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J. Biol. Chem. 266:19079-1908711991),
SEQUENCE 8 AA: 846 MW; C007272DD865BAAA CRC64;
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Bailly J.L., Borman A.M., Peigue-Lafeuille H., Kean K.M.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
Ball; X90724; CAA62259.1; -.
NON TER
SEQUENCE 8 AA; 821 MW; EFC185A2D6DDD876 CRC64;
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Pred. No. 3e+05;
2; Mismatches 1; Indels
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                  8;
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                    Length
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
5'UTR IN IRES SEQUENCES (ISOLATE TH222) (FRAGMENT).
                  DB 2;
3e+05;
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                  Score 14; DB 2
Pred. No. 3e+C
0; Mismatches
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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100.0%; Pre
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Best Local Similarity 40.0
Matches 2; Conservative
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| GAQVS 6
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MEDINE, 87061199.

Morgan W.R., Ward D.C.;

"Three splicing patterns are used to excise the small intron common to all minute virus of mice RNAS.";

J. Virol. 60:1170-1174(1986).

EMBL; M12032; AAA69570.1; -..

EMBL; V02175; AAA67112.1; -..

EMBL; V01115; CAA24311.1; -..

Hypothetical protein.

SEQUENCE 9 AA; 1061 MW; C3FD405863637862 CRC64;
   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SECHAIN-LYMPHOTROPIC VARIANT;
MEDLINE; 86115415.
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, MVM(i), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, PWM(1), and comparison with the DNA sequence of the fibrotropic prototype strain.";
J. Virol. 57:656-669(1986).
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101-NOV-1998 (TTEMBLrel. 08, Last annotation update)
102-NOV-1998 (TTEMBLrel. 08, Last annotation update)
103-NOV-1998 (TTEMBLrel. 08, Last annotation update)
104-NOV-1998 (TTEMBLrel. 08, Last sequence update)
105-NOV-1998 (TTEMBLREL. 01, Last sequence update)
1
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Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 93010967.
Donze O., Spahr P.F.;
"Role of the open reading frames of Rous sarcoma virus leader RNA
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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EMBO J. 11:3747-3757(1992).
EMBL; X6758; CAA47862.1; -.
Hypothetical protein.
NON TER
SEQUENCE 7 AA; 672 MW; 776045A76
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50.0%;
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Matches 2; Conservative
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MEDLINE; 86115415
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MEDLINE: 97442476.
MEDLINE: 97442476.
Plummar N.W., McBurney M.W., Meisler M.H.;
Plummar N.W., McBurney M.W., McBurney M.W.,
"Alternative splicing of the sodium channel SCN8A predicts a truncated
two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24008-24015(1997).
EMBL; U97672; AAB80914.1;
MGD: MGI:103169; Scn8a.
                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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                                                                                                                                                                                                Kanki T., Kuwasawa N., Sekiya Y., Ichikawa Y.;
Kanki T., Kuwasawa N., Sekiya Y., Ichikawa Y.;
"Responsive expression of a MHC class I epitope and genes following
Marek's disease virus infection.";
Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; D90399; BAA14395.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 05, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SODIUM CHANNEL, VOLTAGE-GATED, TYPE VIII, ALPHA POLYPEPTIDE
(TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT) (FRAGMENT).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 1.1 KDA PROTEIN.
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8A55A76455B861B5 CRC64;
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MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.1%;
50.0%;
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9 AA; 859 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 3; Conserv
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NON_TER 1
SEQUENCE 9 AA
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3 TGSN 6
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SEQUENCE
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SEQUENCE FROM N.A. MEDLINE; 88105390. van der Vossen J.M., der Lelie D., Venema G.; "Isolation and characterization of Streptococcus cremoris Wg2-specific
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 9179-79) (FRAGMENT).
                                                                                                                                                                Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
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NON_TER
SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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Pred. No. 3e+05;
1; Mismatches 0; Inde
                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PROMOTER 23 DNA FRAGMENT (FRAGMENT).
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Best Local Similarity 66.7
Matches 2; Conservative
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STRAIN-CDC 9179-79;
MEDLINE; 97089747.
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Best Local Similarity
Matches 2; Conserv
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2 LSGAN (:11:3 ISGVH )
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Q44001;
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Q48686
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MEDLINE; 98208049.
Healewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
Healewood M.M., Elphinston in the Gouldian Finch Erythrura gouldiae
assessed by temperature gradient gel electrophoresis.";
Electrophoresis 19:142-151(1998).
EMBL: U40496; AAC60363.1; -
NON_TER 8
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0.0.0 www. C6C1F2C865B046DE CRC64;
                                       Gaps
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R., "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis."; Electrophoresis 19:42-151(1998).
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Erythrura gouldiae (Gouldian finch).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeridae; Erythrura.
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             DB 12; Length 7;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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Pred. No. 3e+05;
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                                    3; Mismatches
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            28.9%;
33.3%;
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40.0%;
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         Query Match
Best Local Similarity
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Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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1 MAGPSI 6
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3 ISGVH 7
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Ramiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
"Evolutionary divergence in the red algae Caloglossa leprieurii and C.
apomeiotica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caloglossa leprieurii.
Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
Caloglossa.
                                                               [1]
STRAINVARIOUS STRAINS;
MEDLINE; 97089747.
MEDLINE; 97089747.
Marlyshev A.V., Macintyre S.;
"Study of the intergenic exer-exec region and its application as simple preliminary test for Aeromonas Spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89464; CAA61643.1;
EMBL; X89460; CAA61653.1;
EMBL; X89460; CAA61655.1;
EMBL; X89461.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYCENASE LARGE SUBUNIT
                          Aeromonas caviae.
Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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Last annotation update)
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  DNA FOR EXEF-EXEG INTERGENIC REGION (FRAGMENT)
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EMBL; D87813; BAA31279.1; -.
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Best Local Similarity
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01-MAY-2000
01-MAY-2000
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7 VNL 9
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SEQUENCE
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last'sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEC INTERGENIC REGION (STRAIN CDC 1306-83) (FRAGMENT).
                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN ATCC 49659) (FRAGMENT).
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EMBL; X89457; CAA61629.1; -.
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                                                                                                                                   SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE, 97089.
MEDLINE, 97089.
Karlyshev A.V., Macintyre S.;
Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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Pred. No. 3e+05;
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STRAIN=CDC 1306-83;
MEDLINE; 97089747.
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Matches 2; Conserv
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STRAIN-JAW1122, AND 962;
Ramiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kawai I
Reproductive and genetic distinction between broad and narrow
entities of Caloglossa continua (Delesseriaceae, Rhodophyta).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023383; BAA88916.1; -.
EMBL, AB023382; BAA88914.1; -.
                                 Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesserlaceae;
                                                                                                                                 Kawai
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                                                                                                                         Kamiya M., Tanaka J., King R.J., West J.A., Zuccarello G.C., Kaw "Reproductive and genetic distinction between broad and narrow entities of Caloglossa continua (Delesseriaceae, Rhodophyta)."; Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023384; BAA88918.1;
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01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sendence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
(FRACHENT).
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Pred. No. 3e+05;
1; Mismatches
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66.78;
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Caloglossa stipitata.
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Best Local Similarity
2; Conserve
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Matches 2; Conserv
                                                                                              SEQUENCE FROM N.A.
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7 ANV 9
                                                                  Caloglossa.
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7 ANV 9
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                                                             Chloroplast.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
Bostrychia.
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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                                                                                                                                                          Zuccarello G.C., West J.A., King R.J.;
"Blogeography of Bostrychia moritaiana (Ceramiales).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF126705; AAD55863.1; -.
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Pred. No. 3e+05;
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01-MAY-2000 (TrEMBLrel. 13, Last ann
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"Evolutionary divergence in the red algae Caloglossa leprieurii and C. apomeiotica.";
- Phycol. 34:36-370(1998).
EMBL; D89948; BAA31281.1; -.
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Caloglossa monosticha.
Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
                                                                   Caloglossa apomeiotica.
Eukaryota, Rhodophyta, Florideophyceae, Ceramiales, Delesseriaceae,
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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Pred. No. 3e+05;
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Pred. No. 3e+05;
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EMBL; D89950; BAA31285.1; -.
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomelaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
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STRAIN-R.3881.QLD, M3001.MI, R3826.BZ, AND B.R.F.M.BZ;
SUCCATCALLO G.C., West J.A., King R.J.;
"Biogeography of Bostrychia moritziana (Ceramiales).";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF1267015, AAD55883.1; -.
EMBL; AF1267001, AAD55865.1; -.
EMBL; AF1267004, AAD55861.1; -.
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Last annotation update)
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3e+05;
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Pred. No. 3e+05;
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Pred. No. 3e+05
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7 ANV 9
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"Evolutionary divergence in the red algae Caloglossa leprieuril and C.
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Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Lee C.C., Yazdani C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
Caskey C.T.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3e+05;
1; Mismatches 1; Indels
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 07, Last annotation update)
(CLONE XP7B11B) (FRAMBNT).
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Pred. No. 3e+05;
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BAA31293.1;
BAA31295.1;
BAA31297.1;
BAA31299.1;
BAA31301.1;
   "EVCLALL";
J. Phycol. 34:361-370(1998).
ENBL; D89959; BAA31283.1;
""": n89949; BAA31283.1;
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66.7%;
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50.0%;
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                                                        EMBL, D89951; BAA31287.1; --
EMBL, D89952; BAA31289.1; --
EMBL, D89953; BAA31291.1; --
EMBL, D89954; BAA31293.1; --
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EMBL; L32080; AAA73891.1;
NON_TER 1
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Matches 2; Conserv
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EMBL; D89956;
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EMBL; D89958;
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                                  Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.; "Evolutionary divergence in the red algae Caloglossa leprieurii and C. apomeiotica."; J. Phycol. 34:361-370(1998).
EMBL: D89960; BAA31305(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
"Evolutionary divergence in the red algae Caloglossa leprieurii and C.
apomeiotica.";
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STRAIN-1048, 902, 490, 932, 922, 880, 1053, 1052;
Kamiya M., West J.A., King R.J., Zuccarello G.C., Tanaka J., Hara Y.;
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
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Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Delesseriaceae;
Caloglossa.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
8TBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT (FRAGMENT).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RIBULOSE 1,5-BISPHOSPHATE CARBOXYLASE/OXYGENASE LARGE SUBUNIT
                                                                                                                                                          Score 13; DB 10; Length 9; Pred. No. 3e+05;
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Pred. No. 3e+05;
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66.7%;
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EMBL; D89961; BAA31307.1; -.
NON_TER 1
SEQUENCE 9 AA; 977 MW; C7
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llarity 66.7%;
Conservative
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Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Temnopleuroida; Toxopneustidae; Lytechinus.
                                                                                                        TISSUE-BLOOD;
MEDLINE; 90349591.
Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P.,
Hermand P., Salmon C., Cartron J.-P., Colin Y.;
"Molecular cloning and protein structure of a human blood group Rh
Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI phenotype.";
Am. J. Hum. Genet. 60:808-817(1997).
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01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
METALLOTHIONEIN (FRAGMENT).
                                                                                                                                                                                                                       8 8 AA; 1049 MW; C007244691FB5AB1 CRC64;
                                                                                                                                                           polypeptide.";
Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
EMBL; 297030; CAB09726.1;
NOW_TER 8 8
SEQUENCE 8 AA; 1049 MW; CO072446GlFBERD.
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Best Local Similarity 12.5
Matches 1; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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4 HMNL 7
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Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
Enterococcus.
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Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Craiga R.A., Clewell D.B.;
"Isolation and structure of bacterial sex pheromone, CPD1.";
Science 226:849-850(1984).
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Pred. No. 8.8e+04;
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                                                                LPMS_STAEP
PLP_BRANA
UF06_MOUSE
                                                                                                     UPA1_HUMAN
VGLG_HSV2B
AL10_CARMA
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BUK_CLOPA
DSIP_RABIT
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FAR3_PANRE
FAR5_HIRME
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ALL5_CYDPO
ANG2_BOTJA
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Raja clavata (Thornback ray).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Elasmobranchii, Squalea, Hypnosqualea, Pristiorajea, Batoidea;
Rajiformes, Rajidae, Raja
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE: 78026571.
Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
Structural study of circulating thymic factor: a peptide isolated from pig serum. II. Amino acid sequence.";
J. Biol. Chem. 252:8045-8047(1977).
-I. MISCELLANBOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartlodactyla; Suina; Suidae; Sus.
                                                                                Score 15; DB 1; Length 9;
Pred. No. 8.8e+04;
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                     9 AMIDATION.
969 MW; 17FF476EB455B04B CRC64;
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9 AA; 984 MW; 17E9C76EB455B04B CRC64;
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Pred. No. 8.8e+04;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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THYMIC FACTOR.
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ID OXYT_RAJCL
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"Characterization of neurohypophyseal hormones from a fresh water bony fish, the carp (Cyprinus carpio). Comparison with hormones from sea water bony fishs.";

Comp. Biochem. Physiol. 14:245-254(1965).

-I. FUNCTION: ANTIDIURETIC HORMONE.

-I. SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

PIR; A61364; A61364.

INTERPRO; IPRO00981; -.

PRAM: FR00202, hormone4; 1.

HORSITE: PS00204; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                    Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
    Gaps
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Washaryota: Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neoptorygii; Teleostei; Euteleostei; Ostariophysi Cypriniformes; Cyprinidae; Cyprininae; Cyprininae;
                                                                                                                                                                                                                                                                                                                                                                             Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
calliphora vomitoria ";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
    Indels
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MOD_RES 8 8
SEQUENCE 8 AA; 957 MW;
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MEDLINE; 76074708.
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE, 92195954.
MEDLINE, 92195954.
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
Identification of Remide neuropeptides in the medicinal leech.";
Peptides 12.897-508 (1991).
-1. SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
1-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
1-NOV-1995 (Rel. 32, Last sequence)
FWRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
Hirdo medicinalis (Medicinal leech),
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinus maenas (Common shore crab) (Green crab).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidide; Periplaneta.
                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24.4%; Score 11; DB 1; Length 4; 100.0%; Pred. No. 8.8e+04; ive 0; Mismatches 0; Indels
                                                                                                          Score 12; DB 1; Length 9; Pred. No. 8.8e+04;
                                                        9 AA; 1041 MW; 1F49087042DB41BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AMIDATION.
69D4073B30000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limulus polyphemus (Atlantic horseshoe crab), and
          -!- SIMILARITY: WEAK TO OTHER POLYGALACTURONASES.
Hydrolase; Glycosidase; Cell wall.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
PROCTOLIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Periplaneta americana (American cockroach),
                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                          26.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Life Sci. 17:1253-1256(1975)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 AA; 598 MW;
                                                                                                                          Best Local Similarity 50.0 Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES-P. AMERICANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-P. AMERICANA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRCT_PERAM
P01373;
21-JUL-1986 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in insects."
                                                                                                                                                                                               |: |
4 YVIG 7
                                                                                                                                                                                                                                                                                          FAR3_HIRME
P42562;
                                                                                                                                                                            1 YLSG 4
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                           NON_TER
SEQUENCE
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FAR3_HIRME
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Comp. Blochem. Physiol. 118B:861-867(1997).
-!- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1.4-ALPHA-D-GALACTOSIDURONIC LINKAGES IN PECTATE AND OTHER GALACTURONANS.
-!- INDUCTRON: INHIBITED BY CITRUS PGIP.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 9.4, ITS MW IS: 44.5 KDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Avigad G., Markus Z.;
"Identification of a peptide inhibitor of galactose oxidase from "Identification of a peptide inhibitor of galactose oxidase from Dactylium dendroides.";
Fed. Proc. 31:447-447(1972).
-!-FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE GALACTOSE OXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY BINDING FOR TYPE PROSTHETIC COPPER GROUP.

PIR: AND 1341: XEYDGD.
COPPER: Metalloenzyme inhibitor.
SEQUENCE 7 AA; 706 MW; 75BB01A456DB7DB0 CRC64;
                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Doostdar H., McCollum T.G., Mayer R.T.; "Purification and characterization of an endo-polygalacturonase from
                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
GALACTOSE OXIDASE INHIBITOR.
Dactylium dendroides (Cladobotryum dendroides).
Eukaryota; Fungi; Ascomycota; Hypocreales; Hypomyces.
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30-MAY-2000 (Rel. 39, Last annotation update)
10-MAY-2000 (Rel. 39, Last annotation update)
10-POLYCALACTURONSE (PG) (EC 3.2.1.15) (FRAGMENT).
10-Iaprepes abbreviatus (Sugarcane rootstalk borer weevil).
10-MATYOTA: Metazoa; Arthropoda; Trachenata; Haxapoda; Insecta;
10-MATYOTA: Meoptera; Endopterygota; Coleoptera; Polyphaga;
10-Cucujiformia; Curculionidae; Entiminae; Entimini; Diaprepes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 1; Length 7;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
                                         1 1 PYRROLIDONE CARBOXYLIC ACID. 9 AA; 876 MW; D500B87866C5B33D CRC64;
                                                                                                       28.9%; Score 13; DB 1; Length 9; 66.7%; Pred. No. 8.8e+04; Live 1; Mismatches 0; Indels
ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
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                                                                                                                                                                                                                                                                                            7 AA.
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50.0%;
                                                                                                                                           Conservative
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Best Local Similarity
Matches 2; Conserv
                                                                                                         Query Match
Best Local Similarity
Matches 2; Conserv
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1 AGQN 4
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7 GSN 9
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P81179;
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                                       MOD_RES
SEQUENCE
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IGAO_DACDE
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Gaps

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Neuropeptide; Amidation.
MOD_RES 7 7
SEQUENCE 7 AA; 992 MW;
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                                                                                                                                                                                                                                                              TISSUE-LIVER;
                                                                                                                                                                                                                                                                                        Cowthorne M.;
                                                                                                                                RESULT 11
GFRP_MOUSE
ID GFRP_MOUSE
AC P99025;
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P36960;
                                                                                   1 YL 2
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NON_TER
SEQUENCE
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SEQUENCE.
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Cowden C., Stretton A.O.W.;
"AFZ, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present in the Rhabditida).";
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoldea; Ascaridoldae; Ascaris.
                                                                                                                                                               Stangier J., Dircksen H., Keller R.; "Identification of proctolin in
                                                                                                                                                                                 pericardial organs of the shore crab, Carcinus maenas.";
Peptides 7:67-72(1986).
-!- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN THE CRAB PERICARDIAL ORGANS.
                  "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OF
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0
                                                                                                 "Identification of proctolin in the central nervous system of horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                            MEDLINE; 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                              24.4%; Score 11; DB 1; Length 5; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
                                                                                                                                                                                                                                                                  5 AA; 649 MW; 71B7673B44600000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
                                                                                                                                                                                                                                                                                                               0; Mismatches
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         Shea M., Adams M.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Panagrellus redivivus.
                                                    SPECIES=L. POLYPHEMUS;
                                                                                                                                                                                                                                      PIR; A01644; HOROHA.
PIR; A60411; A60411.
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                                                                                                                                                                                                                                                                                                   Local Similarity
nes 2; Conserv
MEDLINE; 81225865.
                                                                                                                                              SPECIES=C.MAENAS;
MEDLINE; 86232789.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 95060998
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SPECIES=A.SUUM;
                                                                                        Shabanowitz J
                                                                                                                                                                                                                                                          Neuropeptide.
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P31890;
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2 YL 3
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                                            SEQUENCE.
                                                                                                                                       SEQUENCE
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FAR2_ASCSU
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Matches
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a Carnobacterium sp.";
Appl. Environ. Microbiol. 58:1417-1422(1992).
-!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
ACTIVE ON GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (AUG-1998) to the SWISS-PROT data bank.
-!- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE (BY SIMILARITY).
-!- SUBUNIT: HOWODIMER (BY SIMILARITY).
SWISS-2DPAGE; P99025; MOUSE.
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Purification and characterization of a new bacteriocin isolated from
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92321768.
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GTP_CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN (P35) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X., Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                               Indels
                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 7;
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AMIDATION.
69D4073B5B11E350 CRC64;
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                                                                                             Score 11; DB 1; L
Pred. No. 8.8e+04;
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Pred. No. 8.8e+04;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
LANTIBIOTIC CARNOCIN UI49 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                 7 AA.
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                                                                                          24.4%; Score 11; DB
llarity 100.0%; Pred. No. 8.8
Conservative 0; Mismatches
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100.0%; Pre
                      992 MW;
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                        Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
                 7 AA;
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Gaps

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ASVATOCIN.
Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
                                                                                                                                                                                                                                                                                                                                                                                     Clypeaster japonicus (Sand dollar).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
Clypeasteridae; Clypeaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.4%; Score 11; DB 1; Length 9; 50.0%; Pred. No. 8.8e+04; Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                           Length
 8 AMIDATION.
902 MW; 736365AB59CAADD8 CRC64;
                                                        Score 11; DB 1; 1
Pred. No. 8.8e+04;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                           (Rel. 17, Last sequence update)
                                                                                                                                                                                                                 9 AA.
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                                                         24.4%;
66.7%;
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Best Local Similarity 50.vv,
                                                                                    Conservative
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                                           Query Match
Best Local Similarity
2; Conserve
 8 AA;
                                                                                                                                                                                                                                                                                         [PHE-6]-MOSACT
                                                                                                                                                                                                                                                           01-FEB-1991
01-FEB-1991
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6 FLIG 9
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P42996;
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MOSF_CLYJA
ID MOSF_CLYJA
                                                                                                                 4 GAN 6
                                                                                                                                          1 GAD 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YLSG
 MOD_RES
SEQUENCE
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                                                                                                                                                                                                                                P19853;
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OXYA_SCYCA
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"Isolation and structure of the bacterial sex pheromone, CADI, that induces plasmid transfer in Streptococcus faecalis.";

PEBS Lett. 178:97-100(1984).

-I- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMOLYSIN PLASMID PADI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holman G.M., Cook B.J., Nachman R.J.; Isolation, primary structure and synthesis of leucokinins VII and YII: the final members of this new family of cephalomyotropic peptides isolated from head extracts of Leucophaea maderae."; Comp. Biochem. Physiol. 88(:31-34(1987). runcTion: THIS CEPHALOMYOTROPIC PEPTIDE STIMULATES CONTRACTILE ACTIVITY OF COCKROACH PROTODEUM (HINDGUT).
                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
SEX PHEROMONE CAD1.
Entercoccus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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01-FEB-1991 (Rel. 17, Last annotation update)
LEUCOKININ VIII (L-VIII).
LEUCOPHAGA maderae (Madeira cockroach).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Orthopteroidea: Dictyoptera; Blattaria;
                                                                     24.4%; Score 11; DB 1; Length 7; 50.0%; Pred. No. 8.8e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24.4%; Score 11; DB 1; Length 8; 66.7%; Pred. No. 8.8e+04; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     047DD732C735B9C7 CRC64;
                             741776D05B05B810 CRC64;
                                                                                                                                                                                                                                8 AA.
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                                                                                                                                                                                                                               PRT;
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                          7 AA; 786 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                   Conservative
Antibiotic; Lantibiotic.
NON_TER 7 7 7
SEQUENCE 7 AA; 786 MW
                                                                                                                                                                                                                                STANDARD;
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Neuropeptide; Amidation.
                                                                     Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 85051889.
                                                                                                                                                                                                                                                                                                                                                Enterococcus
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1 GSEI 4
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P19990;
                                                                                                                                                                                                                                CAD1_ENTFA
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14 LCK8_LEUMA

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2; Indels Length 9;

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-!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PERTOSE-PHOSPHATE PATHWAY.
-!- CATALYTICA CATIVITY: SEDOHEPTULOSE 7-PHOSPHATE + D-GLYCERALDEHYDE 3-PHOSPHATE = D-ERYTHHOSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
-!- PATHWAY: NONOXYDATIVE PART OF THE PERMOSE-PHOSPHATE PATHWAY.
-!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
PIR; A1147; A1147; A1147;
-- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.
-- PROSITE; PS00958: TRANSALDOLASE_2; PARTIAL.
-- PROSITE; PS00954: TRANSALDOLASE_1; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                             325A31A44EB1E058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 11; DB 1;
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                24.48;
40.08;
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ilarity 66.7%;
Conservative
                                                                                                                                                                                                                                                                              Transferase; Pentose shunt.

NON_TER 1 1

NON_TER 9 9
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Best Local Similarity
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Best Local Similarity
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NON_TER
NON_TER
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2 GIHCN 6
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P54714;
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ID UXA4_CHLTR
AC P38005;
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TPIS_CANFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chauvet J., Michel G., Ouedraogo Y., Chou J., Chait B.T., Acher R.,
"A new neurohypophysial peptide, seritocin ([Ser5,Ile8]-oxytocin),
identified in a dryness-resistant African toad, Bufo regularis.";
Int. J. Pept. Protein Res. 45:482-487(1995).
-!- FUNCTION: DEVOID OF OXYTOCIC ACTIVITY.
INTERPO, IPRO00991;
-... SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
MEDLINE; 75145197.
Tsolas O., Sun S.C.;
Tsolation of a peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase.";
Arch. Biochem. Biophys. 167:525-533(1975).
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01-AUG-1990 (Rel. 15, Last sequence update)
01-PEB-1994 (Rel. 28, Last annotation update)
11-FEB-1991 (Rel. 28, Last annotation update)
TRANSALDOLASE III (EC 2.2.1.2) (FRAGMENT)
Pichia jadinii (Yeast) (Candida utilis).
Eukaryota; Fungi; Ascomycota; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bufo regularis (African toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
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                                                                                                                                                            Query Match

24.4%; Score 11; DB 1; Length 9;
Best Local Similarity 14.3%; Pred. No. 8.8e+04;
Matches 1; Conservative 3; Mismatches 3; Indels
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                                                      9 AMIDATION.
982 MW; 17EDD76EB444404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 9 AMIDATION.
9 AA; 983 MW; 17FF476EA5A6D04B CRC64;
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              OXYT_BUFRE STANDARD; PRT; 9 AA. P42955; 01-NOV-1995 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
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Matches 2; Conservative
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                            96
Amidation.
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9
9 AA;
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2 YIQSCPI 8
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MOD_RES
SEQUENCE
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P17441;
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                                                      MOD_RES
SEQUENCE
                         DISULFID
  Hormone;
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TAL3_PICJA
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Dunn M.J., Corbett J.M., Wheeler C.H.;
HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
Electrophoresis 18:2755-2802(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACETONE PHOSPHATE.
-!- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC-2DPAGE; P54714; DOG.
INTERERO: IPR000652;
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
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0
                                       01-077-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
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Pred. No. 8.8e+04;
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PRT;
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TISSUE-OVARY;
MEDLINE; 94211930.
BYLEMBED D., BOLOVSKY D., Hunt D.F., Shabanowitz J., Grauwels L., de Loof A.;
"Sequencing and characterization of trypsin modulating oostatic factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.";
FURCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carcinus maenas (Common shore crab) (Green crab).
Usukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.2%; Score 10; DB 1; Length 7; llarity 50.0%; Pred. No. 8.8e+04; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                22.2%; Score 10; DB 1; Length 6; 100.0%; Pred. No. 8.8e+04; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               6 AA; 695 MW; 61E72451B7642000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                             EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Matches 2; Conservative
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                                                                    SEQUENCE, AND SYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2; Conserv
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P81806;
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P81805;
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                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEOUENCE.
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                                                                                                                                                                                                                                                                                                                                 Hormone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 23
ALL2_CARMA
                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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-- PUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                       Pallini V.;
Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
NON_TER 5
                                                                                                                                 STRAIN-L2/434/BU;
STRAIN-L2/434/BU;
Binl L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
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01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
TRYPSIN-MODULATING OOSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.2%; Score 10; DB 1; Length 6; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                            22.2%; Score 10; DB 1; Length 5; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                         6 6 AMIDATION.
6 AA; 621 MW; 72C9C6876DD81000 CRC64;
                                                                                    Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE II (MIP II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA.
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                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: TO MIP I. PIR; B27696; B27696.
Hormone; Amidation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-PEDAL GANGLION;
                                                                       Chlamydia trachomatis.
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 88240357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIP2_MYTED
P13737;
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SEQUENCE
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TMOF_SARBU
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Gaps
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A., Frigerio J.-M., Plomion C.; "Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Electrophoresis 20:1098-1108(1999).
-1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 6.6, ITS MW IS: 25 KDA.
                                                                                                                                                                                                                                                                                                                                                              0
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0
                                                                                                                                                                                                  allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734 (1997).
-1: FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1: SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                         Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                          Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N141) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                  Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                         Thorpe A.; "Isolation and identification of multiple neuropeptides \mbox{\sc "Isolation}
                                                                                                                                                                                                                                                                                      7 AA; 781 MW; 672879CDCB476420 CRC64;
                                                                                                                                                                                                                                                                                                                   Score 10; DB 1; Ler
Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA; 823 MW; 69D76724486B5740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Le
. 8.8e+04;
                                                                                                                              TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
 30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) CARCINUSTATIN 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
                                                                                                                                                                                                                                                          Neuropeptide; Amidation; Multigene family.

MOD_RES
7 7 AMIDATION.
SEQUENCE 7 AA; 781 MW; 672879CDCB476420
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Pred. No.
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                               22.2%;
50.0%;
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                             MEDLINE; 98121193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-NEEDLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UN06_PINPS
P81675;
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SEQUENCE
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AL12_CARMA
ID AL12_CA
AC P81815;
DT 30-MAY:
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0
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                                                                                                                                                                                                              allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-! FUNCTION: MAY ACT AS A NEGROTRANSMITTER OR NEUROMODULATOR.
-! SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
                                                                                                                                                      MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                      Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae, Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
                                                                                                                                                                                                                                                                                                                            Score 10; DB 1; Length 7; Pred. No. 8.8e+04; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10; DB 1; Length 7; Pred. No. 8.8e+04; 0; Mismatches 2; Indels
                                                                                                                                          TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eubrachyura; Portunoidea; Portunidae; Carcinus.
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA.
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                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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50.0%;
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50.0%;
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Best Local Similarity 50.0.
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Matches 2; Conservative
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                                          CARCINUSTATIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARCINUSTATIN 4.
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P81808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALL4_CARMA
                                                                                                                                                                                      Thorpe A.;
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ID ALLS_C
AC P81808
DT 30-MAY
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Gaps
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                                         Cydia pomonella (Codling moth).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cydia pomonella (Codling moth).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
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P81809; P81810; P81804;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 7 [CONTAINS: CARCINUSTATIN 1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.; "Lepidopteran peptides the allatostatin superfamily."; Peptides 18:1301-1309(1997), Peptides I8:1311-1309(1997), Peptides TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                      Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.;
"Lepidopteran peptides the allatostatin superfamily.";
Peptides 18:130-1309(1997).
-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                              2; Indels
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                                                                                                                                                                                                                                                                                                    Length 8;
                                                                                                                                                                                                                                             8 8 AMIDATION.
8 AA; 934 MW; C82879C45B51F775 CRC64;
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8 AA; 936 MW; 0B2879C45B573767 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 6.
30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
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MOD_RES 8 8
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Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
                                                                                                                                            MEDLINE; 98054539.
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MEDLINE; 98054539.
                                                                                                                              IISSUE=LARVA;
                             CYDIASTATIN 1
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P82157;
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SEQUENCE
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ALL7_CARMA
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                                                                                                                                                                                   "Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                              allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEDROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
SEQUENCE 8 AA; 913 MW; 672879CDCB569AB7 CRC64;
                                                                                                                          TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                       Carcinus maenas (Common shore crab) (Green crab).
Sukaryota: Metazoa; Arthropoda; Crustacea; Malacostraca;
Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                               Indels
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8 AA, 858 MW; C82879D5AB46D865 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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MOD_RES 8 AMIDATION (PO'SEQUENCE 8 AA; 858 MW; C82879D5AB46D86
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P82152;
30-MAY-2000 (Rel. 39, Created)
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50.0%;
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Best Local Similarity
'-has 2; Conserve
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                             CARCINUSTATIN 12.
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P81820;
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SG 2
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ALL1_CYDPO
ID ALL1_C
AC P82152
DT 30-MAY
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                       Carcinus maenas (Common shore crab) (Green crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleccyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.2%; Score 10; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide; Amidation; Multigene family.

MOD_RES 8 AMIDATION.

SEQUENCE 8 AA; 781 MW; 7C2879CDCB476878 CRC64;
                                                                                                                                                                                                                                 TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
                                                                      CARCINUSTATIN 9.
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P81886;
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NON_TER
SEQUENCE
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B44K_PORGI
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-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

Neuropeptide; Amidation; Multipene family.

MOD_RES 8 AMIDATION.

SEQUENCE 8 AA; 795 MW; 922879CTDCTA176877 CTDC.
                                                                                                                                                                                                                          "Isolation and identification of multiple neuropeptides of the allatostatin superfamily in the shore crab Carcinus maenas."; Eur. J. Blochem. 250:727-734(1997).
- !- FUNCTION: MAY ACT AS A NEUROFRANSMITTER OR NEUROMODULATOR.
- I- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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                                                                                                              TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorpe A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
(CARCINUSTATIN 8.
Carcinus maenas (Common shore crab).
                                                                    Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                         Neuropeptide; Amidation; Multigene family.
CHAIN 1 8 CARCINUSTATIN 7.
8 CARCINUSTATIN 6.
CHAIN 4 8 CARCINUSTATIN 1.
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Best Local Similarity
"..heq 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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P81812;
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SEQUENCE
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MEDILINE; 20198497.
Norris J.M., Love D.N.;
"Serum antibody responses of cats to soluble whole cell antigens of felline porphyromonas gingivalis.";
Vet. Microbiol. 73:37-49(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8;
                                                                                     Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; CFB group; Bacteroidaceae; Porphyromonas.
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Pred. No. 8.8e+04;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
44 KDA IMMUNGENIC PROTEIN (FRAGMENT).
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100.0%; Pred. No. ...
0; Mismatches
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| hypothetical prote proctolin - Americ copper resistance proctolin - Atlant spinal cord peptid 27.5 kda structura | 27.5K structural p 27.5K structural p 28.5K structural p 28K structural pro | lipopeptide WS1279 hypothetical prote Ig heavy chain CRD cytotoxic T-lympho | unidentified 5.0/1 microcin C7 - Esch ribosomal protein | 180K excantigen - T-cell receptor be | leucokinin VIII - | acetylcholinestera penalbumin - Adeli Ig heavy chain CRD | major postsynaptic aspartate kinase (blood cell protein calsequestrin, car | dissimilatory suit cell surface adhes transaldolase (EC | neuropeptide Grb-A neuropeptide Grb-A [Phe-6]-mosact · s | crel protein - ch macrophage cytotox T-cell receptor be | i-cell receptor be hemoglobin alpha c T-cell receptor be | y chain C receptor | T-cell receptor be T-cell receptor be | rondanar renan- | | | vomitoria) | 3 #text_change 17-Mar-1999 | Orchard, I.; Rehfeld, | | A.G.; Orchard, I.; Rehfeld, J.F.; Tho | -Phe-Met-Arg-Phe-NH-2 neuropeptides (d | | | | #status experimental | ; Length 8; | +05; 0; Indels 0; Gaps 0; |
|--|--|--|---|--|--|--|---|---|--|---|--|---|--|---|------------------------|--|-----------------|----------------------------|--|--------------------|--|--|---|--------------------|--|---|---|------------------------------|
| 30 11 24.4 4 2 S43014 31 11 24.4 5 1 HOROHA 32 11 24.4 5 2 A41225 33 11 24.4 5 2 A60411 34 11 24.4 5 2 C23751 35 11 24.4 5 2 C33751 | 11 24.4 5 2 11 24.4 5 2 11 24.4 5 2 11 24.4 5 2 | 11 24.4 6 2 1 1 24.4 6 2 1 1 24.4 6 2 1 1 24.4 6 2 2 1 1 24.4 6 2 2 1 1 24.4 6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 11 24.4 7 2 11 24.4 7 2 | 11 24.4 7 2 11 24.4 7 2 | 11 24.4 8 2 | 11 24.4 8 2 1 24.4 8 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 11 24.4 11 24.4 8 8 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 11 24.4 9 2 11 24.4 9 2 11 24.4 9 2 11 24.4 9 2 11 24.4 | 11 24.4 9 2 1 1 24.4 9 2 2 1 1 24.4 9 2 2 1 1 24.4 9 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | 11 24.4 99 2 11 24.4 99 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | 11 24.4 9 4 10 22.2 3 2 | 10 22.2 4 2 10 22.2 4 2 | 10 22.2 4 2 10 22.2 4 2 10 22.2 4 2 10 22.3 4 2 2 10 22.3 4 2 2 10 10 10 10 10 10 10 10 10 10 10 10 10 | 4 + 4 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - | ALIGNMENTS | RESULT 1 | hora | -Sep-199 | Scott, | 30, 19 | ty of | A; Accession: H41978 | Afordus: preliminary Afordus: type: protein A posiduse 1-0 Anny | eptid | (Phe) | 35.6%; | Pred. No. 0; Mismatch | |
| 4.5 Compugen Ltd. | Search time 89.11 Seconds (without alignments) 6.409 Million cell updates/sec | | | W | ers: 793 | | | | | cted by chance to have a sorted, the result being printed, | | 1 | CalliFMFamide 8 | cytochrome oxidase isotocin - common | | Seminal plasma pro T-cell receptor be T-cell receptor be | vicin 72K chain | serine/threonine·s | variant surface gl phosphatidylethano | neuropeptide Grb-A | MHC Class I nistoc glucan 1,3-beta-gl | Ig mu chain V regi | nypochetical plote gene c-rel protein thumic factor - ni | thymocyte growth p | photosystem II pro Ig heavy chain CRD | H4 histone - Afric galactose oxidase | unidentified 6.5/3 capsid protein VP- caldesmon - rabbit | |
| GenCore version 4 Copyright (c) 1993 - 2000 CO | Run on: December 16, 2000, 03:35:12; | Title: US-09-529-121-4 Perfect score: 45 Sequence: 1 YLSGANINL 9 | Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 | Searched: 182106 seqs, 63460219 residues | Total number of hits satisfying chosen parameter | Minimum DB seq length: 0 Maximum DB seq length: 9 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries | IR_65: pir1 | 3: pirs:* 4: pirs:* | Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being ping is a derived by applyeds of the total score distribution | SUMMARIES | Result Query Towarth DE IT | 1 16 35.6 8 2 1 18 35.6 8 2 | 15 33.3 8 2 15 33.3 9 2 | 15 33.3 9 15 33.3 9 | 14 31.1 5 2 14 31.1 6 2 14 31 1 6 2 | 14 31.1 7 2 | 14 31.1 7 2 | 14 31.1 8 2 14 31.1 8 2 | 14 31.1 9 2 | 14 31.1 9 | 13 28.9 4 2 13 28.9 7 2 | 13 28.9 7 2 13 28.9 7 2 | 13 28.9 9 2 | 13 28.9 9 2 C | 12 26.7 6 2 12 26.7 7 1 | 2/ 12 26./ 8 2 P00/01 28 12 26.7 8 2 PL0184 29 12 26.7 9 2 A44873 | |

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Gaps

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Length 9;

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C;Accession: PT0288
R;Yamada, M; Wasserman, R; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity an A;Reference number: PT0222; MUID:91108337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell receptor gamma chain (2t.23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Date: 041946
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Species: Homo sapiens (man)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
A;Molecule type: protein
A;Residues: 1-9 <ACH>
C;Superfamily: oxytocin-neurophysin
C;Superfamily: oxytocin-neurophysin
C;Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F;9/Modified site: amidated carboxyl end (Gly) #status experimental
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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Pred. No. 1.8e+05;
1; Mismatches 3,
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Pred. No. 1.8e+05;
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ilarity 42.9%;
Conservative
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75.0%;
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A,Residues: 1-9 <WHE>
C,Keywords: T-cell receptor
                                                                                                                                                                                                        Best_Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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A:Molecule type: DNA
A:Residues: 1-9 <YAM>
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C;Accession: E60588
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related peotus nudus, Echinometra mathael and Heterocentrotus mammillatus.
A;Reference number: A60527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13818
R;Delarbre, C:; Barriel, V; Tillier, S:; Janvier, P:; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the NDI and the COI A;Title: The main features of the craniate mitochondrial DNA between the NDI and the COI A;Accession: T13818
A;Accession: T13818
A;Accession: T18818
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-8 < DEL>
A;Cross-references: EMBL:Y09527; NID:e1011465; PID:e329906; PIDN:CAA70718.1
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R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A.14, 245-254, 1965
A;Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce A;Reference number: A61364
A;Accession: A61364
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C;Date: 09-Sep_1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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0
                                                                                                                                                                              urchin (Pseudoboletia maculata)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 16; DB 2; Length 8; Pred. No. 1.8e+05; 0; Mismatches 2; Indels
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                                                                                                                                                                      sperm-activating peptide a - sea ur
                                                                                                                                                                                                                             C; Species: Pseudoboletia maculata
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60.0%;
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Best Local Similarity 60.0
Matches 3; Conservative
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A,Note: COI
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E60588
A; Molecule type: protein
A; Residues: 1-8 <YOS>
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Matches 3; Conserv
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Length 9; 1; Indels ô

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TreelI receptor beta chain V-D-J region (121-1BK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Musculus (house mouse)
C;Decession: PT0654
R;Feeney, A.J.
C;Decession: PT0654
R;Feeney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Reference number: PT0659; MUID:91277601
A;Title: Junctional sequences of A;Reference number: PT0659
R;Status: translation not shown
A;Molecule type: mRNA
A;Retaus: translation not shown
A;Molecule type: mRNA
A;Retaus: translation not shown
A;Retaus: translation not shown
C;Retaus: translation not shown
A;Retaus: translation not 
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                                                                                                                                                                                                 Vicilin 72K chain - pigeon pea (fragment)
C;Species: Cajanus cajan (pigeon pea)
C;Species: Cajanus cajan (pigeon pea)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: A34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A;Title: Unusual denaturation properties of vicilin from Cajanus cajan.
A;Reference number: A34818
A;Reference number: A34818
A;Ccession: A34818
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Pred. No. 1.8e+05;
2; Mismatches 1;
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40.0%;
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Matches 3; Conservative
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Best Local Similarity
Matches 2; Conserv
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vicilin 72K chain
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2 SGA 4
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C;Accession: S62883
R;Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.
FEBS Lett. 382, 15-17, 1996
A;Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal plas A;Reference number: S62882; MUID:96196555
A;Accession: S62883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-D-J region (159-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: Pr0593
R;Peeney, A.J.
J; Exp. Med: 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: Pr0599; MuID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Exp. Med. 174, 115-124, 1991
A;Title: Juncitional sequences of fetal T cell receptor beta chains have few N regions.
*Reference number: PT0509; MUID:91277601
A;Accession: PT0609.
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                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-5 <MON>
C;Complex: heterodimer; seminal plasma protein I and seminal plasma protein
C;Keywords: glycoprotein; heterodimer; semen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T-cell receptor beta chain V-D-J region (120-1L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PT0605
R:Feeney, A.J.
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A;Molecule type: mRNA
A;Residues: 1-6 <FED>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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100.0%;
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A;Molecule type: mRNA
A;Residues: 1-6 <FEES
A;Experimental source: newborn t
C;Keywords: T-cell receptor
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Best Local Similarity
Matches 3; Conserv
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Matches 3; Conserv
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Matches 3; Conserv
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| ARIN 4
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2 SGA 4
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glucan 1,3-beta-glucosidase (EC 3.2.1.58) GNIII, extracellular - fungus (Acremonium pon N.Alternate names: (1-3)-beta-D-glucan glucohydrolase GNIII
C.Specias: Acremonium persicinum
C.Specias: Acremonium on Golucias: Acremonium (1-3)-beta-D-gluca
A.Reference number: S56002; MUID:97104268
                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chicken)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Feb-1995
C;Accession: J00914
B;Kanki, T.; Kuwasawa, N.; Sekiya, Y.; Ichikawa, Y.
submitted to JIPID, May 1991
A;Description: Responsive expression of a MHC class I epitope and genes following Mar A;Reference number: J00914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
S43959
If mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959
R;Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
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Pred. No. 1.8e+05;
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                                                                                                               Length 9;
                                                                                                             31.1%; Score 14; DB 2; Lv 100.0%; Pred. No. 1.8e+05; iive 0; Mismatches 0;
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A;Residues: 1-9 <KAN>
A;Experimental source: kidney, strain cornell N
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A; Molecule type: protein
A; Residues: 19 < PTTS
C; Keywords: 91yoosidase; hydrolase
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                           3; Conservative
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-9 <LOR>
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les 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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3 TGSN 6
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5 LSG 7
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| ANI 9
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Best Local Si
Matches 3;
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C;Species: Mus musculus (house mouse)
C;Date: 29-oct-1997 #sequence_revision 29-oct-1997 #text_change 23-Jan-1998
C;Date: 29-oct-1997 #sequence_revision 29-oct-1997 #text_change 23-Jan-1998
C;Accession: PN0043
R;Kato, H
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neurch
A;Accession: PN0041
A;Accession: PN0043
A;Molecule type: protein
A;Residues: 1-8 <AKAT>
A;Experimental source: neuroblastoma cell
C;Commont: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked
C;Keywords: brain
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C; Species: Gryllus bimaculatus (two-spotted cricket)
C; Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C; Accession: C5744
R; Lofenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A; Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A; Reference number: A57444; MuID:95403341
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Score 14; DB 2; Length 7;
Pred. No. 1.8e+05;
1; Mismatches 1; Indels
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Pred. No. 1.8e+05;
2; Mismatches 2; Indels
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7. 1.8e+05;
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Query Match 31.1%;
Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 33.3%;
Matches 2; Conservative
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1 MSGKEV 6
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3 GGNL 6
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5 LSG 7
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thymic factor - pig

N.Alternate names: FTS (facteur thymique serique)
C.Speciess. Sus scrofa domestic pig)
C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-way-1999
C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-way-1999
C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-way-1999
R.Pleau, J.M.; Daddenne, M.: Blouquit, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A.7Title: Structural study of circulating thymic factor: a peptide isolated from pig starcession: A01523
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: Dradenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A.7Title: Biochemical characterisation of a serum thymic factor.
A.Reference number: A60983; MUID:77123829
A.Accession: A60983
A.Molecule type: protein
A.Residues: 2', 2-4', 2', 6-9 < CAMC>
C.Comment: This peptide induces DNA synthesis in immature thymocytes, but not periphe in a variety of immunossays.
C.Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modif C.Superfamily: thymic factor
C.Superfamily: thymic factor
C.Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thymocyte growth peptide - sheep
N;Contains: FTS (facteur thymique serique)
N;Contains: FTS (facteur thymique serique)
N;Contains: FTS (facteur thymique serique)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Accession: A60957
R;Ernstroem, U; Cafvelin, G;Rudja, J.M.
B;Osci. Rep. 10, 403-412, 1990
A;Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationsh
A;Reference number: A60957; MUD:91064427
A;Reference number: A60957; MUD:91064427
A;Residues: 1-9 <ERN>
C;Comment: This peptide induces DNA synthesis in immature thymocytes, but not periphe
C;Comment: This peptide was isolated in two forms. One form contained the pyrrolldone
in a variety of immunoassays.
C;Comment: This peptide was isolated in two forms. One form contained the pyrrolldone
C;Comment: This peptide anion end; pyrroglutamic acid
C;Superfamily: thymic factor
C;Reywords: blocked amino end; pyrroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental
F;1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide)
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C;Species: Chlamydomonas reinhardtii
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Matches 2; Conserv
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7 GSN 9
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7 GSN 9
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C.Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C.Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C.Date: 140504
R.Waye, M.M.; Winter, G.
Eur. J. Blochem. 158, 505-510, 1986
A:Title: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA synt A:Reference number: 140503; MUID:86274732
A:Accession: 140504
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-7 <RES>
A:Cross-references: EMBL:X04193; NID:940233; PIDN:CAA27782.1; PID:9580943
A,Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice. A;Reference number: $43956; MUID:94248036
A,Accession: $43959
A,Molecule type: DNA
A,Residues: 1-4 <WAG>
C;Keywords: immunoglobulin
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
C;Accession: I50210
R;Kabrun, N.; Bumstead, N.; Hayman, M.J.; Enrietto, P.J.
MOI. Cell. Biol. 10, 4788-4794, 1990
A;Title: Characterization of a novel promoter insertion in the c-rel locus.
A;Reference number: I50210; MUID:90355995
A;Accession: I50210
A;Status: preliminary: translated from GB/EMBL/DDBJ
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Pred. No. 1.8e+05;
1; Mismatches 1; Indels
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
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A;Cross-references: GB:M55577; NID:g555438; PID:g211661
C;Genetics:
A;Gene: c.rel
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66.7%;
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
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1 YCAG 4
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2 ANV 4
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A; Accession: A01341
A; Moteoule type: protein
A; Moteoule type: protein
A; Mesidues: 1-7 < AVIX
C; Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose o apoenzyme, may inactivate the enzyme by binding to its prosthetic copper group.
C; Superfamily: galactose oxidase inhibitor
C; Keywords: copper
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C; Species: murine poliovirus, Theiler's encephalomyelitis virus
C; Species: murine poliovirus, Theiler's encephalomyelitis virus
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C; Accession: PLO184
R; Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.
J. Exp. Med. 170, 2037-2049, 1989
A; Title: Alteration of amino acid 101 within capsid protein VP-1 changes the pathogen A; Reference number: PLO184; MUID:90063468
A; Molecule type: genomic RNA
A; Molecule type: genomic RNA
A; Residues: 1-8 < ZUR>
C; Keywords: capsid protein
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unidentified 6.5/31K protein [imported] - rice (fragment)
c;Species: Oryza sativa (rice)
c;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
c;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
c;Accession: Pg0701
Theor. Appl. Genet. 86, 935-942, 1993
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimens
A;Reference number: PQ0696
A;Accession: PQ0701
                                                          galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
C;Species: Cladobotryum dendroides
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
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Pred. No. 1.8e+05;
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Pred. No. 1.8e+05;
0; Mismatches 3; Indels
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Pred. No. 1.8e+05;
1; Mismatches 1;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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                                                                                                                                     C; Accession: A01341
R; Avigad, G.; Markus, Z.
Fed. Proc. 31, 447, 1972
A; Reference number: A01341
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A; Molecule type: protein
A; Residues: 1-8 <KOM>
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1 AGQN 4
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5 VTGA 8
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C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 30-Sep-1993
C;Accession: C41170
C;Accession: C41170
J. Biol. Chem. 266, 16614-16621, 1991
A;Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91358452
A;Accession: C41170
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-9 <DES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C: Species: Homo sapiens (man)
C: Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
R: Yamada, M: Wasserman, R: Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J: Exp. Med. 173, 395-407, 1991
A: Reference number: Pr0222; MUID: 91108337
A: Reference number: Pr0222; MUID: 91108337
A: Residues: 1-9 < VAMA
A: Residues: 1-9 < VAMA
A: Residues: 1-9 < VAMA
A: Residues: heterotetramer; immunoglobulin
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C; Species: Xenopus laevis (African clawed frog)
C; Date: 13-Sep-1996 #text_change 13-Sep-1996
C; Accession: 151434
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; Woodland, H.R.; Warmington, J.R.; Ballantine, J.E.M.; Turner, P.C.
R; McCession: 151391; WUID:84247348
R; McCession: 151434
R; Wolecule type: mRRN
A; McLecule type: mRRN
A; Wollecule type: mRNN
A; Residues: 1-6 < WOOD>
A; Cross-references: GB:K02304; NID:9214227; PID:9555517
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Pred. No. 1.8e+05;
2; Mismatches 0; Indels
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Pred. No. 1.8e+05;
0; Mismatches 2;
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50.0%;
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Similarity 60.0%;
3; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity 66.7
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1 MSG 3
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C; Species: Limulus polyphemus (Atlantic horseshoe crab)
C; Species: Limulus polyphemus (Atlantic horseshoe crab)
C; Accession: A60411
R; Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt Peptides 11, 205-211, 1990
A; Title: Identification of proctolin in the central nervous system of the horseshoe c A; Reference number: A60411; MUID:90287800
R;O'Shea, M.; Adams, M.E.
Science 213, 567-569, 1981
A;Title: Pentapeptide (proctolin) associated with an identified neuron.
A;Title: Pentapeptide (proctolin) associated with an identified neuron.
A;Reference number: A94260; MUID:81225865
A;Contents: annotation; biological source
C;Comment: This peptide is found in the lateral white neurons, which occur (in the co innervate the striated hindgut muscles in insects and stimulate contraction of these C;Superfamily: proctolin
C;Superfamily: proctolin
C;Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 1-5 cGROD.
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the ho
C;Keywords: neuropeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)
C;Species: Pseudomonas syringae pv. tomato
C;Date: 19-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: A41225
R;Cha, J.S.; Cooksey, D.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 8915-8919, 1991
A;Title: Copper resistance in Pseudomonas syringae mediated by periplasmic and outer A;Reference number: A41225; MUID:92020961
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100.0%; Pred. No. 1.8e+05;
iive 0; Mismatches 0;
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Pred. No. 1.8e+05;
1; Mismatches 0
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66.78;
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Best Local Similarity 1
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A;Molecule type: protein
A;Residues: 1-5 <CHA>
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Best Local Similarity
Matches 2; Conserve
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Matches 2; Conserv
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2 YL 3
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A;Residues: 1-5 <STA>
A;Note: the synthetic peptide had the same chromatographic, electrophoretic, and pharmad
                                                                                                                                                                                           C. Accession: A44873
R. Ikebe, M.; Hornick, T.
R. Reference number: A44873; MUID:91378498
R. Reference number: A44873
R. A A4873
R. A A4873
R. Residues: preliminary
R. Residues: 1-9 < IKE>
R. Reperimental source: skeletal myosin
R. Note: sequence extracted from NCBI backbone (NCBIP:63199)
C. Superfamily: caldesmon
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Life Sci. 17, 1253-1256, 1975
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in insects A;Reference number: A93048; MUID:76074708
A;Accession: A01644
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C;Species: Periplaneta americana (American cockroach)
C;Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 23-Aug-1996
C;Accession: A01644
                                                                                                                                                    C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
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Pred. No. 1.8e+05;
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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16.7%;
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llarity 66.7%;
Conservative
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Best Local Similarity 16.7
Matches 1; Conservative
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Best Local Similarity
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1 GSSLKI 6
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spinal cord peptide SCP-6 - pig
C.Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993
C;Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993
C;Accession: C23751
A;Hsi, K.L.; Chen, R.L.; Chen, Z.G.; Zhang, H.L.; Lu, Y.A.; Guo, S.Y.; Wu, S.X.; Tsou, Arch. Biochem. Biophys. 240, 178-183, 1985
A;Reference number: A23751; MUID:85250425
A;Accession: C23751
A;Status: preliminary
A;Nolecule type: protein
A;Residues: 1-5 <HSI>
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27.5 kda structural protein - Leuconostoc oenos phage P32
C.5pecies: Leuconostoc oenos phage P32
C.5pate: 31-Mar-1993 #sequence_revision 22-May-1998 #text_change 22-May-1998
C.Accession: G44817
R.Arendt, E.K.; Lonvaud, A.; Hammes, W.P.
J. Gen. Microbiol. 137, 2135-2139, 1991
A;Title: Lysogeny in Leuconostoc oenos.
A;Reference number: A44817; MUID:92085033
A;Accession: G44817
A;Molecule type: protein
A;Residues: 1-5 <ARE>
A;Note: sequence extracted from NCBI backbone (NCBIP:70333)
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24.4%; Score 11; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels
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24.4%; Score 11; DB 2; Length 5;
Best Local Similarity 40.0%; Pred. No. 1.8e+05;
Matches 2; Conservative 1; Mismatches 2; Indels
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| 4.5 Compugen Ltd. ; Search time 107.12 Seconds (without alignments) 2.873 Million cell updates/sec eters: 61695 eters: 61695 eters: 61695 eters: 61695 eneseqp/Aal980.DAT:* eneseqp/Aal981.DAT:* eneseqp/Aal981.DAT:* eneseqp/Aal980.DAT:* eneseqp/Aal980.DAT:* eneseqp/Aal980.DAT:* eneseqp/Aal980.DAT:* eneseqp/Aal980.DAT:* geneseqp/Aal991.DAT:* geneseqp/Aal991.DAT:* geneseqp/Aal990.DAT:* | results predicted by chance to have a . to the score of the result being printed, of the total score distribution. | S Description | Carcinoembryonic a Human carcina-embr CEA synthetic pept CEA derived HLA-A2 Immunogenic peptid Carcinoembryonic a Carcinoembryonic a HLA binding peptid Carcinoembryonic a Peptide comprising Carcinoembryonic a NCA analogue of re |
| Copyright (c) 1993 - 2000 Compugen Ltd. protein search, using sw model December 16, 2000, 03:07:18; search time 107.12 US-09-529-121-4 1 YLSGANINL 9 Seq. 1913 Million cell u. US-09-529-121-4 1 YLSGANINL 9 Hardenseq. 34193795 residues of hits satisfying chosen parameters: 61695 q length: 0 x ZiDSG/gcgdata/geneseq/geneseqp/AA1980.DAT:* 2: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 3: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 5: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 6: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 7: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 8: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 11: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 8: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 11: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 12: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 13: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 14: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 15: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 16: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 17: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 18: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 11: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 12: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 13: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 14: /SIDSG/gcgdata/geneseq/geneseqp/AA1981.DAT:* 15: /SIDSG/gcgdata/geneseq/geneseqg/geneseqp/AA1981.DAT:* 16: /SIDSG/gcgdata/geneseq/geneseqg/geneseqp/AA1981.DAT:* 17: /SIDSG/gcgdata/geneseq/geneseqg/geneseqgp/AA1981.DAT:* 18: /SIDSG/gcgdata/geneseq/geneseqg/geneseqgp/AA1981.DAT:* 18: /SIDSG/gcgdata/geneseq/geneseqg/geneseqgp/AA1981.DAT:* 18: /SIDSG/gcgdata/geneseq/geneseqg/gene | No. is the number of results pre greater than or equal to the soc derived by analysis of the tota | SUMMARIES Query e Match Length DB ID | 100.0 10 |
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Van Der Burg SH;

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immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W33 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method of selecting T cell peptide epitope(s) - by measuring the stability of HLA class I-peptide complexes on intact B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.6%; Score 43; DB 18; Length 9; 88.9%; Pred. No. 2.1e+05; ive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Toes REM,
                                                                                                                                                                                                                                                                                                                    SCI SEED CAPITAL INVESTMENTS BV.
                                                                                                                                                                                                                                                                                                                                                                              Kast WM, Melief CJM, Offringa R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Page 85; 109pp; English.
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                                                                                                                              97WO-NL00229
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                              28-APR-1997;
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26-APR-1996;
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cytotoxic T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or antigonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancratic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA expressing cells).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist; minumune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 9;
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                                                                                       Carcinoembryonic antigen peptide agonist SEQ ID NO:4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; Page 53; 72pp; English.
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Matches 9; Conservative
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molecules with antigen presenting cells (APCs) pretreated with antigen presenting cells (APCs) pretreated with antigen presenting cells (APCs) pretreated with purified CD8 cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, ALDS, hepatitis, bacterial infection, fungal infection, malaria or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide having a human leukocyte antigen binding motif #2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytocoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
              of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC)
     leukocyte antigen (HLA), HLA-A2.1 and are used to exemplify the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 19;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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88.9%;
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Best Local Similarity
The B; Conserve
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                                                                                                                                                                                                                                                                                                     tuberculosis.
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                                                                                                                                                                                        depleted mutants of a native disease-specific CTL epitope. The cysteine-depleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                       The peptide epitope W77119-W77138 were created for human tumour-specific cytotoxic T lymphocyte response. These peptides are are cysteine-
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immuno disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                     Disease specific immunogen - comprises disease specific cytotoxic lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                  Score 43; DB 19; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
 Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tsai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwood S,
 Kittlesen D,
                                                                                                                        Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 75; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                  95.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-US01959.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
 Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-437445/37.
                                  WPI; 1998-437388/37.
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             presenting cells
                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YLSGANINL
Engelhard VH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                   epitope
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Southwood

Grey HM,

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Gaps

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Length 9; 0; Indels

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Query Match
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response against the antigen from which the peptide is derived.
Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are
Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are
cormally induced by an antigen in the form of a peptide fragment bound
to a HLA molecule, rather than the intact foreign antigen fiself, and
are particularly important in tunnour rejection and in fighting viral
infections. The peptides are therefore useful therapeutically to treat
or prevent viral infections and cancers in mammals (especially humans)
e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
They can be administered as vaccines to elicit an immune response in
individuals susceptible or otherwise at risk of viral infection or
cancer, or used to treat chronic or acute conditions. They are also
useful diagnostically, and can be used to induce a cytotoxic T cell
response, by contacting a cytotoxic T cell with the peptide e.g. to
produce CTLS ex vivo for infusion back into a patient. The
                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                   Score 43; DB 20; Length 9; Pred. No. 2.1e+05;
                                                                                                                                                                                                                   therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carcinoembryonic antigen peptide agonist CAP-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                               A.
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                                                                                                                                                                                                                                                                               95.6%;
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-326544/27
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                           9 AA;
                                                                                                                                                                                                                                                                                                                                   1 YLSGANINL 9
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
Synthetic.
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immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                      Score 43; DB 20; Length 9;
Pred. No. 2.1e+05;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carcinoembryonic antigen peptide agonist SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y09527 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                      95.6%;
88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
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DB 20; Length

88.9%; Score 40;

9 AA;

Sequence

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Carcinoembryonic antigen; CEA; human; agonist; antagonist; fimune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                    Carcinoembryonic antigen peptide agonist SEQ ID NO:2.
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                                                                                                                                                              Y09526 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US19794.
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                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aliele-specific binding motif for the major histocompatibility complex (MHC) molecule HLA, e.g. HLA-A2.1. The peptides have conserved residues at certain positions such as positions 2 and 9. Also, the peptides do not comprise negative binding residues at other positions, such as positions (2.1, 3, 6 and/or 7 (peptides 9 amino acids long) and at polsons 1, 3, 4, 5, 7, 8 and/or 9 (peptides 9 amino acids long). The peptides are used to comprises contacting cytotoxic T cells from a patient (optionally expressing a specific MHC class I allele) with the present peptides. The peptides are used to treat and prevent microbial infection (e.g. in the peptides are used to treat and prevent microbial infection, AIDS, cytomegalovirus (CMV), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cuminatum) and cancer (e.g. prostate cancer, renal carcinoma, carcinoma, 1ymphoma). Patients in the acute phase of infection can be treated with the peptides in conjunction with other treatments. The antigenic opeptides may be used to elicit cytotoxic T lymphocytes (CTLS) ex vivo and in the context of the result of the result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or bacterial) or tumours in patients that do not respond to conventional forms of therapy. The peptides may also be used to produce monoclonal antibodies, which are useful as potential diagnostic or therapeutic agents. The peptides may also be used as diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                       Allele-specific binding motif; major histocompatibility complex; MHC; HLA; HLA-A2.1; cytotoxic T cell response; antiqen; microbial infection; hepatitis; ALDS; malaria; condyloma acuminatum; cancer; prostate cancer; renal carcinoma; cervical carcinoma; lymphoma; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel HLA binding immunogenic peptides used to induce \mathtt{T} cell activation and to induce an immune response
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides Y54171-Y54236 represent immunogenic peptides comprising an
                      ;
                                                                                                                                                                                                                                                                                                                    HLA binding peptide 1233.11 derived from source CEA.605V9.
                        Indels
Pred. No. 2.1e+05;
1; Mismatches 0;
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                                                                                                                                                                                               Y54173 standard; peptide; 9 AA.
  88.88;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-106018/09.
                                                        1 YLSGANINL 9
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Zaremba S;

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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, pladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune ceaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and malive CEA esponse. Cytotoxic T cells generated recognize both (Ia) and malive CEA epipopes. The present
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                                                                                                                                                                                                                                                                                                                                                                                                  sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
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77.88;
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Best Local Similarity 77.00.,
7; Conservative
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Gaps

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88.9%; Score 40; DB 21; Length 9; 77.8%; Pred. No. 2.1e+05; Live 2; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 7; Conserv

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Zaremba

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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, particularly for treating gastrointestinal, breast, particularly for treating of prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 53; 72pp; English.
                                                                                                                                                                                                        98WO-US19794
                                                                                                                                                                                                                                                       97US-0061589
                                                                                                                                                                                                                                                                                                                                                          Barzaga E, Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-326544/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YLSGANINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||||| :||
1 ylsgaclnl
                            sapiens.
                                                                                                   WO9919478-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9626271-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-FEB-1995;
                                                                                                                                                                                                        22-SEP-1998;
                                                                                                                                                                                                                                                       10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1996.
                                                                                                                                                       22-APR-1999
                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W00690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells (CTC), comprises introducing a lst pox virus vector, having at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC the present peptide) to a host to stimulate CTC production, and at least 1 periodic interval after that, contacting the host with an additional antigen. The CEA specific CTC can be used to determine the CTC eliciting epitope of CEA, and to screen for compounds which enhance the ability of the antigen to create a CTC response. A host with a CEA expressing tumour can be treated by introducing the CTC to the host, and at least 1 periodic interval after that introducing a CEA peptide, i.e. the present peptide.

The present peptide is positive for binding to HiA-A2, and scored spropriate peptide results in the upregulation of surface HIA-A2 on the T2 cells, which can be quantified via FACScan using an enti-HIA-A2 antibody (background 280 and 300).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation of human cytotoxic T-cells specific for CEA - useful in therapy, epitope mapping and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing carcinoembryonic antigen (CEA) specific human cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                      Peptide comprising residues 571-579 of Carcinoembryonic antigen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
                                                                                                                       Carcinoembryonic; antigen; human; cytotoxic T cell; pox virus; vector; epitope; determination; screening; tumour; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinoembryonic antigen; CEA; human; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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Pred. No. 2.1e+05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (THER-) THERION BIOLOGICS CORP.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tsang KY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 57; 76pp; English.
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                                                                                                                                                                                                                                                                                                                                                        96WO-US02156.
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87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                       95US-0396385
                       (first entry)
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Best Local Similarity 87.5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-402364/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1||||:||
2 lsganln1 9
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                                                                                                                                                                                                                                                     WO9626271-A1.
                                                                                                                                                                                                                                                                                                                                                   13-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                       22-FEB-1995;
                       01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Panicali D,
                                                                                                                                                                                                                                                                                                      29-AUG-1996
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D X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X D X 
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                                                Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                               NCA analogue of residues 571-579 of carcinoembryonic antigen.
Score 34; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Carcinoembryonic; antigen; epitope; NCA; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (THER-) THERION BIOLOGICS CORP. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                             W00690 standard; peptide; 9 AA.
75.68;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95US-0396385
                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (first entry)
                    Best Local Similarity 77.8
Matches 7; Conservative
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Gaps .; 0

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This sequence represents a V8 proteinase digestion product of an isolated pure enzyme which is capable of catalysing the conversion of DNA to CO-DNA. CO-DNA is a form of DNA in which a carbonyl group is attached to the 1' carbon of the sugar constituent of the DNA. The enzyme can be used to convert DNA to CO-DNA which reduces or eliminates the ability of a cell to divide. The enzyme can be used for inhibiting cell proliferation and for treating tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation; tumour; lysilendopeptidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fragment of enzyme capable of catalysing conversion of DNA to CO-DNA.
did not compromise the structural integrity and folding stability of the progenitor domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, especially novel binding or catalytic properties, and which may be of use in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and evolution of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to reduce or inhibiting cell
                                                                                                                                                                                        Score 23; DB 19; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 18;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New enzyme which converts DNA to CO-DNA - used eliminate the ability of a cell to divide, for proliferation and treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal fragment; V8 proteinase digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tokimatsu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 3; Page 17; 35pp; English
                                                                                                                                                                                                                                                                                                                                                                 W19861 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.9%;
                                                                                                                                                                                        51.1%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-IB01323
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                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                         4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kagawa H, Kagawa K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (KAGA/) KAGAWA K.
(TOKI/) TOKIMATSU H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-319767/29.
                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus domesticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (KAGA/) KAGAWA H.
                                                                                                                                          9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA;
                                                                                                                                                                                                                                                      2 LSGANIN 8
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1 lsggrvn 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JUN-1997
                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CO-DNA;
                                                                                                                                                                                                                                                                                                                                                                                                W19861;
                                                                                                                                                                                                                                                                                                                                  RESULT 14
W19861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are
                                                                                                                                                                                                                                                                                                                    Gaps
                                                              Generation of human cytotoxic T-cells specific for CEA - useful in therapy, epitope mapping and drug screening
                                                                                                                                       The present peptide is negative for binding to HLA-A2, and scored 252 and 225 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HLA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HLA-A2 antibody (background 280 and 300).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vectors used to produce PH domain-like peptide libraries - which screened for therapeutically useful peptide(s), e.g. to produce
                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pleckstrin homology domain; PH domain; peptide library; functional molecular surface; protein structural template; vaccine; gene therapy; cytohesin 1; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cytohesin-1 PH domain randomised AB loop (clone 7).
                                                                                                                                                                                                                                                                                    Score 27; DB 17; Length 9;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                           Example 2; Page 60; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                            W54298 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                  60.0%;
55.6%;
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                                                                                                                                                                                                                                                                                                                   Conservative
    Schlom J,
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                                WPI; 1996-402364/40.
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruhn H, Funk M,
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    Panicali
                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines
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Gaps

Mantyla E;

Mandal A,

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New transgenic plants with increase trehalose contents - prepd. by transforming plants with a trehalose-6-phosphate synthase gene fused to a non-constitutive promoter
                                                                                                                             C, Londesborough J,
Tunnela O, Welin B;
                                                               95WO-FI00377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
   Mycobacterium smegmatis.
                                                                                                        (ALKO-) ALKO GROUP LTD.
                                                                                                                                                           WPI; 1996-077499/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxin protein; ant.
                                                                                                                                                                                                                                                                                                                                                                                                         trehalose content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference
                      WO9600789-A1.
                                                               29-JUN-1995;
                                                                                   29-JUN-1994;
                                          11-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || ||
| ylega
                                                                                                                            Holmstrom F
Palva ET,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YLSGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R29031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R29031
  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tryptic peptide; trehalose-6-phosphate synthase; M. smegmatis; probe; trehalose; transgenic plant; heparin-activated; preservation; food; antigenic determinant; yeast; TSP1; fruit; berry; puree; jelly; jam.
                                                                                                                                                                                                                                                                                                                                                                                                  The alpha-subunit (a-SU), contg. al least one of the polypeptides given in R09404-417, can bind to ICAM-1 (or other natural ligands) on the surface of cells, and can associate with the beta-SU to form a heterodimer (also able to bind to ICAM-1). a-SU, and its derivs., are useful in suppressing inflammation, metastasis and growth of a-SU expressing tumour cells and is used in the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                         Lymphocyte function associated antigen; inflammation; metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                        Pure alpha subunit of lymphocyte function associated antigen and encoding DNA sequences, useful eg for suppressing inflammation or metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%; Score 21; DB 11; Length 6; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Internal tryptic peptide from Tre6P synthase (peak 29) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                   LFA-1 alpha subunit polypeptide (k).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of viral infections.
The pref. dose is 1 pg - 10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 19; 27pp; English.
                                                                      R09414 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R88476 standard; peptide; 6 AA.
                                                                                                                                                                                                                                           88US-0235227.
89US-0321017.
                                                                                                                                                                                                                       89EP-0115160
                                                                                                                                                                                                                                                                          (DANA-) DANA FARBER CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1996 (first entry)
                                                                                                               23-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                Larson R;
                                                                                                                                                                                                                                                                                                                   WPI; 1990-108985/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 AA;
LSGANIN 8
                  3 idganvh 9
                                                                                                                                                                                                                                                                                               Springer TA,
                                                                                                                                                                                                                      17-AUG-1989;
                                                                                                                                                                                                                                                      09-MAR-1989;
                                                                                                                                                                                                                                            23-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111
2 ylsg 5
                                                                                                                                                                                                 11-APR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YLSG 4
                                                                                                                                                                           EP362526-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                           R09414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R88476;
                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 16
                                                                                                      q
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The sequences given in R88473-80 are internal tryptic peptides derived from trehalose-6-phosphate (Tre6P) synthase from M. samegmatis. Tre6P is the key enzyme in the synthase from M. samegmatis. Tre6P is the key enzyme in the synthesis of trehalose via Tre6P. The aim of the invention is to produce a transgenic plant with increase trehalose content. Tre6P in M. samegmatis is were derived from a protein which was purified. These peptides were derived from a protein which was purified with a mol. Wt. of 55 kD which shared antigenic determinants with the yeast Tre6P synthase protein. Using these peptides probes may be designed for the isolation of the Tre6P gene (TSP1) for the production of the transgenic plants. The trehalose may be isolated from the transgenic plants and used in bulk preparation including the preservation of the flavour and structure of food stuffs during drying. Fruits and berries form the transformed of any bear was the process of the form the transformed of the form the fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     form the transformed plants may be processed into purses, jellies and jams which have a fresher and richer flavour due to the increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide encoded by ant-active toxin gene probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'label= Arg or Lys
Example 6; Page 36; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Trp or Tyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46.7%;
80.0%;
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Gaps

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The nucleotide sequence which encodes R78208, a B. thuringlensis (B.t.) endotoxin derived peptide, specifies the degenerate probe og Parobe can be used for the detection of endotoxin producing B.t. microbes. The probe aids in the search for useful microbes hosting toxin encoding genes, specifically from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; pS3; c-ERB2; MAGE-1; melanoma antigen-1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer; allontthm prediction; MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1; LCMV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only peptides with binding affinity of at least 1%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antigen fragment 124, from LCMV has binding affinity for HLA-2.1.
                 Nucleotide sequence used as probes to identify Bacillus thuringiensis - are derived from the B.thuringiensis endotoxin genes, for identifying microbes which encode toxins
                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                                                       Score 21; DB 16; Length 8; Pred. No. 2.1e+05; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sidney J;
                                                                                   Claim 1; Columns 41-42; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 84; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R73808 standard; peptide; 9 AA.
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93US-0073205.
93US-0159184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grey HM, Kast WM, Sette A,
                                                                                                                                                                                                                                                                                         46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-US02353
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                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-302678/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         autoimmune diseases.
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CYTE-) CYTEL CORP.
                                                                                                                                                                                                         nematode species.
                                                                                                                                                                                                                                       8 AA;
                                                                                                                                                                                                                                                                                                                                                           1 YLSGAN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
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                                                                                                                                                                                                                                                                                                                                                                            :::|||
3 wingan
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                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              R73808
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0
                                                                                                                                                                                                                                                                                                                                                                            - for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The peptide (or point mutation variants as shown in the features) is encoded by nucleotide probes used in the rapid identification of Bacillus thuringlensis ant-active toxin genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endotoxin; probes; microbes; peptide; detection; nematode.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; ... Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                         Uick HJ;
                                                                                                                                                                                                                                                                                                                                                                           Toxin proteins isolated from Bacillus thuringiensis – i
amts. e.g. fire, carpenter, argentine and pharaoh ants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schnepf HE, Schwab GE,
                                                                                                                                                                                                                                                                                         Randall JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B. thuringiensis endotoxin derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 56; 71pp; English.
                 /label= Ala or Asn
                                                   /label≖ Asn or Gln
                                                                                                                                                                                                                                                                                       Kennedy MK, Meier H, Payne JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R78208 standard; Peptide; 8 AA
                                                                                                                                                                                    91US-0703977.
91US-0797645.
92EP-0304228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.7%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0427068
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                                                                                                                                                    92WO-US04316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Narva KE,
                                                                                                                                                                                                                                                                                                                                         N-PSDB; Q31414, Q31415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                                                                         (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-245777/32.
                                                                                                                                                                                                                                                                                                                         WPI; 1992-415780/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 3; Conserv
Misc-difference 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 AA;
                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :::|||
3 wingan 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YLSGAN 6
                                                                                                                                                                                    22-MAY-1991;
25-NOV-1991;
12-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaertner FH,
Thompson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1992;
                                                                                                                                                    22-MAY-1992;
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26-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US5430137-A.
                                                                                   WO9220802-A
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                                                                                                                   26-NOV-1992
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Sequence

Query Match

ò g R78208;

18

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This peptide is an example of a peptide which binds to a human leucocyte antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence VG553, by screening with an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune disease, or especially for treatment of viral diseases.
                                                                                                                                                                                                                                                                                                     {\tt HLA-binding} oligopeptide and an immuno:regulator contg it - used in the treatment of auto:immune disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibacterial; antiparasitic; cytostatic; pyrrolobenzodiazepine;
DNA minor groove; combinatorial peptide library screening; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pyrrolobenzodiazepine-peptide #6 from combinatorial library screen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "conjugated to pyrrolobenzodiazepine group"
                                                                                 Human leucocyte antigen; HLA-DQ4; combinatorial library; autoimmune disease; chronic articular rheumatism.
                                                    Human leucocyte antigen DQ4 binding peptide #231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 31; 61pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y83831 standard; peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.78;
80.08;
                                                                                                                                                                                                   94JP-0292657.
                                                                                                                                                                                                                            94JP-0292657.
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                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                              WPI; 1996-329479/33
                                                                                                                                                                                                                                                     (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                Human leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200012506-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                               JP08151396-A.
                              05-JUN-1998
                                                                                                                                                                                                 28-NOV-1994;
                                                                                                                                                                                                                          28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 GANIN 8
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                                                                                                                                                                         11-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ganis
                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytotoxic.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
      W49340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y83831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This peptide is an example of a peptide which binds to a human leucocyte antigen HLA-DD4 molecule. The peptide was isolated from a phagemid combinatorial library comprising the sequence V05953, by screening with an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune disease, or especially for treatment of viral diseases.
(binding affinity is expressed as an ICSO value) as compared to the standard peptide (R71293) in assays. This peptide from LCMV (sic) Np antigen has a binding value of 0.0280. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg.
                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-binding oligopeptide and an immuno:regulator contg it - used the treatment of auto:immune disease
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                                                                                                                                DB 15; Length 9;
                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 21; DB 17; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                            Human leucocyte antigen; HLA-DQ4; combinatorial library; autoimmune disease; chronic articular rheumatism.
                                                                                                                              Score 21; DB 15; L
Pred. No. 2.1e+05;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                   Human leucocyte antigen DQ4 binding peptide #230.
                                                                 prostate cancer or lymphoma, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 31; 61pp; Japanese.
                                                                                                                                                                                                                                                                         W49339 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W49340 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46.7%;
80.0%;
                                                                                                                              Query Match
Best Local Similarity 50.0%;
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94JP-0292657
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                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1996-329479/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEIJ ) TEIJIN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 4; Conserv
                                                                                         9 AA;
                                                                                                                                                                                                          6
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                                                                                                                                                                                  2 LSGANINL 9
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2 isgynfsl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 GANIN 8
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                                                                                                                                                                                                                                                                                                                         05-JUN-1998
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1 ganis
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                   W49339;
                                                                                                                                                                                                                                                 RESULT 20
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W49340
ID W49
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Gaps

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Length 9; Indels

Score 21; DB 17; Pred. No. 2.1e+05; Mismatches

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arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally syno-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy represent expression reference protein isoform peptides, Y42101 to Y42103 represent expression reference protein isoform peptides and 225066 to 225068 represent degenerate probes for RPIS, which are all used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     given in Y54378. Hellomycin is a polycysteine peptide with antifungal and antibacterial activity, isolated from the lepidopteron Heliothis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polycysteine peptides, designated heliomycin, with antifungal antibacterial activity, useful in medicine or plant protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y54379-82 represent fragments of the generic heliomycin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heliomycin; polycysteine peptide; antifungal; antibacterfal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a fragment of a heliomycin peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20; DB 20; Length 7; Pred. No. 2.1e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fungal infection; plant protection; animal protection;
transgenic plant; fungi; bacteria; Cercospora beticola;
Cladosporium herbarum; Fusarium culmorum; F. oxysporum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RHON ) RHONE-POULENC AGROCHIMIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 37; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y54382 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98FR-0004933,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98FR-0004933.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phytophthora cinnamoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heliothis virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-108532/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||:|:
sgadis 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FR2777568-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Y54382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                   The invention relates to novel pyrrolobenzodiazepine (PBD) derivatives which are compounds that bind to the minor groove of double stranded nucleic acid sequences, especially at the sequence Purine-Guanine-Purine where Purine is selected from adenine and guanine. The PBD's can be used in combinatorial peptide library screening for binding interactions with nucleic acids. The PBD's can be used in cytotoxic, antibiotic, antiparastitic and antiviral compositions and also in methods of diagnosis and in methods of target validation in functional genomics. The peptides Y83826-Y83833 represent PBD-peptides isolated from combinatorial peptides library screen on the target nucleic acid sequence 299178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                              New pyrrolobenzodlazepine derivatives used in the preparation of combinatorial libraries of further pyrrolobenzodiazepine derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A method has been developed for the diagnosis of human rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.4%; Score 20; DB 21; L
100.0%; Pred. No. 2.1e+05;
iive 0; Mismatches 0;
                            (UYPO-) UNIV PORTSMOUTH HIGHER EDUCATION CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of human rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Townsend RR;
                                                                                                                                                                                                                                                               Example 8; Page 72; 158pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; Page 150; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y41846 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98GB-0005477.
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                                                                             Howard PW;
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                                                                                                                     WPI; 2000-237841/20.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA;
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                                                                          Thurston DE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-MAR-1999;
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gani 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis
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Sequence
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                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R69970-993 are nonameric mimotopes designed to show high diversity in hydrophobic moment and hydrophobic index, as well as charge distribution and size. The mimotopes are used in the method of the invention to obtain antibodies specifically and strongly reactive with a desired analyte. 16 of the peptides were tested for ability to bind the murine antibody Mab33-6, arbitrarily chosen, and known to bind to the peptides MB4. 3 of the 16 peptides successfully bound Mab33-6. The mimotope is obtd. by reacting a panel of starting antibodies (Abs) representative of the resting B cell repertoire of a mammmal with an analyte (so as to identify analyte-reacting Abs) and
virescens. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in humans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungi and bacteria (specifically Cercospora beticola, Cladosporium herbarum, Fusarium culmorum, F. oxysporum and Phytophthora cinnamoni), and for recombinant
                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                         Nonameric mimotope 24 used to obtain highly specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing antibodies with high specificity and affinity for an analyte - by immunisation with selected mimotope, also analyte detection kits, useful for immunoassay of materials usually
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0
                                                                                                                                                                                                                                                                                                                                                mimotope; antibody; production; high specificity; detection; immunoassay; high performance liquid chromatography.
                                                                                                                                     Length 7;
                                                                                                                                                          1; Indels
                                                                                                                                   Score 20; DB 21;
Pred. No. 2.1e+05;
1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TERR-) TERRAPIN TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Arg-NH2"
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                                                                                                                                                                                                                                                          R69993 standard; peptide; 9 AA.
                                                                                                                                     44.48;
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93US-0072190.
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                                                                            production of the peptides.
                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                           4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-105497/14.
                                                                                                                                   Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                    7 AA;
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                                                                                                                                                                               3 SGANIN 8
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2 sfanvn 7
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04-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kauvar LM;
                                                                                                                                                                                                                                                                                                                                                 mimotope;
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                     Sequence
                                                                                                                                                                                                                                                                                R69993;
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This is a randomised AB loop encoded by clone 8 (see V26502) of a large peptide library (2 million clones) of synthetic Pleckstrin homology (PH) domains with randomised discontinuous surface epitopes. The progenitor AB sequence comprises amino acid residues (16-21 of a stabilised synthetic PH domain (see W54310) of human (2 cytohesin 1. The peptide library was generated by randomisation of AB and CD loop regions using randomised obligonoutlectide primers (see W26493-94). The randomised AB and CD loop regions of 9 clones (see W54292-309) of the peptide library are provided. Randomisation the progenitor domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, especially novel binding or catallytic properties, and which may be of use in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and evolution of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                                   Gaps
then reacting each of a panel of candidate mimotopes representative of a random set of 3D contours with the analyte-reacting Abs. A subject is immunised with one or more mimotopes identified and the product Abs are recovered from the serum of the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vectors used to produce PH domain-like peptide libraries - which screened for therapeutically useful peptide(s), e.g. to produce
                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pleckstrin homology domain; PH domain; peptide library; functional molecular surface; protein structural template; vaccine; gene therapy; cytohesin 1; human.
                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cytohesin-1 PH domain randomised AB loop (clone 8).
                                                                                                                                                                                                                                                                              DB 16; L 2.1e+05;
                                                                                                                                                                                                                                                                              44.4%; Score 20; DB 100.0%; Pred. No. 2.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 5; Fig 12; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W54299 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Henkel T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-EP02840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96EP-0108776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MEDI-) MEDIGENE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-230215/20.
                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruhn H, Funk M,
                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; V26502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-MAY-1996;
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5 sgan 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09745538-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-1997.
                                                                                                                                                                                                                                                                                                                                                                                                          3 SGAN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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9 AA;

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The specification describes vaccines which comprise immunologically effective amounts of T cell receptor (TCR) peptides. The TCRs are present on the surface of T cells. The TCRs are chosen from W beta 6.73, V beta 6.74, V beta
                                                                                   Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6; multiple sclerosis.
                                                    V beta 6 clone found in MS patients after vaccination with TCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TO cell receptor peptide-derived vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 11; Page 85; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                               (IMMU-) IMMUNE RESPONSE CORP. (KIMM-) KIMMEL CANCER CENT SIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                        Gold DP,
                                                                                                                                                                                                                                                                                         97WO-US23147.
                                                                                                                                                                                                                                                                                                                             97WO-US23147.
                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 50.0*
Lona 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Carlo DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-404801/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LSGANI 7
                                                                                                                                                                                                                                                                                                                                                                                                                      Brostoff SW,
                                                                                                                                                                                                                 W09927957-A1
                                                                                                                                                                                                                                                                                       03-DEC-1997;
                                                                                                                                                                                                                                                                                                                             03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| |:
1 lagtn1 (
                 02-SEP-1999
                                                                                                                                                                                                                                                     10-JUN-1999
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                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
R75676
δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-isoforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation - by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                          R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                  Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20; DB 19; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shaw N, Tinschert A;
                                                                  Indels
                              Score 20; DB 19; L
Pred. No. 2.1e+05;
2; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                          K. oxytoca R-specific amidohydrolase peptide T5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10.2; Page 29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robins K,
                                                                                                                                                                                                                              W40267 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Y23411 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.48;
                                44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97WO-EP03670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97CH-0000500
96CH-0001723
                                                                                                                                                                                                                                                                                                    16-JUN-1998 (first entry)
           Ouery Match
Best Local Similarity 42...
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-101063/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGANIN 8
                                                                                                    2 LSGANIN 8
                                                                                                                                      1 Laggkvn 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LONZ ) LONZA
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| ytvgamln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmermann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-MAR-1997;
10-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9801568-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brieden W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                  W40267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y23411;
                                                                                                                                                                                            RESULT 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y23411
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Wilson DB;

Smith LR,

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptokinase; plasmin B; affinity chromatography; purification;
                                                    ö
    Length 6;
42.2%; Score 19; DB 20; Length 6; 50.0%; Pred. No. 2.1e+05; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Streptokinase-binding plasmin B chain peptide.
                                                                                                                                                                                                                                                                R75676 standard; peptide; 7 AA.
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Virus (REHV) DNA polymerase specific antigen. Primers used in the amplification of polymerase specific antigen. Primers used in the amplification of polymerase specific antigen. Primers used in the especially in the diagnosis of herpes viral infection. Herpes virus DNA polymerases of this invention, may be used in vaccines for the protection against infection by a herpes virus of the RFHV/KSHV family. They may also be used in the design and screening of anti-viral drugs. Antibodies raised against the polymerase or fragments of it, may be used in the detection of herpes virus infection and for drug targetting for the therapy of herpes virus infection and for drug targetting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in R35090-100 and R34628-32 are peptides which were used to design the probes given in Q40219-34. These probes can be used to identify Bacillus thuringiansis (BH) DNA which encodes insecticidally active endotoxin. Probe (a) identifies genes encoding a toxin effective against any sort of insect. Sequences (b) and (e)-(l) are specific for toxins against lepidopters, sequences (c), (m) and (n) for toxins active against diptera and sequence (d), (o) and (p) for toxins active against coleoptera.
                                                           The present sequence represents a retroperitoneal fibromatosis herpes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probe; Bacillus thuringiensis; Bt; insecticidal; active; endotoxin; lepidoptera; diptera; coleoptera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene probe for identifying endotoxin sequences in Bacillus thuringiensis - are universal, type specific or gene specific, for rapid detection and characterisation of insecticidal activity
  used in the detection and treatment of herpes virus infection
                                                                                                                                                                                                                                                                          Score 19; DB 18; Length 7;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels

    B. thuringiensis dipteran toxin probe (m) design peptide.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sick AJ;
                               Claim 15; Page 45; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                   R34629 standard; Protein; 8 AA.
                                                                                                                                                                                                                                                                           42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89US-0427068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0427068.
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 42.9%,
Cahes 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schwab GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-143952/17
                                                                                                                                                                                                                                7 AA;
                                                                                                                                                                                                                                                                                                                                                 :||| :
1 hlsggtv 7
                                                                                                                                                                                                                                                                                                                                  1 YLSGANI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaertner FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5204237-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R34629;
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                       R34629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                           R75669-R75678 and R75682 are streptokinase binding peptides derived from the human plasmin B chain in the regions 576-600, 620-640 or 640-655 amino acids. The peptides are also capable of binding other proteins useful particularly when immobilised on a solid support for use in affinity chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes virus DNA polymerase and corresponding nucleotide sequence -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retroperitoneal fibromatosis herpes virus; detection; infection; Kaposi's sarcoma herpes virus; viral DNA; viral RNA; vaccine;
                                                                                                                                                                                                                                                      New peptide sequences from plasmin B chain - able to bind other proteins esp. streptokinase, useful for affinity purifcn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 19; DB 16; Lencored. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes virus DNA polymerase RFHV specific antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retroperitoneal fibromatosis herpes virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Todaro GJ;
                                                                                                                                                                     (OXFO-) OXFORD RES SUPPORT CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W12026 standard; peptide; 7 AA.
                                                                                                                                                                                                                                                                                                   Claim 3; Page 6; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strand K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.2%;
                                                                                                                                          93GB-0024473,
                                                                                                              94GB-0024112
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95US-0001148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                               Cederholm-Williams SA;
                                                                                                                                                                                                                            WPI; 1995-196178/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rose TM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-132644/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9704105-A1.
                            Homo sapiens
                                                                                                              29-NOV-1994;
                                                                                                                                          29-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-JUL-1996;
                                                     GB2284422-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:||
nvn1 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-1996;
14-JUL-1995;
                                                                                 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 NINF 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-FEB-1997
isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bosch ML,
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W12026;
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Gaps

; 0

S

R78218;

RESULT 32

g

õ

R78218

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The sequence given is a complementarity determining region (CDR) designated CDR(f). CDR's are found in the variable domains of light and heavy chains which form the antigen binding site, and act as connectors between the four framework regions.

It has been noted that there seem to be no characteristic features which distinguish human from mouse or rat CDR's and they are therefore immunologically identical. The CDR described is used in a ligand with a binding affinity for the human CD3 antigen within the CDR's decribed in R23736 and R23737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-6; antagonist; cytokine; B cell differentiation; inflammation; tissue injury; B9.9 hybridoma cell line; Castleman's Disease; Lennart's T-cell lymphoma; Non-Hodgkin's lymphoma; allergy; immune deficiency disease; cardiac myxoma; mesangial proliferative glomerulonephritis.
                                                                              determining region; heavy chain variable domain;
                                                                                                                                                                                                                                                                                                                                                                                      Ligands and antibodies with binding affinity for CD3 antigen for treatment of immunosuppression e.g. in graft rejection, and cancer, esp. lymphoid malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 19; DB 13; Length y, Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                              Waldmann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 4; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R37221 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.28;
                                                                                                                                                                                                                   91WO-GB01726.
                                                                                                                                                                                                                                                90GB-0021679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IL-6 antagonist peptide #5
                 (first entry)
                                                                                                                                                                                                                                                                                                            Gorman SD, Routledge EG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Conservative
                                                                                                                                                                                                                                                                                                                                        WPI; 1992-150879/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                              (GORM/) GORMAN S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
                                                                           Complementarity antigen binding
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3 yvssfnv 9
                                              Ligand CDR(f)
                                                                                                                                                                                                                   04-OCT-1991;
                                                                                                                                                                                                                                                05-OCT-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-SEP-1993
                                                                                                                                                      WO9206193-A.
                                                                                                                                                                                    16-APR-1992.
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                                                                                                                         Synthetic.
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                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The nucleotide sequences which encode R78218 and R78219, B. thuringiensis (B.t.) endotoxin derived peptides, specify the probe Q94867 and Q94868 respectively. The probes can be used for the detection of endotoxin producing B.t. microbes. The probes aid in the search for useful microbes hosting toxin encoding genes, specifically from dipteran species.
                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence used as probes to identify Bacillus thuringiensis - are derived from the B.thuringiensis endotoxin genes, for identifying microbes which encode toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sick AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 19; DB 16; Length 8;
Pred. No. 2.1e+05;
!; Mismatches 1; Indels
                                           Score 19; DB 14; Length 8; Pred. No. 2.1e+05; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                        Endotoxin; probe; microbes; peptide; detection; dipteran.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schwab GE,

    B. thuringiensis endotoxin derived peptide.

                                                                         1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Columns 49-50; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schnepf HE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R23738
ID R23738 standard; Protein; 9 AA.
                                                                                                                                                                                                              R78218 standard; Peptide; 8 AA.
                                            42.2%;
60.0%;
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60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8902-0427068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89US-0427068
91US-0737569
                                                                                                                                                                                                                                                                         22-FEB-1996 (first entry)
                                         Query Match 42.2
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 42.2
Best Local Similarity 60.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Narva KE,
                                                                                                                                                                                                                                                                                                                                                                      Bacillus thuringiensis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-245777/32.
8 AA;
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26-JUL-1991;
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2 gtnmn (
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 Sequence
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Gaps

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R23738

RESULT 33

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Gaps

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An aglycosylated IgG antibody having a binding affinity for the human CD3 antigen complex comprises at least one CDR selected from the amino acid sequences given in R50105-R50110. The heavy and light chain variable domains of an aglycosylated antibody is given in R41721-R41722. The antibodies are useful as immunosupressants. Unlike glycosylated antibodies, they do not induce T-cell mitogenesis nor do they cause high level release of cytokines.
preventing graft rejection and treating cancer, and does not induce \ensuremath{\mathtt{T}} cell proliferation and cytokine prodn.
                                                                                                                                                                                                               Score 19; DB 14; Length 9; Pred. No. 2.1e+05; 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                               Search completed: December 16, 2000, 03:07:19 Job time: 8060 sec
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                                        Claim 3; Page 25; 41pp; English
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ilarity 42.9%;
Conservative
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Best Local Similarity
' has 3; Conserv?
                                                                                                                                                                           9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDR; complementarity determining region; heavy chain; light chain; variable domain; immunosuppressant; T-cell; mitogenesis; cytokine; graft; rejection; cancer; proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibody; glycosylation; IgG; binding affinity; CD3; antigen;
                                                                                                                                             New peptide interleukin-6 antagonists - for treating and preventing auto-immune, immuno:inflammatory, neoplastic and infectious diseases etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waldmann H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aglycosylated IgG antibody against human CD3 antigen - for
                                                                                                                                                                                                                                                                                                                                                                            Length 9;
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                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 14; L
Pred. No. 2.1e+05;
2; Mismatches 2;
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                                                                                          Scholz W;
                                                                                                                                                                                                   Example 3; Column 27; 20pp; English.
                                                                                          o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gorman SD,
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                                                                                           Nagarajan
                                                                                                                                                                                                                                                                                                                                                                          42.2%;
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            90US-0480868
                                     90US-0480868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                               (TANA ) TANABE SELYAKU CO.
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLARK M R.
GORMAN S D.
ROUTLEDGE E G.
                                                                                          Lobl TJ,
                                                                                                                    WPI; 1993-166970/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WALDMANN H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BOLT/) BOLT S L.
                                                                                                                                                                                                                                                                                                                                    9 AA;
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1 laennlnl
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            16-FEB-1990;
                                     16-FEB-1990;
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                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDR (f).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CLAR/)
(GORM/)
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                                                                                        Chiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R50110;
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09qvt6 rattus sp.
09qvt6 rattus sp.
09upy3 homo saplen
035903 strongyloce
09uzt7 pyrococcus
09vgm7 drosophila
09vgm7 drosophila
09vgm7 drosophila
09vgm8 deinococcus
09syb9 arabidopsis
03ss04 arabidopsis
09s804 arabidopsis
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                                  caenorhabdi
suillus bov
methanobact
                          076577 caenorhabdi
020618 caenorhabdi
099887 suillus bov
027425 methanobact
090405 drosophila
09uex3 homo saplen
09uby1 cryptococcu
031716 bacillus su
94446 alcaligenes
062831 bos taurus
                                                                                        cryptococcu
bacillus su
alcaligenes
                                                                       homo sapien
homo sapien
 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=MALAWI LIL20 /1;
MEDLINE; 94292916
Bixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow C.,
Hammond J.M., Smith G.L.;
Nucleotide sequence of a 55 kbp region from the right end of the
genome of a pathogenic African swine fever virus isolate (Malawi
                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=MALMI LIL20 /1;
MEDLINE; 94014996.
Vydelingum S., Baylis S.A., Bristow C., Smith G.L., Dixon L.K.;
"Duplicated genes within the variable right end of the genome of pathogenic isolate of African swine fever virus.";
J. Gen. Virol. 74:2125-2130(1993).
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                  000487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 352;
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40682 MW; 61561D08AE1C1599 CRC64;
                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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87.5%; Pred. No. 25;
ive 0; Mismatches 1
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                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                      African swine fever virus (ASFV).
Viruses; dSDNA viruses, no RNA stage;
African swine fever-like viruses.
                                            Q9Y887
Q97425
Q9UEX3
Q9UEX3
Q9UW41
Q31716
P94146
P94146
Q62831
Q62831
Q9V3H2
Q35593
Q00487
                                                                                                                                                                                       Q9RW36
Q9SYB9
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09SS04
097884
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Q9VGN0
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Q9UZT7
                                    020618
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EMBL; X71992; CAA50855.1; -.
THYBRPRO; IPROCSS95; -.
PFAM; PFO1671; ASFV_360; 1.
PRODOM; PD003462; -; 1.
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Best Local Similarity 87.5
Matches 7; Conservative
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763
773
1650
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1 YLSGADIN 8
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SEQUENCE
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Q65258;
RESULT
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099521 homo sapien
002314 caenorhabdi
002315 caenorhabdi
019407 caenorhabdi
019730 caenorhabdi
019729 caenorhabdi
047916 fibrobacter
09ulc6 homo sapien
031988 bacillus su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09sa76 arabidopsis
067835 aquifex aeo
09sddl oryza sativ
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58971 pyrococcus
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006708 saccharomyc
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                                                             ; Search time 113.2 Seconds (without alignments) 7.424 Million cell updates/sec
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       4.5
Compugen Ltd.
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         GenCore version
Copyright (c) 1993 - 2000
                                                             December 16, 2000, 02:00:57
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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sp_bacteria:*
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Match Length
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1006
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Sequence:
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Maximum DB
                                            OM protein
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Gaps

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0; Indels

Length 763;

RESULT 058971

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Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
HwCDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
Nature 399:323-3329(1999).
TIGR; TM0757;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
PFAM; PF00725; 3HCDH; 1.
PROMITE: PS00067; 3HCDH; 1.
PROSITE: PS000667; 3HCDH; 1.
PROSITE: PS000166; ENOYL_COA_HYDRATASE; 1.
SEQUENCE 763 AA; 83041 MW; CDFB85DDE3E512E4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 protein.
860 AA; 100968 MW; 7781CCFA62FB89CF CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
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Last annotation update)
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Pred. No. 1.2e+02;
                                                                                                                                                              Score 34; DB 4;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                          860 AA.
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01-MAY-1997 (TIEMBLRE1 03, Created)
01-MAY-1999 (TIEMBLRE1 10, Last seq
01-MAY-2000 (TIEMBLRE1 13, Last ann
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Bacteria; Thermotogales; Thermotoga.
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PFAM; PF00535; Glycos_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL 101.0 KDA PROTEIN.
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Best Local Similarity 55.0
Free 5; Conservative
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STRAIN=MSB8 / DSM 3109;
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98 FIAGADINM 106
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Best Local Similarity
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SEQUENCE FROM N.A.
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443 YLTGGDIN 450
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SEQUENCE 86
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
BDNA Res. 5:55-76(1998).
HSSP; PO0644; ISNQ.
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"Structures of the human cDNA and gene encoding the 78 kDa gastrin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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20010 MW; CB802A467B17E29E CRC64;
                                                                                                                                                        Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
GASTRIN-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          binding protein and of a related pseudogene.";
Biochim. Biophys. Acta 1219:567-575(1994).
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                                                                                               176 AA
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EMBL: U04627; AAA56664.1; -.
HSSP; P14604; 2DUB.
                                                                                                                                01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequen
01-JUN-2000 (TrEMBLrel. 14, Last annote
176AA LONG HYPOTHETICAL THERMONUCLEASE.
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PROSITE; PS01123; TNASE_1; 1.
                                                                                             PRELIMINARY;
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 258 YLLGADIN 265
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| 128 YLNGTDIN 135
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EMBL; Z69383; CAA93405.1; -.
01-JUL-1997 (TrEMBLrel. 01-JAN-1999 (TrEMBLrel.
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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Jones M., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
      Monstein H.J., Nylander A.G., Hakanson R.;
"Widespread tissue expression of gastrin-binding-protein mRNA.";
Eur. J. Biochem. 246:502-507(1997).
Embl. y89225; CA466885.1;
HSSP: P14604; ZDUB.
INTERPRO; IPRO01753;
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                                                                                                                                               Length 171;
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SEQUENCE 401 AA; 45608 MW; E1D3F8AD84C0873D CRC64;
                                                                                                                 171 AA; 18141 MW; 7CC22F2E66B98447 CRC64;
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Last annotation update)
                                                                                                                                              Score 33; DB 4;
Pred. No. 28;
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                                                                     PFAM; PF00378; ECH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
                                                                                                                                                                                                                                                                                        Created)
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55.6%;
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77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                               Query Match
Best Local Similarity
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65 FVAGADINM 73
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Bonfield J., Burton J., Connell M., Copeey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
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Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
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Smaldon N., Smith A., Sonnhammer E., Staden R., Sullston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
P. 2. Mb of contiguous nucleotide sequence from chromosome III of C.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Gardner A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latrellle P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riften L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditidae; Peloderinae; Caenorhabditis.
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   Last sequence update)
Last annotation update)
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Pred. No. 78;
0; Mismatches
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 368:32-38(1994).
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                                                                                                                                                                                                                                                                                                                                                     Submitted (NOV-1996)
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Wilkinson J.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Matches 6; Conserv
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                                                                                                    SEQUENCE FROM N.A. MEDLINE; 94150718.
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334 LSGSDLNL 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YLSGADINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LSGADINL 9
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Q47916;
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Q9ULC6
ID Q9ULC6
AC Q9ULC6
DT 01-MAY
DT 01-MAY
DE PEPTIDI
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Q47916
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Graxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Laireille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Walson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.,
elegans.",
                                                                                                                                                                                                                         Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                        Length 441;
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
INTERPRO; IPR001611; -.
PFAM; PF00560; LRR; 4.
SEQUENCE 441 AA; 50845 MW; 66AC257B7884CCFA CRC64;
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EMBL; Z71262; CAA95817.1; -.
SEGUTENCE 445 AA; 51330 MW; 4380A86BAF05DC6D CRC64;
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Last annotation update)
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Last annotation update)
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87;
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Pred. No. 8
                                                                                                                                                        73.3%; Score 33; 62.5%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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77.88;
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01,
09,
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Matches 5; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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01-NOV-1996 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
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427 YISGEDVN 434
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DT 01-NOV
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"Endoglucanase G from Fibrobacter succinogenes S85 belongs to a class of enzymes characterized by a basic C-terminal domain.";
Can. J. Microbiol. 42:934-943(1996).
EMBL: 013887; AAB38548.1; ---
HSSP: P17901; lebG.
Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J. Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Rershaw J., Kirsten J., Roopra A., Sunders B., O'Callaghan M.,
Parsons J., Percy C., Riften L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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EMBL; Z71262; CAA95816.1; -.
SEQUENCE 454 AA; 52822 MW; FA0134DBF31D0925 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR001547; -.
PFAM; PF00150; cellulase; 1.
SEQUENCE 519 AA; 56848 MW; B06D2113B10FF27E CRC64;
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Bacteria, Fibrobacteria, Fibrobacter.
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PEPTIDYLARGININE DEIMINASE TYPE I (EC 3.5.3.15).
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Pred. No. 90;
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77.8%;
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Best Local Similarity 77.8.
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Created)
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PFAM; PF00664; ABC_membrane; 1
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                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.00,
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Best Local Similarity 75.0
Matches 6; Conservative
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 SEQUENCE FROM N.A.
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                 STRAIN=168;
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RA Acevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borulser S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Codani J.J., Forner C., Ferrari E., Foulger D.,

RA Entian K.D., Errington J., Febret C., Ferrari E., Foulger D.,

RA Fitz C., Fullta M., Fullta Y., Funma S., Galizzi A., Galleron N.,

RA Ghims S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

RA Milseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,

RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,

RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,

RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,

RA Presecan E., Pujic P., Purnelle B., Powollik S., Persortt A.M.,

RA Presecan E., Pujic P., Purnelle B., Ropeport G., Rey M., Reynolds S.,

RA Scanlan E., Schleich S., Schroeter R., Scoffone F.,

Schluchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Scrokin A., Tanaka T., Tarakanshi H., Takemaru K.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Wairi A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,

RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,

Wanters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,

RA Vari A., Voshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

RA Subliles R., Solicher S., Schroeter P., Shin Bacillus

RA Voshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

Ra Subliles R., Solich R., Salane R., Solich B., Rapubliles R., Roshikawa H., Danchin A.;

Ra Subliles R., Solich R., Salane R., Solich R., Solich R.,

Ra Subliles R., Solich R., Solich
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                                                                                                             Ishigami A., Guerrin-Weber M., Sebbag M., Serre G., Senshu T.; "Molecular cloning of peptidylarginine deiminase type I cDNA from human epidermis."; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AB033768; BAA88771.1; -.
               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                73.3%; Score 33; DB 4; Length 663; 66.7%; Pred. No. 1.4e+02; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                 663 AA; 74607 MW; 0BD8D460634EE2D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
SUBLANCIN 168 LANTIBIOTIC TRANSPORTER.
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                                                                                                                                                                                                                                                                                                  6; Conservative
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Best Local Similarity
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||11 YLTGVDISL 119
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MEDLINE; 98044033.
                                                                                 SEQUENCE FROM N.A.
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                                                                                                  TISSUE-EPIDERMIS;
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HPAD-COLONY10.
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Lazarevic V., Duesterhoeft A., Soldo B., Hilbert H., Mauel C.,
Karamata D.;
SIGNATION STATEMENT OF STATEMEN
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EMBL, AF020713; ARC12993.1; -.
INTERPRO; IPR001140; -.
INTERPRO; IRRO1617; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00339; AA TRNA_LIGASE_II_2; UNKNOWN_1.
PROSITE; PS00675; SIGMA54_INTERACT_1; UNKNOWN_1.
SEQUENCE 705 AA; 81563 MW; 0F94D9964AFBBD3A CRC64;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
SUBLANCIN TRANSPORTER PROTEIN.
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Last annotation update)
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OC Bacillus/Staphylococcus group; Bacillus.

RP [1]

RP [1]

RP [2]

RC STRAIN-168;

RA MEDLINE; 9389743.

RA MEDLINE; 9389742.

RA MEDLINE; 9389743.

RA Paik S.H., Chakicherla A., Hansen J.N.;

RT "identification and characterization of the structural and transporter genes for, and the chemical and biological properties of, sublancin 168 a novel lantiblotic produced by Bacillus subtilis 168.";

RL J. Biol. Chem. 273:23134-23142(1998).

BR INTERPRO; IPR00140;

INTERPRO; IPR00140;

INTERPRO; IPR001617;

BR INTERPRO; IPR001617;

INTERPRO; IPR00056;

BR INTERPRO; IPR00664;

BR INTERPRO; IPR00654;

BR INTERPRO; IPR00655;

BR INTERPRO; IPR00654;

BR INTERPRO; IPR00655;

BR I
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Search completed: December 16, 2000, 02:00:57 Job time: 5931 sec

1 YLSGADIN 8 ||:| ||| 543 YLNGLDIN 550

Qy

0;

Gaps

; 0

Query Match 73.3%; Score 33; DB 2; Length 707; Best Local Similarity 75.0%; Pred. No. 1.5e+02; Matches 6; Conservative 1; Mismatches 1; Indels

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homo sapien
mus musculu
gallus gall
pasteurella
                                                                                   pasteurella
pasteurella
                                                                                                                   homo sapien
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mus musculu
                                                                                                                                                                                         rattus norv
     vesicular
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 90258861.
Schrawe H., Thompson J., Bona M., Hefta L.J.F., Maruya A.,
Hassauer M., Shively J.E., von Kleist S., Zimmermann W.;
"Cloning of the complete gene for carcinoembryonic antigen: analysis of its promoter indicates a region conveying cell type-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE: 89122014.
MEDLINE: 89122014.
MEDLINE: B.J., Goobel S.J., Nothdurft M.A., Elting J.J.;
Carcinoembryonic antigen family: characterization of CDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Olkawa S., Nakazato H., Kosaki G.;
"Primary structure of human carcinoembryonic antigen (CEA) deduced
from CDNA sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100)
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P55121
P18510
Q03450
P39470
P35242
                                 P80144
Q91955
P16533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31ochem. Biophys. Res. Commun. 142:511-518(1987)
                                                                                                                                                                                                                                                                                                                       702 AA
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                                                V1P_CHICK
LKC1_PASHA
LKC3_PASHA
LKC8_PASHA
LLLX_HUMAN
TRF4_ECOLI
RS13_SULAC
PSPA_MOUSE
 RRPL_VSVJH
LRP2_HUMAN
V1P_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression.";
Mol. Cell. Biol. 10:2738-2748(1990).
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 RESULT 1
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COMPRISING 60% CARBOHYDRATE. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 7 IG-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC ANTIGEN
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MIM; 114890; -
PINTERPRO; IPR003006; -
PFAM; PF00047; 1g; 7.
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M9710; NOT_ANNOTAFED_CDS.
M95940; AAA51967.1;
M15042; AAA51963.1;
M16234; AAA51963.1;
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M99255, AAA62835.1; JOINED.
M99257, AAA62835.1; JOINED.
M99258, AAA62835.1; JOINED.
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M99259, AAA62835.1; JOINED.
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M99709, MOT_ANNOTATED_CDS.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              Pichia pastoris (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
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                                                       Length 702;
                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
  MISSING (IN REF. 4).
6299AE26CDDBDB5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIÀL.
CYTOPLASMIC (POTENTIAL).
6853C5EA5C67EC34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         "Protein translocation into peroxisomes.";
J. Biol. Chem. 271:32483-32486(1996).
-!- FUNCTION: INVOLVED IN PEROXISOME BIOSYNTHESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MATRIX (POTENTIAL).
                                                       DB 1;
                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PAS2 (PEROXIN-3)
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Last annotation update)
                                                                                                                                                                                                       455 AA
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                                                       Score 38;
                                                                    Pred. No
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequ
15-JUL-1999 (Rel. 38, Last ann
GLYPICAN-5 PRECURSOR.
                                                                                                                                                                                                                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last anno
320 M
76795 MW;
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                                                      84.48;
77.88;
                                       Query Match
Best Local Similarity 77.8%,
Acconservative
                                                                                                                                                                                                                                                                                                                         Saccharomycetaceae; Pichia.
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Best Local Similarity 77.8.
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               702 AA;
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SEQUENCE FROM N.A.
                                                                                                           1 YLSGADINL 9
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34
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Q92262;
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CONFLICT
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PEX3_PICPA
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GPC5_HUMAN
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MEDLINE; Y. Alba H., Baba T., Hayashi K., Inada T., Isono K., Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K., Yamamoto Y., Alba H., Bakawa M., Makino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Yamagata S., Horluchi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horluchi T.; Yamagata S., Horluchi T.; Yamagata S., Horluchi T.; Alba Sequence of the Escherichia coli - Kl2 genome corresponding to 50.0-68.8 min on the linkage map and analysis of its sequence features.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA - TRANS-2(OR 3)-ENOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -! - CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) - 3-OXOACYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- CATALYTIC ACTIVITY: (S)-3-HYDROXYBUTANOYL-COA =
(R)-3-HYDROXYBUTANOYL-COA.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ENOYL-COA
HYDRATASE/ISOMERASE FAMILY.
-!- SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE 3-
HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                    Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 (EC 1.1.1.35); 3-HYDROXYBUTYRYL-COA EPIMERASE (EC 5.1.2.3)]
                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE000322; AAC75401.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 55.6%;
Matches 5; Conservative
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INTERPRO; IPR001753; -.
INTERPRO; IPR002135; -.
PFAM; PF00725; 3HCDH; 1.
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                                                                                         SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE; 97426617.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                Escherichia coli
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                                                              Escherichia.
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GLYPICAN-5.

REMOVED IN MATURE FORM (POTENTIAL).

POLY -LEU.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

G-LO (GLYCOSAMINOGLYCAN) (POTENTIAL).

G-Y C (IN REF. 2).
                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                                                      "Characterization of glypican-5 and chromosomal localization of human GPC5, a new member of the glypican gene family."; Genomics 40:24-30(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
91-OCT-2TY OXIDATION COMPLEX ALPHA SUBUNIT (INCLUDES: ENOYL-COA HYDRATASE (EC 4.2.1.17); 3-HYDROXYACYL-COA DEHYDROGENASE
                                                                                                                                                                                                                                                                           SIMILARITY).
-i- TISSUE SPECIFICITY: IN ADULT, PRIMARILY EXPRESSED IN THE BRAIN
                            Veugelers M., Vermeesch J., Reekmans G., Steinfeld R., Marynen P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF001462; AAC12261.1; -.
MIM; 602446; -
INTERPRO; IPRO11863; -.
PFAM; PF01153; Glypican; 1.
PROSITE; PS01207; GLYPICAN; 1.
PROCEOGLYCAN; Heparan sulfate; Glycoprotein; Signal; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                              MEDLINE: 97470873.
Saunders S., Paine-Saunders S., Lander A.D.;
Saunders S., Paine-Saunders S., Lander A.D.;
Expression of the cell surface proteoglycan glypican-5 is developmentally regulated in kidney, limb, and brain.";
Dev. Biol. 190:78-93(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 572;
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                                                                                                                                                                                                                                                                                                         ALSO DETECTED IN FETAL BRAIN, LUNG, AND LIVER.
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illarity 75.0%;
Conservative 1
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486
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572 AA;
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Matches 6; Conserv
                                                                                                                      SEQUENCE FROM N.A.
              97224481
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                                                                                                                                      TISSUE-BRAIN;
 FISSUE-BRAIN;
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P77399;
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PROSITE; PS00166; BHCH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; FALSE_NEG.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; FALSE_NEG.
OXIGOTECTICAL protein; Fatty acid metabolism; Multifunctional enzyme; OXIGOTECTICASE; NAD; Lyase; Isomerase.
ACTIVATES A WATER MOLECULE (BY ACTIVATES A WATER MOLECULE (BY Gaps ö Score 34; DB 1; Length 714; Pred. No. 22; 4; Mismatches 0; Indels PROVIDES THE ALPHA-PROTON (BY F4E0A75680039A0D CRC64; 1 YLSGADINL 9 ŏ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COA + H(2)0.
-1- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
[INCLUDES: LONG-CHAIN ENVYL-COA HYDRATASE (EC 4.2.1.17); LONG CHAIN
3-HYDROXYACYL-COA DEHYDROGENASE (EC 11.1.35)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 92:841-845(1995).
-!- FUNCTION: BIFUNCTIONAL SUBUNIT.
-!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBCELLULAR LOCATION: MITCHONDRIAL MATRIX.
-:- DISEASE: DEFECTS IN HADHA ARE A CAUSE OF MATERNAL ILLNESS OCCURING
LIVER OF PRECHANCY (AFLP), A SEVERE MATERNAL ILLNESS OCCURING
DURING PREGNANCIES WITH AFFECTED FETUSES. THIS DISEASE IS
CHARACTERIZED BY SUDDEN UNEXPLAINED INFANT DEATH OR HYPOGLYCEMIA
AND ABNORMAL LIVER ENZYMES (REYE-LIKE SYNDROME).
-:- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ENOYL-COA
HYDRATASE/ISOMERASE FAMILY.
-:- SIMILARITY: IN THE CEBRRAL SECTION; BELONGS TO THE 3-
HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sims H.F., Brackett J.C., Powell C.K., Treem W.R., Hale D.E., Brancht M.J., Gibson B., Shapiro S., Strauss A.W., The molecular basis of pediatric long chain 3-hydroxyacyl-CoA dehydrogenase defictency associated with maternal acute fatty liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00067; 3HCDH; 1.
PROSITE; PS001667; BNOYL_COA_HYDRATASE; 1.
Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase; NAD; Lyase; Mitochondrion; Transit peptide; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                 Kamijo T., Aoyama T., Miyazaki J.I., Hashimoto T.;
Structural analysis of cOMAs for subunits of human mitochondrial
fatty acid beta-oxidation trifunctional protein ";
Blochem. Biophys. Res. Commun. 199:818-825(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- PATHWAY: CATALYZES TWO STEPS OF THE FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! - SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
                                                                                                    763 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D16480; BAA03941.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00725; 3HCDH; 1. PFAM; PF00378; ECH; 1.
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERPRO; IPR001753; -.
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HSSP; P14604; 2DUB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 95148633.
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FIAGADINM 73
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P40939;
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                                                                                     ECHA_HUMAN
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"The large subunit of the pig heart mitochondrial membrane-bound beta-oxidation complex is a long-chain enoyl-CoA hydratase: 3-hydroxyacyl-CoA dehydrogenase bifunctional enzyme "; comp. Biochem. Physiol. 109B:557-566(1994). -!- FUNCTION: BIFUNCTIONAL SUBUNIT; CANNOT USE CROTONYL-COA OR 3-HYDROXYBUTRYRYL-COA AS SUBSTRAFE. -!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MIJOCHODRIAL TRIFUNCTIONAL ENZYME ALPHA SUBBUNIT PRECURSOR (TP-ALPHA)
(78 KDA GASTRIN-BINDIG PROTEIN) [INCLUDES: LONG-CHAIN ENOYL-COA
HYDRATASE (EC 4.2.1.17); LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA Gaps MEDLINE; 93290643. Baldwin G.S., Casey A., Weinstock J., Partial structure of the gene encoding the 78 kDa gastrin binding protein excludes a close relationship with the peroxisomal Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. ; 0 Yang S.-Y., He X.-Y., Styles J., Luo M.J., Schulz H., Elzinga la Primary structure of the large subunit of trifunctional beta-coxidation complex from pig heart mitochondria "; Biochem. Biophys. Res. Commun. 198:431-437(1994). Baldwin G.S.; ACTIVATES A WATER MOLECULE (BY SIMILARITY). PROVIDES THE ALPHA-PROTON (BY Length 763; Indels /FTId=VAR_002273. 98D7881F7CB5949B_CRC64; MITOCHONDRION (POTENTIAL) ; Biochem. Biophys. Res. Commun. 193:560-564(1993) Mantamadiotis T., Sobieszczuk P., Weinstock J., "Nucleotide sequence encoding a novel member of Score 34; DB 1; Pred. No. 24; -> Q (IN AFLP). 763 AA 4; Mismatches hydratase/dehydrogenase family."; Biochim. Biophys. Acta 1170:211-215(1993). SIMILARITY E -> Q (IN MM: 75.6%; PARTIAL SEQUENCE FROM N.A. 82959 Conservative STANDARD; 36 763 151 510 trifunctional enzyme HADHA OR LCHYD-HAD. Sus scrofa (Pig). Query Match Best Local Similarity Matches 5; Conserv TISSUE=STOMACH; MEDLINE; 94002212. TISSUE=HEART; MEDLINE; 95187623. 763 AA; SEQUENCE FROM N.A. MEDLINE; 94128080. 98 FIAGADINM 106 SEQUENCE FROM N.A. CHARACTERIZATION. 1 YLSGADINL 9 510 151 173 37 TISSUE=LIVER TISSUE-HEART -Y.; ECHA_PIG ACT_SITE SEQUENCE ACT_SITE VARIANT lang S. 9 CHAIN RESULT ECHA_PIG DAT DDT TO DD TO D ö g

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RA MEDLINE; 93101122.
RA MAYOLGA M.E., Timberlake W.E.;
RY "The developmentally regulated Aspergillus nidulans wA gene encodes a ray of general control of the second synthases.";
RL MOI. Gen. Genet. 235:205-212(1952).
CC INTERMEDIATE PRILION CONDENSES CARBON UNITS TO FORM AN CC INTERMEDIATE YELLOW POLYKETIDE PIGMENT THAT IS POLYMERIZED BY CONIDIAL LACCASE TO FORM THE GREEN PIGMENT IN MATURE
CC ASEXUAL SPORES (CONIDIA).
CC -: COFACTOR: CONTAINS 2 COVALENTLY BOUND PHOSPHOPANTETHEINES
                                                                                                                                                                                                                                                                                                                                                                                            MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae; Emericella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
           CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA
                                                       -!- SÜBÜNIT: HETERODIMER OF AN ALPHA AND A BETA SÜBÜNIT.
-!- SÜBCELLÜLAR LÖCATION: MITOCHONDRIAL MATRIX.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELÖNGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
-!- SIMILARITY: IN THE CENTRAL SECTION; BELÖNGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                             PROSITE; PS00067; 3HCDH; 1.
PROSITE; PS00167; 2HCDH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase; NAD; Lyase; Mitochondrion; Transit peptide.
                                   PATHWAY: CATALYZES TWO STEPS OF THE FATTY ACID BETA-OXIDATION
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ACTIVATES A WATER MOLECULE
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Pred. No. 24;
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01-JUN-1994 (Rel. 29, Last sequence update)
12-JUL-1998 (Rel. 36, Last annotation update)
CONIDIAL GREEN PIGMENT SYNTHASE (EC 2.3.1.-).
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INTERPRO; IPRO01753; -.
PFAM; PPO0725; 3HCDH; 1.
PFAM; PFO0728; ECH; 1.
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Rodriguez J.F., Vinuela E.;
"Analysis of the complete nucleotide sequence of African swine fever
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BETA-KETOACYL SYNTHASE (BY SIMILARITY).
ACYL/MALONYL TRANSFERASES
(BY SIMILARITY).
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ACYL CARRIER (ACP).
BETA-KETOACYL SYNTHASE (BY SIMILARITY).
ACYL/MALONYL TRANSFERASES (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHOPANTETHEINE (BY SIMILARITY).
PHOSPHOPANTETHEINE (BY SIMILARITY).
W; 74EF0940FF40EE9A CRC64;
PATHWAY: BIOSYNTHESIS OF CONIDIAL GREEN PIGMENT. SIMILARITY: WITH BOTH EUKARYOTIC AND PROKARYOTIC POLYKETIDE SYNTHASES AND VERTEBRATE FATTY ACID SYNTHASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           African swine fever virus (strain BA71V) (ASFV).
Viruses; dsDNA viruses, no RNA stage;
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01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR000255; -.
INTERPRO; IPR000255; -.
INTERPRO; IPR001025; -.
INTERPRO; IPR001257; -.
FFAM; PF00109; Retoacyl-synt; 1.
PFAM; PF00500; PF050000; PROSTHE; PS00001; PROSTHE; PS00001; PROSTHE; PS00001; PROSTHE; PS00001; PROSTHE; PS00001; ACP DOMAIN; 2.
PROSTHE; PS00075; ACP DOMAIN; 2.
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Pred. No.
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African swine fever-like viruses.
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Best Local Similarity 75.v.
6; Conservative
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P23163;
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send an email to license@isb-sib.ch).
                                              EMBL; D16478; BAA03939.1; -.
                                                                            INTERPRO; IPRO01753; -.
INTERPRO; IPRO02135; -.
PFAM; PF00725; 3HCDH; 1.
PFAM; PF00378; ECH; 1.
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Q06708;
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                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by non-profit institutions as long as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MITOCHONDEAL TRIFUNCTIONAL ENZYME ALPHA SUBENIT PRECURSOR (TP-ALPHA)
[INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE (EC 4.2.1.17); LONG CHAIN
3-HYDROXYACYL-COA DEHYDROGENASE (EC 11.1.35)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNE: 94075534.

Kamijo T., Aoyama T., Miyazaki J., Hashimoto T.;

"Molecular cloning of the cDNAs for the subunits of rat mitochondrial fatty acid beta oxidation multiensyme complex. Structural and functional relationships to other mitochondrial and peroxisomal beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxidation enzymes.";
J. Biol. Chem. 268:26452-26460(1993).
-!- FUNCTION: BIFUNCTIONAL SUBUNIT.
-!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
-!- SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -! - PATHWAY: CATALYZES TWO STEPS OF THE FATTY ACID BETA-OXIDATION
                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                               Length 311;
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
                                                                                                                                                                                                                                                                                        311 AA; 35574 MW; 02651F4C5F2A3DA7 CRC64;
-1- FUNCTION: NOT KNOWN.
-1- SIMILARITY: BELONGS TO THE MULTIGENE FAMILY 360.
                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1;
Pred. No. 15;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 AA.
                                                                                                                                                                                 EMBL; M57544; AAA42677.1; -.
EMBL; U18466; AAA65374.1; -.
PIR; E43680; E43680.
                                                                                                                                                                                                                                                                                                                                         73.3%;
75.0%;
                                                                                                                                                                                                                                    INTERPRO; IPR002595; -
PFAM; PF01671; ASFV_360; 1.
Multigene family.
                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              1: |||||
258 YILGADIN 265
                                                                                                                                                                                                                                                                                                                                                                                                         1 YLSGADIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECHA_RAT
Q64428;
                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ECHA_RAT
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO AB972;

MEDLINE: 97313267.

A Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Brenes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Brenes V., Bruckner M., Delius H., Dubois E., Dusterhoft A., Britan K.D., Floeth M., Goffeau A., Hebling U., Heumann K., A. Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Kotter P., A. Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Mostl D., Muller Auer S., Neitwich U., Obermaler B., Pirayandi E., Pohl T.M., RA Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Charles M., Scherens B., Scholler P., Schwarz S., Underwood A.P., Ulrestarazu L.A., Vandenbol M., Verhasselt P., RA Vierendeels F., Voet M., Volckeart G., Voss H., Wambutt R., Wedler E., Redelr H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D., The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                                                                                              MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA
                                                                                                                                                                                                                                                                                                                                                           Gaps
PROSTIE; PS00067; 3HCDH; 1.
PROSTIE; PS00166; ENOYL_COA_HYDRATASE; 1.
Fatty acid metabolism; Multifunctional enzyme; Oxidoreductase; NAD; Lyase; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 99.8 KDA PROTEIN IN IK13-RPS29A INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                          ACTIVATES A WATER MOLECULE (BY SIMILARITY).
                                                                                                                                                                                                PROVIDES THE ALPHA-PROTON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                        73.3%; Score 33; DB 1; Length 763; 55.6%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                          MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                            F4A489C360AFF4A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              880 AA.
                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 387:87-90(1997).
                                                                                                                                      SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50077; HEAT_REPEAT; 1.
Hypothetical protein; Transmembrane.
                                                                                                                                                                                                                                          763 AA; 82512 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U19104; AAB67272.1;
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                            36
                                                                                                                                                      151
                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity
'-has 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                             98 FVAGADINM 106
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PGL1_COLLN

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PARTIAL SEQUENCE, REVISION TO C-TERMINUS, AND FUNCTION
   414 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 AA
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   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequ
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                    F23F12.6; CE01253.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U12965; AAA20608.1;
                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR001939; -..
PFAM; PF00004; AAA; 1.
PROSITE; PS00674; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
   STANDARD;
                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=BRISTOL N2;
Du Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||||||
366 ISGADIN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LSGADIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRS6_HUMAN
P43686;
                                                                                                                                                                                                                                                                                                                                                                                                  WORMPEP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRS6_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                         Centis S., Dumas B., Fournier J., Marolda M., Esquerre-Tugaye M.T.; "Isolation and sequence analysis of Clpg1, a gene coding for an endopolygalacturonase of the phytopathogenic fungus Colletotrichum lindemuthlanum."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROBABLE.
N-LINKED (GLCNAC. . .) (POTENTIAL).
A17A60386791B897 CRC64;
                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                               Colietotrichum lindemuthianum (Anthracnose fungus).
Eukaryota; Fungi; Ascomycota; Phyllachorales; Phyllachoraceae;
                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ENDOPOLYGALACTURONASE 1 PRECURSOR (EC 3.2.1.15) (PECTINASE)
                                                   Length 880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 363;
                                                                             2; Indels
POTENTIAL.
E625AB6F032D2E1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
ENDOPOLYGALACTURONASE 1.
                                                   ;;
                                                                                                                                                                                           363 AA.
                                               DB 45;
                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Phyllachorale
anamorphic Phyllachoraceae; Colletotrichum.
                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                  Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 17 PO
18 26 PO
27 363 EN
224 224 PR
212 212 NP.
363 AA; 36712 MW;
 84 PC
99771 MW;
                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
01-NOV-1997 (Rel. 35, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.18;
71.48;
                                                  73.3%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X89370; CAA61552.1; -.
                                                 Query Match 73.3
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
                                                                                                                                                                                           STANDARD;
64
880 AA;
                                                                                                                          380 YIPCODINL 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 96200868.
                                                                                                   1 YLSGADINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||||:
| 192 YISGADV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YLSGADI 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein.
                                                                                                                                                                                          PGL1_COLLN
TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROPEP
CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE 26S COMPLEX (BY SIMILARITY).

-!- SUBSCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR (POTENTIAL).

-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
26S PROTEASE REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7) (TBP-7).
PSMC4 OR TBP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein is
family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein; Proteasome; ATP-binding; Nuclear protein. NP_BIND 202 209 ATP (POTENTIAL). SEQUENCE 414 AA: 46358 MW. RAJAARMANA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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MEDLINE; 93126329.
Ohana B., Moore P.A., Ruben S.M., Southgate C.D., Green M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 32; DB 1; Length 414; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The type 1 human immunodeficiency virus Tat binding transcriptional activator belonging to an additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    evolutionarily conserved genes.";
Proc. Natl. Acad. Sci. U.S.A. 90:138-142(1993).
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last Sequence update)
12-UUL-1998 (Rel. 36, Last annotation update)
PROBABLE 26S PROTEASE REGULATORY SUBUNIT 6B.
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MEDLINE; 94338582.

RESULT 12 PRS6_CAEEL

Best Loca Matches

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PRS6_RAT
063570;
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Matches
                                                                                    Matches
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Or send an email to license(isb-sib.ch).
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Dubiel W., Ferrell K., Rechsteiner M.;
"Tat-binding protein 7 is a subunit of the 26S protease.";
Biol. Chem. Hoppe-Seyler 375:237-240(1994).
-!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
DEGRADATION OF UBIOUTINATED PROTEINS. THE REGULATORY (OR ATPASE)
COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
26S PROTEASE REGULATORY SUBUNIT 6B (CIP21) (MIP224) (MB67 INTERACTING PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Choi H.S., Seol W., Moore D.D.;
"A component of the 26s proteasome binds on orphan member of the nuclear hormone receptor superfamily.";
J. Steroid Biocham. Mol. Biol. 56:23-30(1996).
-I- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE RAIP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGLATORY (OR ATPASE) COMPLEX COMPERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE 26S COMPLEX. INTERACTS WITH THE ORPHAN NUCLEAR HORMONE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosťomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                INTERPRO; IPKULL,,
PFAM; PFO0004; AAA; 1.
PROSITE; PS00674; AAA; 1.
Proteasome; ATP-binding; Nuclear protein.
Proteasome; ATP-binding; Nuclear protein.
ATP (POTENTIAL).
ATP (POTENTIAL).
ATP (ATTACH MW; 932C5233C0AD8F08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TP (POTENTIAL).
C2D57FB9591729F4 CRC64;
                                                                                                                                                                                               -!- PTM: THE N-TERMINUS IS BLOCKED.
-!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
MIM; 602707; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
                                                                                                                                                26S COMPLEX.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  418 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteasome; ATP-binding; Nuclear protein NP_BIND 206 213 ATP (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47281 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.18;
85.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L76223; AAA88243.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00004; AAA; 1.
PROSITE; PS00674; AAA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         418 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=LIVER;
MEDLINE; 96184184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 ISGADIN 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LSGADIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRS6_MOUSE
P54775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
26S PROTEASE REGULATORY SUBUNIT 6B (TAT-BINDING PROTEIN-7) (TBP-7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makino Y., Yogosawa S., Kanemaki M., Yoshida T., Yamano K., Kishimoto T., Moncollin V., Egly J.M., Muramatsu M., Tamura T.; "Structures of the rat proteasomal ATPases: determination of highly conserved structural motifs and rules for their spacing.", Blochem. Blophys. Res. Commun. 20211049-1054[956].

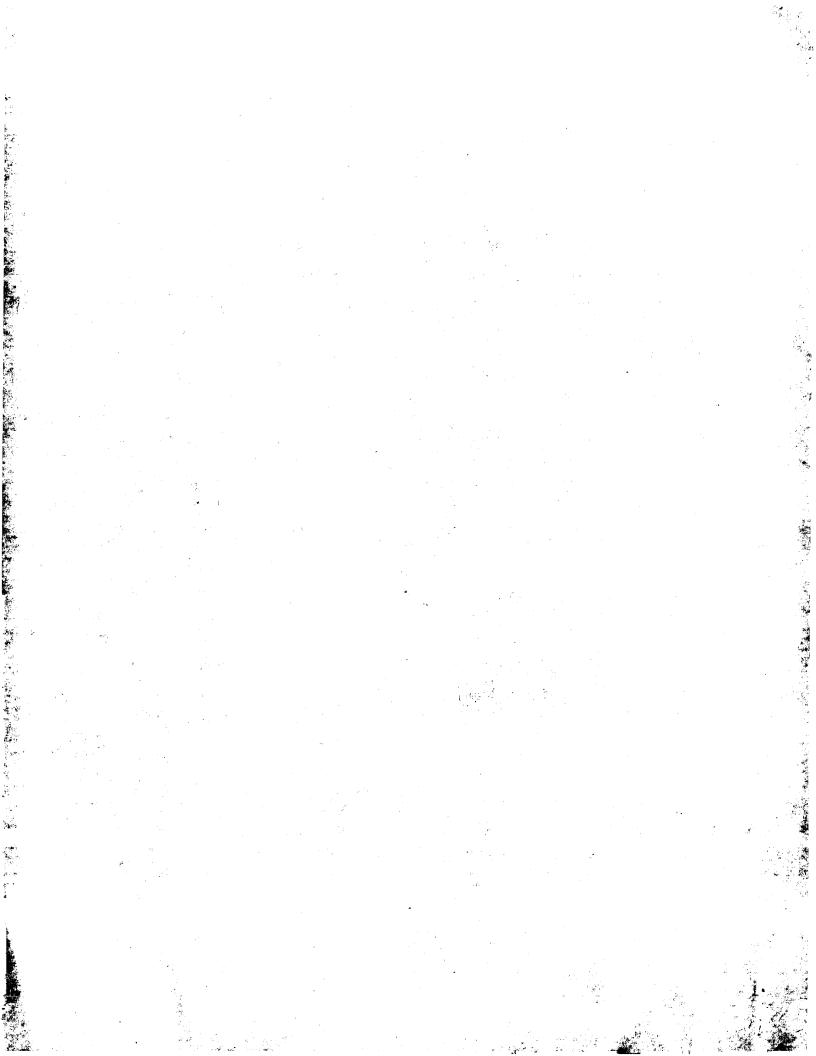
-I- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
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     Length 418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.1%; Score 32; DB 1; Length 418; 85.7%; Pred. No. 33;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERNATION PEROUNGA; AAAN; AAAN; AAAN; AAAN; BROSITE; PS00674; AAAN; A. PROSITE; PS00674; AAAN; A. Proteasome; ATP-binding; Nuclear protein.

Proteasome; ATP-binding; Nuclear protein.

ATP (POTENTIAL).

ATANB MW; 6FD2CIE3EBIFFSF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: CYTOPLASMIC AND NUCLEAR. SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
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  DB 1;
                          d. No. 33;
Mismatches
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  Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                           ;
71.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D50695; BAA09340.1; -.
                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPR001939;
PFAM; PF00004; AAA;
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 96183075.
                                                                                                                                                    370 ISGADIN 376
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                                                                                                             2 LSGADIN 8
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; Search time 91.14 Seconds (without alignments) 6.267 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                           01:51:14
                                                                                     OM protein - protein search, using sw model
                                                                                                                           December 16, 2000,
                                                                                                                           Run on:
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US-09-529-121-3 45 1 YLSGADINL 9 Perfect score: Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

182106 Total number of hits satisfying chosen parameters:

182106 seqs, 63460219 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries PIR_65:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | carcinoembryonic a | micrococcal nuclea | gastrin-binding pr | hypothetical prote | | hypothetical prote | probable polyketid | D'311 protein - Af | Ω. | | | | hypothetical prote | ထ | long-chain-fatty-a | probable membrane | conserved hypothet | hypothetical prote | hypothetical prote | polygalacturonase | hypothetical prote | monooxygenase-rela | ABC transporter (A | IgG Fc binding pro | nar | gp330 protein prec | retinol-binding pr | hlyU protein - Vib | Ω, |
|-----------|----------------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------|--------------------|-------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------|
| SUMMARIES | QI | A36319 | F71064 | PN0511 | C65007 | JC2108 | C72338 | S28353 | E43680 | T24929 | T24930 | T20840 | T21262 | T21261 | T12784 | A49681 | S51473 | G70475 | T33344 | T22450 | JC4748 | E69049 | C81704 | E69861 | T30257 | S53457 | T42737 | A03148 | m | PQ0493 |
| | DB | . 7 | 7 | 7 | 7 | ~ | ~ | 7 | 7 | ~ | 7 | 7 | ~ | 7 | ~ | - | 7 | 7 | 7 | ~ | ~ | 7 | ~ | ~ | 7 | 7 | ~ | 7 | 7 | 7 |
| | S Ouery Match Length | 702 | 176 | 275 | 714 | 763 | 860 | 1986 | 311 | 401 | 402 | 441 | 445 | 454 | 705 | 763 | 880 | 188 | 312 | 350 | 363 | 374 | 206 | 540 | 1023 | 1650 | 4660 | 30 | 108 | 112 |
| ď | Query Match | 84.4 | 75.6 | 75.6 | 75.6 | 75.6 | 75.6 | 75.6 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 73.3 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 71.1 | 6.89 | 68.9 | 68.8 |
| | Score | 38 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 31 | 31 | 31 |
| | Result No. | 7 | 7 | m | 4 | S | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 53 |

| phycoerythrocyanin micrococcal nuclea hypothetical prote | histone deacetylas melanoma antigen h cyclin A-like prot hypothetical prote | probable acidCoA hypothetical prote hypothetical prote development-specif | translation elonga LDL receptor precu serine proteinase LDL receptor precu LDL receptor precu |
|--|--|--|---|
| A41841 D75083 S08389 | H75470 A49179 T02746 S50519 | A70904 S19381 T23685 A30814 | B71723 QRHYLD T10585 QRHULD QRMSLD |
| 7 7 7 | 0000 | 0000 | 21215 |
| 172 175 210 | 301 491 502 502 | 554 586 596 597 | 699 856 860 862 |
| 68 68 68 68 68 68 | 6.88.9 6.89.9 6.09.9 | 688 688 69 69 69 69 | 68 68 68 68 68 68 68 68 |
| 31 | 31 31 31 31 | 3333 | 311111 |
| 30 31 32 | 9 9 9 9 9 | 37 38 39 40 | 4 4 4 4 4 1 4 4 3 2 1 |

ALIGNMENTS

| RESULT 1 |
|--|
| A36319 |
| carcinoembryonic antigen precursor - human |
| N; Alternate names: CEA; meconium antigen 100 |
| C;Species: Homo sapiens (man) |
| C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000 |
| C; Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59098; |
| R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; Shive |
| Mol. Cell. Biol. 10, 2738-2748, 1990 |
| A; Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of its p |
| A; Reference number: A36319; MUID:90258861 |
| A; Accession: A36319 |
| A; Molecule type: DNA |
| A; Residues: 1-702 <sch></sch> |
| A; Cross-references: GB:M17303; NID:q178676; PIDN:AAB59513.1; PID:q178677 |
| A; Note: the authors show the codons TTA for residue 641-Phe and CAG for residue 646-T |
| R; Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P. |
| Mol. Cell. Biol. 7, 3221-3230, 1987 |
| A; Title: Isolation and characterization of full-length functional cDNA clones for hum |
| A; Reference number: A27773; MUID:88038876 |
| A; Accession: A27773 |
| A; Molecule type: mRNA |

A; residues: 1-70 ckeps.

A; residues: 1-70 ckeps.

A; residues: 1-70 ckeps.

A; residues: 1-70 ckeps.

A; Reference number: 3. 59-66, 1988

A; Reference number: A31037; MuID:89122014

A; Recession: A31037; MuID:89122014

A; Recieved number: A31037; MuID:89122014

A; Recieved number: A31037; MuID:89122014

A; Recieved number: A31037; MuID:89122014

A; Residues: 1-702 ckBR>
A; Residues: 1-702 ckBR>
A; Residues: 1-702 ckBR>
A; Rolecule type: mRNA
A; Residues: 1-702 ckBR>
A; Note: the authors translated the codon GTG for residue 130 as Leu
B; Oikawa, S.; Nakazato, H.; Rosaki, G.
B; Oikawa, S.; Nakazato, H.; Rosaki, G.
A; Title: Primary structure of human carcinoembryonic antigen (CEA) deduced from cDNA
A; Reference number: A25845; MuID:87128144
A; Residues: 5-702 colks
A; Residues: 5-702 colks
A; Residues: 5-702 colks
A; Reference number: S08106
A; Residues: Soluce
A; Reference number: S08106
A; Residues: 5-319; 321-702 colts
A; Residues: 5-319; 3 A; Residues: 1-702 <BEA>

A;Cross-references: EMBL:X16455; NID:929854; PIDN:CAA34474.1; PID:9825638
R;Barnett, T.
Submitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcin A;Reference number: S31737

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A Molecule type: DNA
A;Residues: 1-176 <KMM>
A;Cross-references: GB:AP000005, NID:93236132; PIDN:BAA30312.1; PID:93257629
A;Cross-references: Grain OT3
A;Cross-timental source: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBa
                                                                                                                                                                                                                                               C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: F71064 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 C;Accession: F71064 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000 R;Xawarabayasi, Y:; Sawada, M:; Hanka, Y:; Hino, Y:; Yamanoto, S:; Se M:; Obluk, Y:; Yamazaki, J:; Kushida, N:; Ogu N. Poh Res. 5, 55-76, 1998 A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili A;Reference number: A71000; MUID:98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrin-binding protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-pec-1993 #sequence_revision 31-pec-1993 #text_change 17-Mar-1999
C;Accession: PNO511
R;Baldwin, G.S.; Casey, A.; Weinstock, J.
Biochem. Biophys. Res. Commun. 193, 560-564, 1993
A;Title: Partial structure of the gene encoding the 78KDa gastrin binding protein enc A;Reference number: PNO511; MUID:93290643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 23/1; 37/1; 60/3; 105/2; 151/3; 191/3; 226/1
C; Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA
F;1-36/Domain: signal sequence #status predicted <SIG>
F;37-275/Product: gastrin-binding protein #status predicted <MAT>
F;62-218/Domain: enoyl-CoA hydratase homology <ECH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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Pred. No. 21;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: micrococcal nuclease
C;Keywords: hydrolase
F;1-27/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7
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Pred. No. 13;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.68;
55.68;
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C65007
hypothetical protein b2341 -
C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
5, Conserve
      605 YLSGANLNL 613
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A; Residues: 1-275 <BAL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: F71064
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                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 35-141 <KHA>
R;Willcocks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
A;Reference number: 154224; MUID:91139118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: M60964; NID: 9180215; PIDN: AAA51964.1; PID: 9180217
R; Zimmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.
Proc. Natl. Acad. Sci. U.S.A. 84, 2960-2964, 1987
A; Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon A; Reference number: IS9098; MUID: 87204247
A; Accession: IS9098
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A; Molecule this is the amino terminal end of a fragment shown to mediate uptake by Kupffer C; Comment: This heavily 91ycosylated membane protein of unknown function is a widely use C; Comment: This protein may be processed at its C-terminus. It is anchored to the membra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.Cross-references: GDB:119054; OMIM:114890

A.Map position: 19q13.2-19q13.2

A.Map position: 19q13.2-19q13.2

A.Map position: 19q13.2-19q13.2

A.Map position: 19q13.2-19q13.2

C.Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin C.Keywords: blocked carboxyl end; glycoprotein; lipoprotein; membrane protein; phosphatif F.1-134 Domain: carcinoembryonic antigen precursor amino-terminal homology <CEAN>
F.3-55-678/Product: carcinoembryonic antigen extended <SIG>
F.35-678/Product: carcinoembryonic antigen #status predicted <MAT>
F.160-217/Domain: immunoglobulin homology <IMMI>
                                                                                                                                                                                                                        estimation of the size of the carcinoembr
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F;679-702/Domain: carboxyl-terminal propeptide #status predicted <CTP>
F;678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
                                                                                                                                                           s.
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A; Residues: 35-64 <SIE>
A; Rischidues: 35-64 <SIE>
R; Thomas, P.: Toth, C.A.
Biochem. Biophys. Res. Commun. 170, 391-396, 1990
A; Title: Carcinoembryonic antigen binding to Kupffer cells is via a peptide located at A; Reference number: A35490; MUID:90321257
A; Accession: A33490.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M16234; NID:g180240; PIDN:AAA51972.1; PID:g180241
R;Siepen, D.; Paxton, R.J.; Neumaier, M.; Shively, J.E.; Wagener, C.
Biochem. Blophys. Res. Commun. 147, 212-218, 1987
A;Title: Carcinoembryonic antigen (CEA) and two crossreacting antigens of 165 KD and
                                                                                                                                                           K.; Hammarstroem,
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                                                                                                                 A,Cross-references: EMBL:X62151
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the s1 A;Reference number: A44476; MUID:93052339
A;Accession: A44476
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Pred. No. 8.6;
2; Mismatches
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A;Accession: A26831
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77.88;
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A; Residues: 331-702 <RE2>
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Best Local Similarity
7; Conserv?
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A; Residues: 1-37 <RES>
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A; Accession:
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Gaps

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Gaps

- Escherichia coli (strain K-12)

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1 YLSGADINL

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C. Accession: S28353
R. Mayorga, M.E.; Timberlake, W.E.
Mol. Gen. Genert. 235, 205-212, 1992
A. Title: The developmentally regulated Aspergillus nidulans wA gene encodes a polypep A; Reference number: S28353; MuID:93101122
A; Accession: S28353
A; Molecule type: DNA
A; Residues: 1-1986 < MAX>
A; Residues: 1-1986 < MAX>
A; Cross-references: EMBL:X65866; NID:95508; PID:95509
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A;Introns: 96/2; 193/3; 1336/3; 1588/3
C;Superfamily: 3-oxoacyl-jacyl-carrier-protein] synthase I homology; acyl carrier pro
C;Keywords: carrier protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-860 <ARN>
A;Residues: 1-860 <ARN>
A;Cross-references: GB:AE001745; GB:AE000512; NID:g4981278; PID:g4981284; TIGR:TM0757
A;Experimental source: strain MSB8
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316
A;Accession: C72338
                                                                                                                                                                                                                                                                                                                                                                                                  R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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F;911-1199/Domain: [acyl-carrier-protein] S-malonyltransferase homology <AMT>
F;1648-1718/Domain: acyl carrier protein homology <ACP>
F;1766-1840/Domain: acyl carrier protein homology <ACP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
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Pred. No. 1.7e+02;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                     hypothetical protein - Thermotoga maritima (strain MSB8)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 399, 323-329, 1999
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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FIAGADINM 106
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443 YETGGDIN 450
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                                  1 YLSGADINL
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A;Cross references: GDB:434026; OMIM:600890
A;Cross references: GDB:434026; OMIM:600890
C;Complex: heterocotamer of 4 alpha and 4 beta chains
C;Complex: heterocotamer of 4 alpha and 4 beta chains
C;Complex: heterocotamer of alpha and 4 beta chains
C;Superfamily: encyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA def;Superfamily: encyl-CoA hydratase/3-hydroxyacyl-CoA deficies acyltransferase; carbon-oxygen lyase; fatty acid beta-oxidation; heterocctam
F;1.36/Domain: transit peptide (mitochondrinon) #status predicted <TPP>
F;37.763/Product: fatty acid beta-oxidation trifunctional protein, alpha chain #status eff;6.52-218/Domain: anoyl-CoA hydratase homology <HCD>
F;361-640/Domain: 3-hydroxyacyl-CoA dehydrogenase homology <HCD>
F;361-640/Domain: beta-alpha-beta NAD nucleotide-binding fold
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A; Residues: 37-64 <RA2>
A; Note: peptide sequence from amino end of mature protein
A; Oct: peptide sequence from amino end of mature protein
B; Zhang, O.X.; Baldwin, G.S.
Biochim. Biophys. Acta 1219, 567-575, 1994
A; Title: Structures of the human cDNA and gene encoding the 78 kDa gastrin-binding prote
A; Reference number: $50127; MUID:95002180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dong-chain-fatty-acid beta-oxidation multienzyme complex alpha chain precursor, mitochon N;Alternate names: 78K gastrin-binding protein
N;Alternate names: 78K gastrin-binding protein
N;Contains: long-chain-3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.211); long-chain-encyl-C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 20-Jun-2000
R;Kamijo, T.; Aoyama, A.; Hashimoto, T.
Biochem. Blophys. Res. Commun. 199, 818-825, 1994
A;Titles: Structural analysis of cDNAs for subunits of human mitochondrial fatty acid bet A;Reference number: JC2108; MUID:94183263
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                                                                                                                                                                                                                                                                                                                             A:Residues: 1-714 <BLAT>
A:Residues: 1-714 <BLAT>
A:Cross-references: GB:AE000322; GB:U00096; NID:g1788672; PIDN:AAC75401.1; PID:g1788682;
A:Experimental source: strain K-12, substrain MG1655
C;Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA de F:29-185/Domain: enoyl-CoA hydratase homology <ECH>
F:29-185/Domain: anoyl-CoA hydratase homology <ECH>
F:308-587/Domain: 3-hydroxyacyl-CoA dehydrogenase homology <ECH>
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A;Molecule type: mRNA
A;Rosidues: 1-145,'L',147-151,'L',153-170,'A',172-177,'I',179-196,'VF',199-205,'N',207-2
A;Cross-references: EMBL:U04627; NID:9595266; PIDN:AAA56664.1; PID:9595267
C;Genetics:
                                                       Riblatine: F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; G.; Rose, D.J.; Mau, B.; Shao, Y.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Tille: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 22-Jun-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 714;
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Pred. No. 58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
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55.6%;
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A; Residues: 1-763 <KAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :::|||||:
65 FIAGADINM 73
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                               Accession: C65007
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hypothetical protein F13E9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 15-0ct-1999
C;Accession: T20840
C;Accession: T20840
A;Reference number: Z19332
A;Accession: T20840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F22D6.11 - Caenorhabditis elegans cippothetical protein F22D6.11 - Caenorhabditis elegans cippoties caenorhabditis elegans cippoties 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 (C; Accession: T21262 R;Wilkinson, J. Submitted to the EMBL Data Library, April 1996 A; Reference number: 219397 A; Accession: T21262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 2; Length 441;
Pred. No. 55;
2; Mismatches 1; Indels
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A;Introns: 65/3; 95/2; 136/3; 180/3; 256/3; 281/3; 403/3
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A:Molecule type: DNA
A:Residues: 1-445 <WIL>
                                A; Introns: 55/3; 85/2; 121/3; 161/3; 237/3; 262/3
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A;Introns: 39/3; 93/1; 146/3; 252/3; 296/2; 426/2
                                                                                                                                                                  Score 33; DB 7
Pred. No. 50;
0; Mismatches
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                                                                                                                                                                       73.3%;
77.8%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
                                                                                                                                                                  Query Match 73.3
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 7/...
7; Conservative
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196 YLSGVDIPL 204
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215 YLSGVDIPL 223
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427 YISGEDVN 434
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A;Gene: CESP:F22D6.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP:F13E9.1
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D'311 protein - African swine fever virus (strain BA71V)
C; Species: African swine fever virus, ASFV
C; Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 26-Aug-1999
C; Accession: E43680
R; Conzalez, A.; Calvo, V.; Almazan, F.; Almendral, J.M.; Ramirez, J.C.; De La Vega, J.; J. Virol. 64, 2073-2081, 1990
A; Title: Multigene families in African swine fever virus: family 360.
A; Reference number: A43680; MUID:90219205
A; Reference preliminary
A; Reference preliminary
A; Rejatus: preliminary
A; Residues: 1-311 <CGN>
A; Residues: 1-311 <CGN>
A; Residues: 1-31 <CGN>
A; Residues: 1-311 <CGN>
A; Residues: 1-3
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C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T24930
R:Dobson, R.
submitted to the EMBL Data Library, November 1996
R:Accession: T24930
A:Reterence number: 219956
A:Accession: T24930
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-402 <WIL>
A:Coss references: EMBL:283125; PIDN:CAB05621.1; GSPDB:GN00019; CESP:T15D6.3
A:Cross references: EMBL:283125; A:Genetics:
A:Genetics:
A:Genetics:
A:Genetics:
A:Map position: 1
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A:Molecule type: DNA
A:Residues: 1-401 <WILL>
A:Coss-references: EMBL:283125; PIDN:CAB05620.1; GSPDB:GN00019; CESP:T15D6.2
A:Experimental source: clone T15D6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T15D6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24929
R;Dobson, R.
submitted to the EMBL Data Library, November 1996
A;Reference number: 219956
A;Accession: T24929
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A:Introns: 45/3; 75/2; 111/3; 151/3; 227/3; 252/3; 296/2; 359/3
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Pred. No. 38;
1; Mismatches
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75.0%;
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Best Local Similarity 75.0°
Matches 6; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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186 YLSGVDIPL 194
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258 YILGADIN 265
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A; Acadus: 112/05 class
A; Readus: 112/05 class
A; Readus: 112/05 class
A; Readus: 112/05 class
A; Readuces: L705 class
A; Readuces: EMBL.AF020713; NID:93025478; PID:93025498; PIDN:AAC12993.1
A; Cross-references: EMBL.AF020713; NID:93025478; PID:93025498; PIDN:AAC12993.1
B; Rkunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Broullatt, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A: Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A; Ehrlich, S. D.; Fitz, C.; Fujita, M.; Fujita, Y.; Fuma S.; Galizzi, A.; Galler
A; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Lander, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekwaka, A.; Serori
akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tarpstra, P.; Tognoni, A.; Tosato, V.; Voliyama,
T.; Winters; Yoshikawa, H.F.; Zunstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A; Accession: A69720
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C:Species: Bacillus subtilis phage SPBc2
C:Date: 13.Aug-1999 #sequence_revision 13.Aug-1999 #text_change 20.Jun-2000
C:Accession: T12784; A69720
R:Lazarevic, V.: Duesterhoeft, A.; Soldo, B.; Hilbert, H.; Mauel, C.; Karamata, D.
Bubmitted to the EMBL Data Library, August 1997
A:Description: The complete nucleotide sequence of the Bacillus subtilis SPbetac2 propha
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A;Experimental source: strain 168
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                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:271262; PIDN:CAA95816.1; GSPDB:GN00019; CESP:F22D6.12 A;Experimental source: clone F22D6
                  C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T21261
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C;Superfamily: hemolysin secretion protein B; ATP-binding cassette homology
C;Keywords: ATP; P-loop
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- Caenorhabditis elegans
                                                                                                                                     R;Wilkinson, J.
submitted to the EMBL Data Library, April 1996
A;Reference number: 219397
A;Accession: T21261
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-454 <WIL>
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Pred. No. 57;
0; Mismatches
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A;Introns: 62/3; 92/2; 190/3; 266/3; 291/3; 412/3
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
       hypothetical protein F22D6.12
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A. Accession: A49661.
A. Status: preliminary
A. Molecule type: mRMA; protein
A. Molecule type: mRMA; protein
A. Molecule type: mRMA;
A. Molecule type: mRMA;
A. Cross-references: GB:D16478; NID:9510107; PIDN:BAA03939.1; PID:9510108
A. Experimental source: Wistar, liver
A. Note: sequence extracted from NCBI backbone (NCBIN:140844, NCBIP:140846)
C. Complex: heterooctamer of 4 alpha and 4 beta chains
C. Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA (S. Superfamily: enoyl-CoA hydratase homology cECA-starbon-oxyagen lyase; fatty acid beta oxidation; heterooctamer; hydro-lyas F: 361-840/Domain: anyl-CoA hydratase homology cECA-starbon-oxyacyl-CoA hydratase homology cECA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxyacyl-COA-starbon-oxya
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F;499-690/Domain: ATP-binding cassette homology <ABC>F;516-523/Region: nucleotide-binding motif A (P-loop)
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iive 4; Mismatches
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A;Reference number: A49681; MUID:94075334
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Amino acid sequenc

Enoyl CoA hydrase Human glypican 5 p Human GPC5 protein Human GPC5 protein

Human transport-as Gastrin-binding pr Human kidney calci Soybean Padi homol

sed

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Database

Minimum DB Maximum DB

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

homo1

Calcium sensor pro Wheat Type I gluta Low density lipopr

Peptide comprising Human calcium sens

PHA depolymerase. Z. mays Padl Soybean Padl

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Carcinoembryonic antigen; CEA; human; agonist; antagonist; fimmune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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2.827 Million cell updates/sec
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Peptide agonists and antagonists of carcinoembryonal antigen

Score

Result Š 262437

Claim 5; Page 53; 72pp; English

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                     The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and
             peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                         Gaps
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Pred. No. 2.1e+05;
0; Mismatches 0;
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generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes peptides (A) that comprise agonists (Ia)
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1; Mismatches 0; Indels
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barzaga E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                   Query Match
                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                    Y09528;
                                                                                                                                     Best Loca
Matches
                                                                                                                                                                                                                                                                                    Y09528
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W39723;

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RESULT

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The peptide epitope W77119-W77138 were created for human tumour-specific cytotoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific firmunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disease specific immunogen - comprises disease specific cytotoxic \tau lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antiqen; HLA; tumour associated antiqen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                              tyrosinase cytotoxic lymphocyte response; lymphocyte; cysteine-depleted; melanoma.
                                                                                                                                                                                                                                                                                                                                                                                                  Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 19;
Pred. No. 2.1e+05;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                    Hunt DF, Kittlesen D,
                                                                                                                                                                                                                                                                                                                                                             (UYVI-) UNIV VIRGINIA PATENT FOUND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 27; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.4%; Scc. 77.8%; Pred 2;
                                                                          CEA synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                       97US-0037781.
                                                                                                                                                                                                                                                                                    98WO-US01592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Trees 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-437388/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YLSGADINL 9
                                                                                                                                                                                                                                                                                                                                                                                                  Engelhard VH,
                                                                                                                                                                                                         WO9833810-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                Tyrosinase;
cytotoxic T
                                                                                                                                                                                                                                                                                                                       30-JAN-1997;
                                     16-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-OCT-1998
                                                                                                                                                                                                                                              06-AUG-1998
                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epitope
W77134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptides W39430-W39734 are used in a novel method for the selection of immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukcoyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral fammune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A21.
                                                                                                                                                                                                                                                                              T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method of selecting T cell peptide epitope(s) - by measuring the stability of HLA class I-peptide complexes on intact B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Der Burg SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                              Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18; Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.1e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Offringa R, Toes REM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38; DB 1
Pred. No. 2.1e+
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCI SEED CAPITAL INVESTMENTS BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 85; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W77134 standard; peptide; 9 AA.
                                                                                                                                W39723 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-NL00229.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96EP-0203670.
96EP-0201145.
                                                                                                                                                                                                       11-JUN-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melief CJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-549891/50.
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Best Local Similarity
Matches 7; Conserv
6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA;
                 1 YLSGADINL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YLSGADINL
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| ylsganini
                                                                                                                                                                                                                                                                                                                                                                                                WO9741440-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-DEC-1996;
26-APR-1996;
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        06-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kast WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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RESULT

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Gaps

Example 6; Page 75; 104pp; English.

presenting cells

Sette A, Sidney J,

Celis E,

WPI; 1998-437445/37

(EPIM-) EPIMMUNE INC.

98WO-US01959 97US-0036696

30-JAN-1998; 31-JAN-1997;

06-AUG-1998

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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukcoyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes CPC) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and care particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunosehic peptides are also useful
                                                                                                                                                                                                                                                                                                                        immunogenic peptides with HLA binding motif, useful in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen; CEA; human; agonist; antagonist; mimmune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                  Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                  Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84.4%; Score 38; DB 20; 77.8%; Pred. No. 2.1e+05; iive 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen peptide agonist CAP-1.
                                                                                                                                                                                                                                                                                                                                                 and diagnosis of cancers and viral diseases
                                                                                                                                                                                                               Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 118; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y09525 standard; peptide; 9 AA.
                                                                                                                                                                                                               Sette A, Kubo RT, Sidney J,
                                                       98WO-US05039
                                                                                                      98WO-US05039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 77.0.
7: Conservative
                                                                                                                                                           (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                 WPI; 1999-551214/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||||||::||
| ylsqanlnl
                                                    13-MAR-1998;
                                                                                                      13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y09525;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y09525
òλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human leukcoyte antigen (HAA). HAA-A2.1 and are used to exemplify the method control for invention of producing antigen-specific cytotoxic T cells (CTLS) in vitro. The method comprises contacting immunogenic peptides from an control for the binds class I major histocompatibility complex (MHC) antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCS) pretreatment growth factors, and incubating the APCS with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen specific CTLS. A method for specifically killing target cells in a human patient is also previded which comprises contacting the cytocoxic T cells with APCS pretreated with pre-treatment growth factors, where the APCS comprise class I MHC molecules. The pretreated APCS are incubated with the cytotoxic growth factors, thereby producing activated CTLS where the APCS comprise class I MHC molecules. The pretreated CTLS where the activated composition can then be administered to the patient. The activated composition and then be administered to the patient. The activated composition be used for treating cancers, immune disorders, viral infections, and the contacted with funded infection, funded in the contacted composition malaria or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                             Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84.4%; Score 38; DB 19; Length 9; 77.8%; Pred. No. 2.1e+05; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                               Tsai V;
                                                                                                                                                                                                            Southwood S,
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0

Gaps

Y47655 standard; Peptide; 9 AA.

RESULT 7 Y47655

Query Match 84.4 Best Local Similarity 77.8 Matches 7; Conservative

9 AA;

Sequence

uberculosis.

||||||::|| | ylsganln| 9 1 YLSGADINL 9

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Óγ

01-DEC-1999 (first entry)

vaccine; immunisation.

Homo sapiens W09945954-A1

Synthetic

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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes the antigen from which the peptide is derived. Thyphocytes (CTLS) which destroy antigen bearing cells are response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighthing viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or landividuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The charactering as a mannical and a patient of the and an analysis of the contacting a mannical and a patient of the and an analysis of the charactering as a mannical and a patient of the and an analysis of the contacting a mannical and an analysis of the contacting a mannical and an analysis of the contacting and the immunogent of peptides are also useful
     immunogenic peptides with HLA binding motif, useful in treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunoglobulin; therapeutic; streptokinase; vaccine; 708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing immunogenicity of proteins - by modifying the amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 20; Length 10;
Pred. No. 0.041;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapeutically and for immunisation as above.
                         and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein sequence of vaccine 2 708 VI.
                                                                    Claim 1; Page 76; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W86133 standard; Protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.48;
77.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0007751.
97GB-0010480.
97GB-0016197.
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97US-0067235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-045301/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YLSGADINL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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02-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-1997
31-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                               The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide having a human leukocyte antigen binding motif #1166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytocoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                          Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1e+05;
ches 0; Indels
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                                                                                          (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                          Schlom J, Zaremba S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y46555 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                          Claim 1; Page 53; 72pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sette A, Kubo RT, Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.48;
77.88;
98WO-US19794
                                               97US-0061589
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; Immunisation
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                                                                                                                                                                                          WPI; 1999-326544/27.
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22-SEP-1998;
                                               10-OCT-1997;
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                                                                                                                                             Barzaga E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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Gaps

178 AA;

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                                                                                                  proteins. The method comprises determining at least part of the amino acid sequence of sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins. e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the protein sequence of vaccine 2 708 VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .CEA fragments can be used in assays to determine the presence and ant. of CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128~\rm kD antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinoembryonic antigen fragments - used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens.
                                                                                       The invention relates to a method for the production of non-immunogenic
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
sequence of the protein to eliminate potential epitopes for T-cells of a given species
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                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 107;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carcinoembryonic antigen; domain III; domain A; domain
                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of carcinoembryonic antigen domain III.
                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 2C
Pred. No. 0.67;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; page 4; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="domain A"
90..178
/note="domain B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P93499 standard; protein; 178 AA.
                                                        77pp; English
                                                                                                                                                                                                                                                                                                                                                    84.48;
77.88;
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8'
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                                                      Example 4; Fig 19;
                                                                                                                                                                                                                                                                                                         107 AA;
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89 ylsganini 97
                                                                                                                                                                                                                                                                                                                                                                                                                1 YLSGADINL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CITY ) CITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAY-1989;
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                                                                                                                                                                                                                                                                                                          Sequence
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                                              Gaps
                                                                                                                                                                                                                                                                                     Primer; amplify; polymerse chain reaction; PCR; human; blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CER; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
                                            ;
              Length 178;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stewart LMD;
                                           ó
                DB 10;
                                                                                                                                                                                                                                                         BGP (1-314)/CEA (490-643) chimaeric protein.
                             Pred. No. 1.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Snary D,
                Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "CEA (490-643)"
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315..468
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                                                                                                                                                                       R77436 standard; Protein; 468 AA.
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              84.48;
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                                                                                                                                                                                                                              (first entry)
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Query Match
Best Local Similarity 77.8.
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                                                                                       107 ylsganini 115
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                                                                     1 YLSGADINL
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                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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R77436
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ed. No. 4; Mismatches

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Best Local Similarity 77.8
Matches 7; Conservative
                                                                  1 YLSGADINL
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Young S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
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                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; amplify; polymerse chain reaction; PCR; human;
blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimaeric protein; PRLA3 epitope; anti-PRLA3 antibody;
colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
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                     Score 38; DB 16; Length 468;
Pred. No. 3.8;
                                                                  Indels
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                                                                  2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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315..493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                      R77435 standard; Protein; 493 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Durbin H,
                84.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-GB01816
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Query Match
Best Local Similarity 77.07
Best Local 7; Conservative
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| 396 ||Sganln| 404
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Length 493;

DB 16;

84.4%; Score 38;

Query Match

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The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membranebound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRAM3 epitope. The PRAM3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRAM3 antibodies indicating that the PRAM3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRAM3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific FRAM3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                       Primer; amplify; polymerse chain reaction; PCR; human; blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimmeric protein; PRLA3 epitope; anti-PRLA3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
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                                                                                                                                                                                                       BGP (1-314)/CEA (490-644)/BGP (391-430) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart LMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durbin H, Snary D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   "CEA (490-644)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "BGP (391-430)"
                                                                                                                                                                                                                                                                                                                                                                                                 /note= "BGP (1-314)"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                               R77437 standard; Protein; 509 AA.
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                                                                                                                                                                      (first entry)
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396 ylsganln| 404
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                    Gaps
                                                                                                                                                                                                                                                                                         Primer; amplify; polymerse chain reaction; PCR; human;
blilary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimmeric protein; PRLA3 epitope; anti-PRLA3 antibody;
colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in R77435-38 are chimaeric proteins comprising
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Pred. No. 4.2;
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468.511
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/note= "BGP (1-314)"
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77.88;
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                                                                                                                                                                                                                          19-JAN-1996 (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
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DB 16; Length 511;

84.48; Score 38;

Query Match

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77.8%; Pred. No. 4.2; tive 2; Mismatches
                                                                                                                                             Search completed: December 16, 2000, 00:51:14 Job time: 18774 sec
Best Local Similarity 77.8
Matches 7; Conservative
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Q1-FEB-1997 (
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05883 methanococc
06348 ratus norv
98725 saccharcomyc
09umc7 homo sapien
09u156 homo sapien
09x3k1 prochloroco
066807 echovirus 2
P82079 limnodynast
09ps69 gallus gall
09ps69 gallus gall
09ps79 limnodynast
095954 artus mori
044001 aeromonas e
044468 aeromonas v
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              297973 seqs, 93374136 residues
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                                                                                                                                      December 16, 2000, 04:22:12
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Listing first 75 summaries
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33,3%;
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                                   SEQUENCE 7 AA; 758 MW;
                                                                   Query Match 33.3
Best Local Similarity 33.3
Matches 2; Conservative
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Matches 3; Conserv
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2 IRGGDL 7
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MEDLINE; 85230552.

Bollschweller C., Kuehn R., Klein A.;

Bollschweller C. Ar-rich sequences are found in intergenic regions of Methanococcus voltae DNA.";

MEMBO J. 4:805-809(1985).

EMBL; X02518; CAA26355.1; -.

BONLTER

SEQUENCE 9 AA; 1087 MW; 99ED005DC404405A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE; 9(198747.
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
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0. 3e+05;
0; Indels
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                                                                                                                                                    2; Indels
                                                                                                                            Score 16; DB 5; Length 8;
Pred. No. 3e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
INTERGENIC AT-RELH DNA SEQUENCE (FRAGMENT).
Methanococcus voltae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TR4-NS ORPHAN RECEPTOR (FRAGMENT).
                                                                                            SEQUENCE 8 AA; 878 MW; F4C6C2CAAB187B16 CRC64;
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33.3%;
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Best Local Similarity
Matches 2; Conserv
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Matches 3; Conserv
            MEDLINE; 96182101.
SEQUENCE FROM N.A.
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1 MEGEDV 6
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2 DIN 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Wedler H., Wedler H., Wedler E., Scharfe M., Wambutt R.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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672AA87864005350 CRC64;
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                                                                      Score 15; DB 11;
Pred. No. 3e+05;
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"Isolation and characterisation of human ge
cytosolic serine hydroxymethyltransferase."
Bliochem. Soc. Trans. 25:53-53(1997).
EMBL; Y14492; CAB54844.1; -..
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Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from
the banjo frogs Limnodynastes interioras, Limnodynastes dumerilli and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limnodynastes interioris (Giant banjo frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
Enterovirus.
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                                                                                                                                                                                                                                   Bailly J.L., Borman A.M., Peigue-Lafeuille H., Kean K.M.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases. EMBL; X90724; CAA62259.1; -.
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Last annotation update)
                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
5'UTR IN IRES SEQUENCES (ISOLATE TH222) (FRAGMENT).
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SEQUENCE 8 AA; 729 MW; 7C28772865B72728 CRC64;
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA.
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Aust. J. Chem. 46:833-842(1993).
-!- MASS SPECTROMETRY: MW=729; METHOD=FAB.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAY-2000 (TrEMBLrel. 13, Last seno
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Q9PS69;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 40.0.
اتامع 2; Conservative
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Best Local Similarity
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2 GAQVS 6
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09PS69
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Stream.";
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                                                                                                                                                                                                                                                                                                                             "Two novel mutations in Thai patients with hereditary methemoglobinemia types I and II: a subtle amino acid change causes instability of NADH-cytochrome b5 reductase."; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL, AF061830; AAF06818.1; ...
                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
Prochlorococcus.
                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT).
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                             1; Indels
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  Length
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOCHROME B (FRAGMENT).
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888 MW; 76C5B73B5051F6D8 CRC64;
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Score 15; DB 4;
Pred. No. 3e+05;
2; Mismatches
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"Genetic diversity in Prochlorococcus isorted from the Sargasso Sea and Gulf: Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070193; AAD23233.1; -.
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                           5;
33.3%;
50.0%;
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                                                      4 GADINL 9
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1 GSDNHL 6
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09UL56;
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Gaps

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Indels

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Plummer N.W., McBurney M.W., Meisler M.H.;
"Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24408-24015(1997).
EMBL; U97672; AAB80914.1;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                     MEDLINE: 92250478.

Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;

"A calcyclin-associated protein is a newly identified member of the Ca2+/phospholipid-binding proteins, annexin family.";

J. Biol. Chem. 267:8919-8924(1992).

SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TTEMBLEEL. 05, Last sequence update)
01-NOV-1999 (TTEMBLEEL. 12, Last annotation update)
SODIUM CHANNEL, VOLTAGE-GATED, TYPE VIII, ALPHA POLYPEPTIDE
(TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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MEDLINE; 96198747.
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31.1%; Score 14; DB 11; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
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     Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
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(TrEMBLrel. 08, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                            9 AA.
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Best Local Similarity 100.
Matches 3; Conservative
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SEQUENCE FROM N.A.
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NON_TER 1
SEQUENCE 9 AA
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01-NOV-1998
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"Identification of a prothoracicostatic peptide (PTSP) from the larval
brain of the silkworm, Bombyx mori.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 0:0-0(1999).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALCYCLIN-ASSOCIATED PROTEIN, CAP50=CA2+/PHOSPHOLIPID-BINDING PROTEIN
L-7 FRAGMENT.
                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                           Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J., Schneider W.J.;

"The laying hen expresses two different low density lipoprotein receptor-related proteins.";
J. Biol. Chem. 266:19079-19087(1991).

SEQUENCE 8 AA: 846 MW; C007272DD865BAAA CRC64;
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Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Bombycoidea; Bombycidae; Bombyx.
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"Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-MAY-2000 (TrEMBLrel. 13, Last annotation update) LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PROTHORACICOSTATIC PEPTIDE (PTSP).
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3878C5B4472AB6C3 CRC64;
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches 0
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ilarity 66.7%;
Conservative
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9 AA; 1090 MW;
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
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SGA 5
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 1306-83) (FRAGMENT).
                                             Karlyshev A.V., Macintyre S.;
"Study of the intergenic exeF-exeG region and its application as a simple preliminary test for Aeromonas spp.";
EMBL Microbiol. Lett. 137:37-44(1996).
EMBL; X89468; CAA61651.1: -.
NON_TER 1 1 1 1. -.
SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;
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STRAIN=CDC 1306-83;

MEDLINE, 97089747.

Karlyshev A.V., Macintyre S.;

Study of the intergenic exef-exeG region and its application as simple preliminary test for Aeromonas spp.";

FEMS Microbiol. Lett. 137:37-44(1996).

BMBL; X89457; CAA61629.1; -.

NON_TER 1 SEQUENCE 9 AA; 1059 MW; 785852C69444472B CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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Pred. No. 3e+05;
1; Mismatches 0; Indels
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043928; 043918; 043920; 043921;
01.NOV-1996 (TEMBLrel. 01, Created)
01.NOV-1996 (TEMBLrel. 01, Last sequence update)
01.NOV-1998 (TEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (FRAGMENT).
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Pred. No. 3e+05;
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66.7%;
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STRAIN-VARIOUS STRAINS;
MEDLINE; 97089747.
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
    SEQUENCE FROM N.A. STRAIN-ATCC 49659; MEDLINE; 97089747.
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Q44468;
Q1-NOV-1996 (
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7 VNL 9
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7 VNL 9
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Q44468
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Q43928
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Detera-Wadleigh S.D.; "Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEC INTERGENIC REGION (STRAIN CDC 9179-79) (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN ATCC 49659) (FRAGMENT).
                                                                                                                      Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.; "New variants of the human and rat nuclear hormone receptor, TR4: expression and chromosomal localization of the human gene.";
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"Study of the intergenic exeF-exeG region and its application as simple preliminary test for Aeromonas Spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89461; CAA61637.1;
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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                                                                                                                                                                                                                                                                                            2; Indels
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Pred. No. 3e+05;
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                                                            Endocrinology 137:1562-1571(1996).
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66.7%;
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40.0%;
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Best Local Similarity 40.0
Matches 2; Conservative
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STRAIN-CDC 9179-79;
MEDLINE; 97089747.
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Matches 2; Conserv
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SEQUENCE FROM N.A.
MFNI, INE; 96299786.
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ICGGD 6
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01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
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SEQUENCE
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Query Match
Best Local Similarity 33.30,
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Best Local Similarity 50.0%,
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EMBL; S74094; AAD14973.2;
NON_TER 1
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SEQUENCE FROM N.A.
TISSUE=BONE MARROW;
MEDLINE; 95002916.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                TISSUE=PLACENTA;
                                                                                                           2 LSGADI 7
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1 MAGPSI 6
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2 FLPG 5
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SEQUENCE
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Q15901
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                                                                                                                                                                                                                                                                                                                                                                               of
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 95180691.

Rosenow C., Roberts I.S., Jann K.;

Rosenow C., Roberts I.S., Jann K.;

"Isolation from recombinant Escherichia coli and characterization of the synthetase, involved in the expression of the capsular K5 polysaccharide (K-CKS)."

FEMS Microbiol. Lett., 125:159-164(1995).

EMBL; $76943; CAB33515.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viruses; Retroid viruses; Retroviridae; Avian type C retroviruses
                                                                                                                                                                                                                                                                                                     Plasmid pCR3.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
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                                                                                                           Length 9;
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                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
                                                                         9 AA; 1059 MW; 785852C69444472B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA; 899 MW; 3EBBB72042C33DD8 CRC64;
                                                                                                                             0
                                                                                                       Score 13; DB 2;
Pred. No. 3e+05;
1; Mismatches
Simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89462; CAAG1643.1; -.
EMBL; X89460; CAAG1639.1; -.
EMBL; X89460; CAAG1635.1; -.
EMBL; X89460; CAAG1635.1; -.
EMBL; X89460; CAAG1641.1; -.
SEQUENCE 9 AA; 1059 MW; 785852C69444472B
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                                                                                                      Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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Matches 3; Conservative
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STRAIN-PRAGUE C;
MEDLINE; 93010967.
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2 GAKVIL 7
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7 VNL 9
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NON_TER
SEQUENCE
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Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Lee C.C., Zazdani A., Wehnert M., Baldini A., Lindsay E.A., Zhao Z.Y.,
Caskey C.T.H.;
Hum. Mol. Genet. 0:0-0(0).
EMBL; L32080; AAA73891.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tighe J.E., Calabi F.; "Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia M2.";
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
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Last annotation update)
EMBL; X67587; CAA47862.1; -.
Hypothetical protein. 7
7 SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;
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Pred. No. 3e+05;
2; Mismatches 2;
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33.3%;
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[1]
SEQUENCE FROM N.A.
MEDLINE; 92040090.
Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
"Functional and structural mapping of Chlamydia trachomatis species-
specific major outer membrane protein epitopes by use of neutralizing
                                                                                                                                      MYOGLOBIN (FRAGMENT).
Manorina melanocephala (noisy miner).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.
                                                                                                                                                                                                                       MEDLINE: 98208049.

MEDLINE: 98208049.

Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;

"Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis.";

Electrophoresis 19:142-151(1998).

EMBL; U40497; AAC60364.1; -.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN VARIABLE DOMAIN IV, MOMP VD IV.
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Last annotation update)
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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01-NOV-1996 (TrEMBLrel. 01, Created)
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Infect. Immun. 59:4147-4153(1991)
SEQUENCE 9 AA; 976 MW: 9c61BA.
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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3 ISG 5
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MEDLINE: 98208049.
Heslewood M.m., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
Hyoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                        Gaps
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Erythrura gouldiae (Gouldian finch).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeridae; Erythrura.
                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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       Score 12; DB 4; Length 8; Pred. No. 3e+05;
                                       Indels
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Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
Mol. Immunol. 0:0-0(0).
EMBL; U62585; AAB18735.1; -.
                                                                                                                                                    8 AA.
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50.0%;
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66.7%;
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milarity 66.7%;
Conservative
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Best Local Similarity 66.7
Matches 2; Conservative
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Query Match
Best Local Similarity
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01-FEB-1997
01-AUG-1998
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4 YSTG 7
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SEQUENCE
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Erickson J.W., Cline T.W.; "Key aspects of the primary sex determination mechanism are conserved across the genus Drosophila"; Development 125:3259-3268(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93387464.
Vidal H., Crepin K.M., Rider M.H., Hue L., Rousseau G.G.;
"Cloning and expression of novel isoforms of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase from bovine heart.";
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                            SEQUENCE FROM N.A.
Bell M., Cline T.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF046045; AAC97605.1; -.
                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. EMBL; L77326; AAA96415.1; SEQUENCE 9 AA, 931 MW; 6D5BD2C865B05044 CRC64;
                                                                                                                                                                                                                          Length
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                9A8BD1AAA9C449CA CRC64;
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Pred. No. 3e+05;
0; Mismatches
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66.7%;
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Bost Local Similarity 60.,
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Best Local Similarity
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SEQUENCE FROM N.A.
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Bukaryota, Medazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                          Gaps
                                                                                                             SEQUENCE FIGURE 1993.

MEDLINE, 94320083.

Nagalla S.R., Spindel B.R.;

"Functional analysis of the 5'-flanking region of the human gastrin-releasing peptide gene in small cell lung carcinoma cell lines.";

Cancer Res. 54:4461-4467(1994).

EMBL; S73265; AAD14116.1;

"TPE77672B040864 CRC64;
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                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
EMBL, 077631, ADD15626.1;
Hydrolase; Glycosidase.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) HGRP PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
GALACTOCEREBROSIDASE (EC 3.2.1.46) (FRAGMENT).
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Last annotation update)
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Pred. No. 3e+05
1; Mismatches
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Best Local Similarity 66.7%;
Matches 2; Conservative
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                                                       Homo sapiens (Human).
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Best Local Similarity
Matches 2; Conserv
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Clark M.A., Moran N.A., Baumann P.; "Sequence evolution in bacterial endosymbionts having extreme base
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                                                             Weber P.C., Palchaudhuri S.;
"Incompatibility repressor in a Repa-like replicon of the IncFI
plasmid Colv2-K94.";
J. Bacteriol. 166:1106-1112(1986).
EMBL; M13472; AAA23194.1; -.
                                                                                                                                                                                                                                                                                                                   Indels
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OFRO49;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NIFS PROTEIN HOMOLOG (FRAGMENT).
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U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
NIFS PROTEIN HOMOLOG (FRAGMENT).
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8 AA; 998 MW; 0F37205AA73416D7 CRC64;
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3e+05;
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EMBL; AF130814; AAF13805.1; -.
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EMBL; AF130812; AAF13797.1; -.
NON_TER 8
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50.0%;
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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    [1]
SEQUENCE FROM N.A.
MEDLINE; 86223772
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SEQUENCE
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| YL 7
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Q9RQ57;
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Q9RQ57
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Enjuanes L.;
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MEDLINE; 95159435.
Bleouet J., Rasschart D., Lambert P., Levy L., Vende P., Laude H.;
"Complete sequence (20 kilobases) of the polyprotein-encoding gene 1 of transmissible gastroenteritis virus.";
Virology 206:817-822(1995).
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MEDLINE; 88078100.
Rasschaert D., Gelfi J., Laude H.;
Rasschaert Coronavirus TGEV: partial sequence of the genomic RNA, its
                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL FUSION PROTEIN.
HYPOTHETICAL Transmissible gastroenteritis virus.
Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
coronaviridae; Coronavirus.
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Escherichia.
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Last annotation update)
                                                                859CA5BDC7644865 CRC64;
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                                                                                                                           Score 12; DB 6;
Pred. No. 3e+05;
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Biochimie 69:591-600(1887).
EMBL, AJ011482; CAA09625-1;
SEQUENCE 7 AA; 927 AW;
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051594;
015094;
01-NOV-1996 (TrEMBLEEL 01, C.
01-NOV-1999 (TrEMBLEEL 10, L.
01-MAY-1999 (TrEMBLEEL 10, L.
COPB PROTEIN (FRAGMENT).
Escherichia coli.
FEBS Lett, 330:329-333(1993).
EMBL, X74564; CAA52652.1; -.
NON, TER
SEQUENCE 9 AA; 837 MW; 85
                                                                                                                       26.7%;
llarity 66.7%;
Conservative
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Matches 2; Conserv
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Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Craig R.A., Clewell D.B.;
"Isolation and structure of bacterial sex pheromone, CPDI.";
Science 225:849-850(1984).
-1- FUNCTION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF BACTERIOCIN PLASMID PPDI.
 P41495
P811351
P811351
P811806
P811807
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P02731
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Pred. No. 8.8e+04;
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ALL4_CARMA
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AL12_CARMA
AL17_CARMA
ALL7_CARMA
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Copyright (c) 1993 - 2000 Compugen Ltd
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A CALEAR R., Chauvet J., Chauvet M.-T., Crepy D.;
A CALEAR R., Chauvet J., Chauvet M.-T., Crepy D.;
The carp (Cyprius carpio). Comparison with hormones from sea water bony fish, the carp (Cyprius carpio). Comparison with hormones from sea water bony fishs.";
Comp. Biochem. Physiol. 14:245-254(1965).
Comp. Biochem. P
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Wararyota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinis.
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01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
LEUCOKININ VIII (L-VIII).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Plerygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
 Indels
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8 AA; 902 MW; 736365AB59CAADD8 CRC64;
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                                                 FLSG
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                                1 YLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
SEQUENCE
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                                                                                                            RESULT 2
LCK8_LEUMA
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pollen coat of Brassica napus.";
Planta 208:588-598(1999).
-!- FUNCTION: MAY PLAY & STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-
SPECIFIC PLASTIDIAL LIPID ORGANELLE.
-!- TISSUE SPECIFICITY: TAPETUM OF ANTHERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFWREFAUIDE 6.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycery a; Muscomorpha;
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly calliphora vomitoria.", Proc. Natl. Acad. Sci. U.S. A. 89:2326-2330(1992).
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MEDLINE; 99349136.
Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-THORACIC GANGLION;
BUDDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;
                                                                                                                         Score 16; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; Score 15; DB 1; Length 8; 66.7%; Pred. No. 8.8e+04; Live 1; Mismatches 0; Indels
9 AMIDATION.
969 MW; 17FF476EB455B04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PLASTIDIAL LIPID-ASSOCIATED PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 AA.
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Gaps

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Appl. Environ. Microbiol. 58:1417-1422(1992).
-!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBIOTIC (LANTIBIOTIC).
ACTIVE ON GRAM-POSITIVE BACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 92321768.
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nes I.F.,; ^{\mathrm{Purification}} and characterization of a new bacteriocin isolated from
-!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBOESOPHAGEAL GANGLION.
PIN; A60065; AKLQIM.
Amidation; Neuropeptide.
9 AMIDATION.
SEQUENCE 9 AA; 1060 MW; 387D7DD4472AB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
LANTIBLOTIC CARNOCIN U149 (FRAGMENT).
Carnobacterium sp. (strain U149).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae; Carnobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE, 77185324.

Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J., Schoenenberger G.A.;

Schoenenberger G.A.;

"The delta sleep inducing peptide (DSIP). Comparative properties of the original and synthetic nonapeptide.";

Experientia 33:548-552(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                            Score 14; DB 1; Length 9;
Pred. No. 8.8e+04;
.; Mismatches 0; Indels
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21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DELTA SLEEP-INDUCING PEPTIDE (DSIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA.
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50.0%;
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66.7%;
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                                                                                                                                                                     Query Match
Best Local Similarity
Thes 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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| GSEI 4
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P01158;
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P36960;
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SEQUENCE
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4 DLN
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DSIP_RABIT
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LANC_CARUI
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MEDLINE; 92179466.
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
Isolation, identification and synthesis of locustamyoinhibiting
peptide (LOM-MIP), a novel biologically active neuropeptide from
Locusta migratoria.";
Regul. Pept. 36:111-119(1991).
-:- FUNCTION: SUPPRESSES SPONTANEOUS CONTRACTIONS OF THE HINDGUT AND
OVIDUCT.
                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cydia pomonella (Codling moth).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D., Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides of the allatostatin superfamily.";

Peptides 18:1301-1309(1997).

-: SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
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Bukaryota, Metazoa, Arthropoda; Tracheata, Hexapoda; Insecta;
Pterygota, Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3: Indels
                                                                                                                                                                                                                     1; Indels
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                                                                                                                                                                       Length 9;
                                                                         AMIDATION.
96D10699CAB6D865 CRC64;
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8 AA; 898 MW; 922879CABB58640D CRC64;
                                                                                                                                                                     Score 15; DB 1; I
Pred. No. 8.8e+04;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 14; DB 1; I
Pred. No. 8.8e+04;
0; Mismatches 3;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUC-1993 (Rel. 27, Last annotation update)
LOCUSTAMYOINHIBITING PEPTIDE (LOM-MIP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA.
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50.0%;
                                                                                                                                                                  33.3%;
ilarity 75.0%;
Conservative
                                                                       MOD_RES 9 9 SEQUENCE 9 AA; 1058 MW;
                                                Neuropeptide; Amidation.
MOD_RES 9 9
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MOD_RES 8 8
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  FAMILY.
PIR; F41978; F41978.
                                                                                                                                                                  Query Match
Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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2 SGQD 5
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P31799;
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P82156;
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ALLS_CYDPO
AC P82156;
DT 30-MAY.
DT 30-MAY.
DF CYDIAS;
OC CYDIAS;
OC CYDIAS;
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RN FR SEQUENC
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- FUNCTION: ACTURS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED IN VARIOUS TYPES OF CELL MOTILITY AND ARE UBIQUITOUSLY EXPRESSED IN ALL EUKARYOTIC CELLS.
- SUBCELLULAR LOCATION: CYTOPLASMIC.
- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS: 6.8, ITS MW IS: 46 KDA.
- SIMILARITY: BELONGS TO THE ACTIN FAMILY.
                             SEQUENCE.
MEDLINE; 66123415.
ACHEL R., Chauvet J., Chauvet M.-T., Crepy D.;
Phylogeny of neurophyophyseal peptides: isolation of a new hormone, glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish, the ray (Raia clavata).";
Biochim. Biophys. Acta 107:393-396(1965).
-I-FONCTION: ANTIDIORETIC HORMONE.
-I-SIMILARITY: BELDINGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lachaise F., Somme G., Carpentier G., Granjeon E., Webster S., Bapdidassarian D.;
"A transaldolase. An enzyme implicated in crab steroidogenesis.";
Endocrine 5:23-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                               28.9%; Score 13; DB 1; Length 9; 66.7%; Pred. No. 8.8e+04; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.7%; Score 12; DB 1; Length 8; 25.0%; Pred. No. 8.8e+04; Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                             9 AA; 984 MW; 17E9C76EB455B04B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AA.
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PROSITE; PS00432; ACTINS_2; PARTIAL.
PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.
                                                                                                                                                                                            PFAM, PF00220; hormone4, 1.
PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                  AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
Rajiformes; Rajidae; Raja.
                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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Best Local Similarity
'-has 1; Conserve
                                                                                                                                                                                                                                Hormone; Amidation.
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2 YIS 4
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                                                                                                                                                                                                                                                               MOD_RES
SEQUENCE
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DVDI
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P80709;
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SEQUENCE
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-i-SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                             OF
ELECTRIC
     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D., Garrison R.D., Williams J.F., Friedman A.R.;
"Two FMRFamide-like peptides from the free-living nematode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raja clavata (Thornback ray).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
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0
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Pred. No. 8.8e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 13; DB 1; Length 9;
Pred. No. 8.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Panagrellus redivivus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Panagrolaimoidea; Panagrolaimidae; Panagrellus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DA0B0729C4576AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF2 (SADPNFLRF-AMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA.
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                                                                                                                                                                                                                                         28.9%;
50.0%;
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Similarity 75.0%;
3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 9 AA; 1066 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panagrellus redivivus, ";
Peptides 13:209-214(1992).
-! FUNCTION: MYOACTIVE.
                                                                                                                                                                                                                                       Query Match 28.99
Best Local Similarity 50.09
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 93027659.
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Matches 3; Conserv
                                                                                                                                                                                                                                                                                                        3 SGAD 6
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2 AGGD !
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P42994;
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Query Match 26.7'
Best Local Similarity 50.0
Matches 2; Conservative
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                                                                                                          STANDARD;
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Best Local Similarity
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                                      3 SGAD 6
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                                                                                                        OXYA_SCYCA
P42996;
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SEQUENCE
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Matches
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Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                           AND THE RELEASE OF PANCHEATIC ENZYMES IN THE GUT. ITS FUNCTION
IN THE BRAIN IS NOT CLEAR.
-1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
PIR; A43001; A43001.
PIR; PO0012.
PIR; PO0012.
PROSITE; PS00259; GASTRIN; 1.
Amidation; Sulfatation; Hormone.
                                                                           Macropus eugenii (Tammar wallaby), and sayvusa vivertinus (Southeastern quoll). Eusayvota: Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 88234141.
Fan Z.W., Eng J., Shaw G., Yalow R.S.;
"Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                 Score 12; DB 1; Length 8; Pred. No. 8.8e+04; 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                           AMIDATION.
DDCAA68378768B5A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFWRFAMIDE 13.
                           01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-CCT-1996 (Rel. 34, Last annotation update)
CHOLECYSTOKININ (CCK).
           8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AA
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           PRT;
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9 AA; 1028 MW;
                                                                                                                                                                                                                                                                                                    8 AA; 1064 MW;
                                                                                                                                                                                 Peptides 9:429-431(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neuropeptide; Amidation.
MOD_RES 9 9
SEQUENCE 9 AA; 1028 MW
                                                                                                                                                                                                                                                                                                                                                     Conservative
           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2; Conserv
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|2 YMGWMD 7
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                                                                                                                          SEQUENCE.
TISSUE-BRAIN;
          CCKN_MACEU P30369;
                                                                                                                                                                                                                                                                                                                                                                                                                                          FARD_CALVO
P41868;
                                                                                                                                                                           marsupials
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SEQUENCE.
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CCKN_MACEU
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                                         Gaps
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                                                                                                                                                                                                                                                                                                                        Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichtyes;
Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
Scyliorhinidae; Scyliorhinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
SERITOCIN
Bufo regularis (African toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 95062247.

MEDLINE; 95062247.

MEDLINE; 95062247.

"Special evolution of neurohypophysial hormones in cartilaginous fishes: asvatocin and phasvatocin, two oxytocin-like peptides fishes: asvatocin the spotted dogfish (Scyllorhinus cantculus):"; proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).

"FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTENUS.
                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY. INTERPRO; IPR000981; -. PFAM: PF00220; hormone4; 1. PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1. HORMONE, Amidation. 6
Score 12; DB 1; Length 9; Pred. No. 8.8e+04; L; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 12; DB 1; Length 9; 14.3%; Pred. No. 8.8e+04; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AMIDATION.
982 MW; 17EDD76EB444404B CRC64;
                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
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 26.7%;
50.0%;
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Gaps

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PGLR_DIAAB

Matches

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"Plasma protein map: an update by microsequencing.";
Electrophoresis 13:707-714(1992).
-- MISCELLANBOUGS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5, ITS MW IS: 48 KDA.
SWISS-2DPAGE; P30092; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 92195954.

Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Evans B.D., Pohl Jo, Kartsonis M.A., Calabrese R.L.;

Identification of RFamide neuropeptides in the medicinal leech.";

Peptides 12:897-908 (1991).

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Limulus polyphemus (Atlantic horseshoe cráb), and Carcinus maenas (Common shore crab) (Green crab). Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Plerygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
   Hughes G.J., Frutiger S., Paquet N., Ravier F., Pasquali C.,
Sanchez J.-C., James R., Tissot J.-D., Bjellqvist B.,
Hochstrasser D.F.;
                                                                                                                                                                                                                                Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 11; DB 1; Length 4; ilarity 100.0%; Pred. No. 8.8e+04; Conservative 0; Mismatches 0; Indels
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SEQUENCE 4 AA; 598 MW; 69D4073B3000000 CRC64;
                                                                                                                                                                               9 AA; 935 MW; 5282F2CAA8676447 CRC64;
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21-JUL-1986 (Rel. 01, Last Sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
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                                                                                                                                                                                                                                  Query Match 26.7%;
Best Local Similarity 33.3%;
Matches 2; Conservative
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Matches 2; Conserv
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P42562;
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NON_TER
SEQUENCE
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FAR3_HIRME
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PRCT_PERAM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 36, Last sequence update)
BUDO-POLYGALACTURONASE (PG) (EC 3.2.1.15) (FRAGMENT).
Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Curculionidae; Entiminae; Entimini; Diaprepes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF PLASMA (SPOT 14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                               4; Indels
                                                                                                                                                           Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA; 1041 MW; 1F49087042DB41BB CRC64;
                                                                                     9 9 AMIDATION.
9 AA; 983 MW; 17FF476EA5A6D04B CRC64;
INTERPRO; IPR000981; -. PF40220; hormone4; 1. PROSITE; PS00264; NEUROHYP_HYS_HORM; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA.
                                                                                                                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                                                                                                                                                         PRT;
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50.0%;
                                                                                                                                                           26.7%;
28.6%;
                                                                                                                                                                                               2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                   Hormone; Amidation.
DISULFID 1
MOD_RES 9
SEQUENCE 9 AA; 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                           Query Match
Best Local Similarity
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4 YVIG 7
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P81179;
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P30092;
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SEOUENCE
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Gaps

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SEQUENCE. SPECIES=P.AMERICANA; MEDLINE; 76074708.

SEQUENCE. TISSUE=PLASMA; MEDLINE; 93092937.

RESULT 18

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UPA6_HUMAN

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us-09-529-121-3.lim9.rsp

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Gaps
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Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.;
Submitted (AUG-1998) to the SWISS-PROT data bank.
I- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
SEX PHEROWONE CAD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN (P35) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                  24.4%; Score 11; DB 1; Length 7; llarity 100.0%; Pred. No. 8.8e+04; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.4%; Score 11; DB 1; Length 7; 100.0%; Pred. No. 8.8e+04; tive 0; Mismatches 0; Indels
                                                                                                                         AMIDATION.
69D4073B5B11E350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                806 MW; 71B5B057273B4700 CRC64;
                                                                                                                                                                                                                                                                                                                                                        7 AA.
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-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
SWISS-ZDPAGE; P99025; MOUSE.
                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                      7 AA; 992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                         Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                       GFRP_MOUSE
ID GFRP_MOUSE
AC P99025;
                                                                                                                         MOD_RES
SEQUENCE
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P13268;
                                                                                           FAMILY
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NON_TER
SEQUENCE
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CAD1_ENTFA
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MEDLINE; 93324431.
Cowden C., Stretton A.O.W.;
Cowden E. Sacaris neuropeptide: isolation, sequence, and bioactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95060998.
Maule A.G., Shaw C., Bowman J.W.;
"The FMRRamide-like neuropeptide AF2 (Ascaris suum) is present in the
Starratt A.N., Brown B.E.; "Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                  SPECIES-P.AMERICANA;
MEDLINE; 81225865.
O'Shea M., Adams M.E.;
"Pentapeptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                            Shabanowitz J.; "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                 SPECIES-L.POLYPHEMUS;
MEDLINE; 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 AA; 649 MW; 71B7673B44600000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.4%; Score 11; DB 1; Le
100.0%; Pred. No. 8.8e+04;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                            Life Sci. 17:1253-1256(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-P. REDIVIVUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 2; Conserv
                                                                         BIOLOGICAL SOURCE
                                                                                                                                                                                                                                                                                                                                                        SPECIES=C.MAENAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuropeptide.
SEQUENCE 5
                               in insects.
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11
2 YL 3
                                                                                                                                                                                  SEQUENCE.
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FAR2_ASCSU
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PIR; E41978; E41978
                                                                                                                                                                      Local Similarity
les 2; Conserv
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Matches 2; Conserv
      TISSUE=STOMACH;
MEDLINE; 92082847.
                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAR7_CALVO S P41862;
01-NOV-1995 (Rel O1-NOV-1995 (Rel O1-NOV-1995 (Rel O1-NOV-1995 (Rel CALLIFMRFAMIDE 7
                                                                                                                                                                                                                                                                    RESULT 26
FAR5_CALVO
ID FAR5_CALVO
                                                                                                                                                                                                          4 GAD 6
                                                                                                                                                                                                                                 4 GOD 6
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                                                                                                              Hormone.
SEQUENCE
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Matches
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                                                                                                                                                                                                                                                                                                                                     Calliphora vomitoria (Blue blowfly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                           Gaps
Mori M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C., Craell D.B., Suzuki A.;

"Isolation and structure of the bacterial sex pheromone, CADI, that induces plasmid transfer in Streptococcus faecalis.";

FEBS Lett. 178:97-100(1984).

-i- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE HEMCLYSIN PLASMID PADA
                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-THORACIC GANGLION;
MEDLINE: 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oll-MAR-1992 (Rel. 21, Created)
Ol-MAR-1992 (Rel. 21, Last sequence update)
Ol-MAR-1992 (Rel. 21, Last sequence update)
Ol-MAR-1992 (Rel. 21, Last annotation update)
GASTRIN/CHOLECYSTOKININININIE PEPTIDE D1.
Nephrops norvegicus (Norway lobster).
Bukaryotta, Metazoa; Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Astacidea;
Nephropoidea; Nephropidae; Nephrops.
                                                                                                                                                       Indels
                                                                                                                                 Score 11; DB 1; Length 8;
Pred. No. 8.8e+04;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 11; DB 1; Length 8; Pred. No. 8.8e+04; 1; Mismatches 0; Indels
                                                                                              8 AA; 819 MW; 047DD732C735B9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72D40699CAA44DD8 CRC64;
                                                                                                                                                                                                                                                                                     01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                 8 AA.
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                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                 24.48;
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66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 AA; 957 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; H41978, H41978.
Neuropeptide; Amidation.
MOD_RES 8
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                            CALLIFMRFAMIDE 8.
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6 LAG 8
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                                                                                    Pheromone.
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P24816;
                                                                                               SEQUENCE
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRFAMIDE 5.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Calliphora vomitoria (Blue blowfly).
Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda, Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae, Calliphora.
                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
MEDLINE; 92082847.
Favrel P., Kegel G., Sedlmeier D., Keller R., van Wormhoudt A.; "Structure and biological activity of crustacean gastrointestinal peptides identified with antibodies to gastrin/cholecystokinin."; Blochimie 73:1233-1239(1991).
-i. FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
-i. SIMILARITY: ERLONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-THORACIC GANGLION;
MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.E., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
Proc. Natl. Acad. SGI. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (EMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                             Score 11; DB 1; Length 9;
Pred. No. 8.8e+04;
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                                                                                                                                                                                                         9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;
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39D10699CAB6D867 CRC64;
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Pred. No. 8.8e+04;
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                        24.4%; Scor.
66.7%; Pred. No. o..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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9 AA; 1068 MW;
                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide; Amidation.
MOD_RES 9 9 9
SEQUENCE 9 AA; 1068 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Indentification of 2 new neurohypophyseal hormones, valitocin (valgoxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
INTERPRO: IPRO00981;
PFAM; PF00220; hormone4; 1.
PROSITE: PS00264: NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDILNE; 73031727.
Acher R., Chauvet J., Chauvet M.-T.;
Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Biochem. 29:12-19(1972).
                         Acher R., Chauvet J., Chauvet M.-T.; "Phylogeny of the neurohypophysial hormones. Two new active peptides "Phylogeny of the neurohypophysial hormones. Two new actilaginous fish, Squalus acanthias."; Eur. J. Blochem. 29:12-19(1972).
                                                                                                           Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
Indentification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
C. R. Acad Sci., D. Sci. Nat. 274:313-316(1972).
I-SIMILARIY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PRAM: PF00220; hormone4; 1.
PROSITE: PS00264: NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                           Score 11; DB 1; Length 9;
Pred. No. 8.8e+04;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24.4%; Score 11; DB 1; Length 9; 14.3%; Pred. No. 8.8e+04; ive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                    9 9 AMIDATION.
9 AA; 996 MW; 17F8376EB444404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 9 AMIDATION.
9 AA; 996 MW; 17EDD76EB456D04B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                              24.4%;
14.3%;
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Best Local Similarity 14.37
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Best Local Similarity 14.3
Matches 1; Conservative
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                                                                                                                                                                                                                                                         Amidation.
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             MEDLINE; 73031727.
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2 YINNCPL 8
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P43000;
                                                                                                                                                                                                                                                                                    MOD_RES
SEQUENCE
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SEQUENCE
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                                                                                                SEQUENCE.
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OXYV_SQUAC
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Squalus acanthias (Spiny dogfish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Buve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Thorpe A.;

"Isolation, Structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly Calliphora vomitoria.";

Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

--- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clypeaster japonicus (Sand dollar).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24.4%; Score 11; DB 1; Length 9; 50.0%; Pred. No. 8.8e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                        Length 9;
                                                                                                                                                                                                 AMIDATION. E1D10699CAB6D86A CRC64;
                                                                                                                                                                                                                                                      Score 11; DB 1; L
Pred. No. 8.8e+04;
); Mismatches 1;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Rel. 17, Last sequence update)
(Rel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                   9 AA.
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                                                                                                                                                                                                                                                        24.48;
66.78;
                                                                                                                                                                                                  9 9
9 AA; 1081 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clypeasteridae; Clypeaster.
                          TISSUE-THORACIC GANGLION;
                                                                                                                                                                                  Neuropeptide; Amidation.
MOD_RES 9 9
SEQUENCE 9 AA; 1081 MW
                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 2; Conservat
                                                                                                                                                                      PIR; G41978; G41978.
                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-EGG JELLY;
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P42999;
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01-FEB-1991
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P19853;
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6 FLIG
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OXYA_SQUAC
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last sequence update)
11-NOV-1995 (Rel. 33, Last annotation update)
TRYPSIN-MODULATING OOSPATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Bukaryota; Metazoa; Anthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
00estroidea; Sarcophagidae; Sarcophaga.
                                                                                                             Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
                                      STRAIN=L2/434/BU;
Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN'1990 (Rel. 13, Created)
01-JAN'1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING EFFILDE II (MIP II).
Mytilus edulis (Blue mussel).
Eukaryota, Metazoa, Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 10; DB 1; Length 6; Pred. No. 8.8e+04;
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                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                         SEQUENCE 5 AA; 474 MW; 75BAA865AA800000 CRC64;
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72C9C6876DD81000 CRC64;
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                                                                                                                                                                                                                                   22.2%; Scor.
100.0%; Pred. No. v...
0; Mismatches
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                                                                                                                                                                                                                                                                                      Conservative
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PIR; B27696; B27696.
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TISSUE=OVARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hormone; Amidation.
                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 2; Conserv
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P13737;
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SEQUENCE
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     [1]
SEQUENCE.
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- 5
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CIP2_MYTED
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Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata H., Iwashita T., Nomoto K.;

Iwashita T., Nomoto K.;

Crystal structure and molecular conformation of achatin-I

(H-Gly-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
D-amino acid residue. ",

Int. J. Pept. Protein Res. 39:258-264(1992).

--- FUNCTION: NEUROEXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
AND FRODUCES A SPIKE BROADENING OF THE IDEMITIEDE HEART EXCITATORY

NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND PREQUENCY

HEART BEAT. HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.

PIR; A32480; A32480.
                                                                                                                                                                                                                                                               Gastropoda; Pulmonata; Stylommatophora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fujimoto, K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K., Yoshida M., Harada A., Muneoka Y., Kobayashi M.; Purification of achatin-I from the atria of the African giant snail, Achatina fulica, and its possible function."; Biochem. Biophys. Res. Commun. 177:847-853(1991).
                                                                                                                                                                                                                                                                                                                                                                        Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue."; Biochem. Biophys. Res. Commun. 160:1015-1020(1989).
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01-0CT-1994 (Rel. 30, Last sequence update)
030-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARX BODY (FRAGMENT).
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 2 D-PHENYLALANINE.
4 AA; 408 MW; 6AADD9C81000000 CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                4 AA.
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                                                                                                                                                                                                                                                                                                                 SEQUENCE, CHARACTERIZATION, AND SYNTHESIS. STRAIN-FERUSSAC; TISSUE-GANGLION;
                                                                                                                                                                                                                                         Achatina fulica (Giant African snail)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=HEART ATRIUM;
                                                                                                                                                                                                                                                                            Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Mollusca;
                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FERUSSAC; T
MEDLINE, 91264856.
                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 89273551.
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CHARACTERIZATION.
YLSGADI 7
                                 2 YIQNCPV 8
                                                                                                                            ACH1_ACHFU P35904;
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P38005;
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                                                  "Sequencing and characterization of trypsin modulating oostatic factor (TWOF) from the ovaries of the grey fleshfly, Neobellieria (Sarcophaga) bullata.
(Sarcophaga) bullata.
1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS IN THE MIDGUF WHICH INDIRECTLY REDUCES THE VITELLOGENIN CONCEMPRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCTTE DEVELOPMENT.
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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"Two-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806(1998)
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
PROTEIN IS: 5.0, ITS MM IS: 75.9 KDA.
                                                                                                                                                                                                                               -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
UNKNOWN PROTEIN CP 6 FROM 2D-PAGE (FRAGMENT).
Clostridium pasteurianum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
MEDLINE; 94211930.
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
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                                                                                                                                                                                                                                                                                                                                                          Query Match

22.2%; Score 10; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 8.8e+04;
Matches 2; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                 6 AA; 695 MW; 61E72451B7642000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE.
STRAIN=W5;
MEDLINE; 98291870.
                                           de Loof A.;
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P81351;
                                                                                                                                                                                                                                                                                                 SEQUENCE
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Search completed: December 16, 2000, 04:23:31 Job time: 4566 sec

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Mon Dec 18

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chains have few N regions
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copper resistance
20K protein - Rick
proctolin - Atlant
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spinal cord peptid
7-cal receptor be
hypothetical prote
Ig heavy chain CRD
globulin IV alpha
ribosomal protein
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Ig heavy chain CRD
T-cell receptor be
T-cell receptor be
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T.cell receptor be
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calliFMRFamide 8
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: P70542
R;Feeney, A.J.
J. Exp. Med. 174, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: P70509; MUID:91277601
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Experimental source: day 18 fetal thymus, strain BALB/c
Keywords: T-cell receptor
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S29735
PA040128
PA010128
PA010129
PA100701
PA10202
PA10
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A43848
E41978
G41978
A58718
A41117
PT0547
QDRB
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A61386
PH0935
PH0918
A26209
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I51434
S16364
B35890
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ilarity 75.0%;
Conservative
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A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-7 <FEES
A,Experimental source: day 18 fe
C,Keywords: T-cell receptor
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                   Search time 89.11 Seconds (without alignments) 6.409 Million cell updates/sec
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                        4.5
Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                              182106 seqs, 63460219 residues
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                      GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                     December 16, 2000, 03:35:12
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Maximum Match 100%
Listing first 75 summaries
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Gapop 10.0 , Gapext 0.5
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A21440
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1: pir1:*
2: pir2:*
3: pir3:*
3: pir4:*
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Perfect score:
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Gaps

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3; Indels

Length 9;

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C,Accession: PT0540
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A;Feference number: PT0509; MUID:91277601
A;Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hemoglobin alpha chain - human (fragment)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Species: Homo sapiens
R.Whitelaw, E.; Hogben, P.; Hanscombe, O.; Proudfoot, N.J.
Mol. Cell. Blol. 9, 241-251, 1899
A.Title: Transcriptional promiscuity of the human alpha-globin gene.
A.Reference number: 157650; MUID:89181576
A.Scession: 157650
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: Lanslated from GB/EMBL/DDBJ
A.Status: Lanslated from GB/EMBL/DDBJ
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T-cell receptor beta cháin V-D-J region (126-1L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
           C:Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F:9/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.6%; Score 16; DB 4; Length 9; 80.0%; Pred. No. 1.8e+05; live 0; Mismatches 1; Indels
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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A,Residues: 1-5 <FEE>
A:Experimental source: day 18 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                      Score 16; DB 2; I
Pred. No. 1.8e+05;
1; Mismatches 3;
                                                                                                                                                   35.6%;
42.9%;
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                                                                                                                                                   Query Match 35.6
Best Local Similarity 42.9
Matches 3; Conservative
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2 YISNCPI 8
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3 LSPAD 7
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(Species: Cyprinus carpio (common carp)
(Species: Cyprinus carpio (common carp)
(Species: Cyprinus carpio (common carp)
(Species: O9-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
(Species: O9-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
(Species: Office: Carcaterisation for Air (Species: Office: Carcaterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce A: Reference number: A61364
A: Reference number: A61364
A: Reference protein
A: Reference protein
A: Residues: 1-9 < ACH>
C: Superiamily: oxytocin-neurophysin
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C.Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
R.Holman, G.M.: Cook, B.J.: Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A.Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin A.Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the fin A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: Leucokinins, a family of cephalomyotropic peptide
C.Comment: Leucokinins, a family of cephalomyotropic peptide
C.Keywords: amidated carboxyl end; cephalomyotropic peptide
F.8/Modified site: amidated carboxyl end (Gly) #status experimental
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                                                                                                                                                                                                                                    Variant surface glycoprotein pSLc1 - Trypanosoma brucei (fragment)
C;Species: Trypanosoma brucei
C;Daces: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
C;Accession: A2140
R;Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.
Celli38, 309-316, 1984
A;Reference number: A90853; MUID:84282716
A;Molecule type: mRNA
A;Residues: 1-8 <PARS
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C;Keywords: glycoprotein
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Matches 2; Conservative
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Best Local Similarity
Matches 3; Conserv
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1 MSGKEV 6
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2 SGGD 5
3 SGAD 6
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C; Species: Calliphora vomitoria
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C; Accession: F41978
R; Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Tho
Proc. Natl. Acad. Sci. U.S.A. 89, 2330-2330, 1992
A; Title: Isolation, structure, and 2021vity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (d
A; Reference number: A41978; MUID:92196111
                                                                                                                                                                                                Cytochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13818
R;Delazbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Title: The main features of the craniate mitochondrial DNA between the NDI and the A;Reference number: Z17775; MUID:97398704
A;Accession: T13818
A;Accession: T13818
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Cross-references: EMBL:Y09527; NID:e1011465; PID:e329906; PIDN:CAA70718.1
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C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacte: 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0288
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G. J. Exp. Med. 173, 395-407, 1991
A;Fitle: Preferential utilization of specific immunoglobulin heavy chain diversity A;Reference number: PT0222; MUID:91108337
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A:Molecule type: protein
A:Residues: 1-9 <DUV->
CJKCywords: amidated carboxyl end; neuropeptide
F:9/Modified site: amidated carboxyl end (Phe) #status experimental
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100.0%; Pred. No. 1.8e+05;
ive 0; Mismatches 0;
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Pred. No. 1.8e+05;
0; Mismatches 1
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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A; Note: COI
C; Keywords: mitochondrion
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Best Local Similarity
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SGED
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601
A;Accession: PT0726
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
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T-cell receptor beta chain V-D-J region (161-2D) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0526
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0676
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Pred. No. 1.8e+05;
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-7 <FEES
A;Experimental source: day 18 fetal thymus, strain BALB/C
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                A;Experimental source: newborn thymus, strain BALB/c C;Keywords: T-cell receptor
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C.Keywords: T-cell receptor
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75.0%;
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75.0%;
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A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
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Best Local Similarity 75.0%
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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J. Exp. Med. 174, 115-124, 1991
Afrille: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0609
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions
A;Reference number: PT0509; MUID:91277601
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Blosci. Blotechnol. Blochem. 59, 231-235, 1995
A;Title: Identification of DNA-binding proteins changed after induction of sporulatio
A;Reference number: PC2369; WUID:95218265
                                                                        T-cell receptor beta chain V-D-J region (120-1L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0605
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cell receptor beta chain V-D-J region (159-1F) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Bate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0593
R;Feeney, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.1%; Score 14; DB 2; Length 6; 100.0%; Pred. No. 1.8e+05; Live 0; Mismatches 0; Indels
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A;Residues: 1-6 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
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100.0%; Pred. No. 1.8e+05;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      A)Residues: Î-6 <FEE>
A)Experimental source: newborn thymus, strain BALB/C
C)Keywords: T-cell receptor
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A,Status: preliminary
A,Molecule type: procein
A,Residues: 1-7 <AMAS>
C,Keywords: ATP blosynthesis; hydrolase
                                                                                                                                                                                                                                                                                                                                    A; Status: translation not shown A; Molecule type: mRNA
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A; Status: translation not shown
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Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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| SGA 4
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4 SGA 6
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
J;Exp. Med. 114, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Reference number: PT0509; MUID:91277601
A;Reference number: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c, 154-2J
A;Recession: PT0708
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-5 <FEE>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: G41946
R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma of A:Accession: G41946
A:Reference number: A41946; MUID:92049316
A:Accession: G41946
A:Status: preliminary: not compared with conceptual translation
A:Residues: 1-9 cwHE>
C:Keywords: T-cell receptor
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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A,Accession: PT0288
A,Molecule type: DNA
A,Residues: 1-9 <YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                         33.3%;
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75.0%;
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Best Local Similarity 75.0%;
Matches 3; Conservative (
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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5 YSSG 8
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5 YSSG 8
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T-cell receptor beta chain V-D-J region (126-1BD) - mouse (fragment)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Accession: PT0557
R; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions A; Reference number: PT0509; MUID:91277601
A; Rittle: Junctional sequences of A; Reference number: PT0509; MUID:91277601
A; Reference number: PT0557
A; Status: translation not shown
A; Molecule type: mRNA
A; Residues: 1-8 CFEE
A; Experimental source: day 18 fetal thymus, strain BALB/C
C; Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                  phosphatidylethanol amine-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C;Accession: PN0043
R;Kato, H.
Rawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne A;Reference number: PN0041
A;Reference number: PN0043
A;Reference number: PN0043
A;Residues: 1-8 <KAT>
A;Residues: 1-8 <KAT>
C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is bloc C;Keywords: brain
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                                                                                                                                         31.1%; Score 14; DB 2; 7 50.0%; Pred. No. 1.8e+05; tive 1; Mismatches 1
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Best Local Similarity
Matches 3; Conserva
      A; Accession: S65647
A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-8 <MUE>
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Best Local Similarity
Matches 3; Conserva
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Best Local Similarity
Matches 2; Conserv
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4 GIDV 7
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5 LSG 7
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C.Species: Acidaminococcus fermentans
C.Sate: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 07-May-1999
C.Accession: 865647
R.Mueller, U.: Buckel, W.
Eur J. Blochem. 230, 6970, 1995
A.Title: Activation of (R)-2-hydroxyglutaryl-CoA dehydratase from Acidaminococcus fermen A:Reference number: 865647; MUID:95331308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C,Accession: PT0722
C,Accession: PT0722
R;Fenney, A.J.
R;Fenney, A.J.
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                           J. Exp. Med. 174, 115-124, 1991
A; Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A; Reference number: PT0509; MUID:91277601
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C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0654
S:Feeney, A.J.
J. Exp. Med. 174, 115-124. 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell receptor beta chain V-D-J region (135-1G) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                     Gaps
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      Length 7;
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A;Status: translation not shown
A;Bolcule type: mRNA
A;Residues: 1-7 <FEE>
A;Residues: 1-7 <FEE>
C;Keywords: T-cell receptor
  Score 14; DB 2; Le
Pred. No. 1.8e+05;
1; Mismatches 0;
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A;Status: translation not shown
A;Molecule type: DNA
A;Espatius: 1-7 <FEE>
A;Experimental source: newborn thymus, strain BALB/C
C;Keywords: T-cell receptor
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31.1%;
milarity 66.7%;
Conservative 1
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75.0%;
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Best Local Similarity 75.0°
Matches 3; Conservative
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Best Local Similarity 100.
Matches 3; Conservative
    Query Match
Best Local Similarity
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SGDD 5
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2 SGA 4
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PT0268
Type and CRD3 region (clone 3-94B) - human (fragment)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Hough #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
CyAccession: PT0268
Fyrsmadav M.; Wassermann, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A,Title: Preferential utilization of specific immunoglobulin heavy chain diversity and A. Feference number; PT0222; MUID:91108337
                                                    "curupeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C5744
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Reference number: A57444; MUID:95403341
A;Reference preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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C; Species: Homo sapiens (man)
C; Species: 20-0ct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C; Accession: S43959
R; Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, Nucleic Acids Res. 22, 1389-1393, 1994
A; Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A; Reference number: S43956; MUID:94248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 1.8e+05;
0; Mismatches 2; Indels
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Pred. No. 1.8e+05;
1; Mismatches 1; Indels
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A,Residues: 1-9 <YAM>
A,Experimental source: B lymphocyte
C,Keywords: heterotetramer; immunoglobulin
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60.0%;
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50.0%;
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A; Residues: 1-4 <WAG>
C; Keywords: immunoglobulin
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Matches 2; Conserv
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                                          R.Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
Regul. Pept. 36, 111-119, 1991
A.Yiltle: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI A.Yiltle: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI A.Reference number: A60065; MUID: 92179466
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
A.Molecule type: protein
C.Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and C.Superfamily: locustamyoinhibiting peptide
C.Superfamily: locustamyoinhibiting peptide
C.Superfamily: amidated carboxyl end; hormone
F:9/Modified site: amidated carboxyl end (Trp) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C:Species: Gryllus binaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996
R:Lorenz, Mw.; Kellner, R.; Hoffmann, K.H.
J. Blol. Chem. 270, 21103-21108, 1995
A:Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              neuropeptide Grb-AST B2 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: B5744
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
B. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri
A;Reference number: A57444; MUID:95403341
A;Accession: B57444
A;Accession: B5744
A;Accession: preliminary
A;Acleule type: protein
A;Residues: 1-9 <LOR>
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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 20-Mar-1998 C;Accession: A60065
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
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Pred. No. 1.8e+05;
1; Mismatches 0;
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llarity 66.7%;
Conservative 1
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66.7%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity 66.77
Conservative
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A; Status: preliminary
A; Molecule type: protein
A; Residues: 1-9 <LOR>
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Best Local Similarity
Matches 2; Conserv
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4 DLN 6
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C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Jr-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C; Saccession: PT0547
S; Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A; Exp. Med. 174, 115-124, 1991
A; Afference number: PT0509; MUID:91277601
A; Accession: PT0547
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C:Species: Oryctolagus cuntculus (domestic rabbit)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A01422
R:Monnier, M.; Dudler, L.; Gachter, R.; Maier, P.F.; Tobler, H.J.; Schoenenberger, G.
Experientia 33, 548-552, 1977
A:Title: The delta sleep inducing peptide (DSIP). Comparative properties of the original A:Reference number: A01422; MUID:77185324
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photosystem II protein psbM - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Dates: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 30-Sep-1993
C;Accession: C41170
R;de Vitry, C; Diner, B.A.; Popot, J.L.
J. Biol. Chem. 266, 16614-16621, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-D-J region (126-1AI) - mouse (fragment)
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                                 Score 13; DB 2; Len
Pred. No. 1.8e+05;
                                                                                                                                2; Mismatches
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Matches 2; Conserv
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| GAEM 4
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A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobac A;Reference number: A58718; MUID:92321768
A;Accession: A58718
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R; Krelenkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A; Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo A; Reference number: A41117; WUID: 91296772
A; Accession: A41117
A; Molecule type: protein
A; Residues: 1-8 KRE>
C; Keywords: carboxylic ester hydrolase
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                                                                                                                                                                                                          C.Species: Gallus gallus (chicke)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
C.Accession: 150210
R.Kabrun, N.; Bunstead, N.; Hayman, M.J.; Enrietto, P.J.
R.Kabrun, N.; Bunstead, N.; Hayman, M.J.; Enrietto, P.J.
A.Title: Characterization of a novel promoter insertion in the c-rel locus. A.Reference number: 150210; MUID:90355995
A.Accession: 150210
A.Accession: 150210
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Status: preliminary; translated from GB/EMBL/DDBJ
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C;Date: 23.Jan-1998 #sequence_revision 30.Jan-1998 #text_change 30.Jan-1998
C;Accession: A58718
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C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
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A;Cross-references: GB:M55577; NID:g555438; PID:g211661
C;Genetics:
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A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine
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A;Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91358452
A;Accession: C41170
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <DE5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macrophage inhibitory factor (F5 cells) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: A61386
R;Oki, S.; Hirose, S.I.; Higuchi, M.; Osawa, T.
Lymphokine Cytokine Res. 10, 273-280, 1991
A;Title: Macrophage migration inhibitory factor (MIF) produced by a human T cell hybridc
A;Reference number: A61386
A;Accession: A61386
A;Accession: A61386
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <OKI>
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28.9%; Score 13; DB 2; Length 9;
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Matches 2; Conservative 2; Mismatches 0; Indels
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28.9%; Score 13; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.8e+05;
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| W70078 Y41847 R07966 W38383 | X47062 R67605 | K6/613 W00690 Y70832 R09414 | K884/b W54298 Y41962 Y42028 | W70077 Y55545 Y55587 | X47818 X05407 | Y70831 Y54210 | W56879 W56879 R26159 | W56983 R30155 R87430 | W54299 | W40267 Y30946 Y54211 Y56575 | Y28182 R90466 | W83890 Y55201 | Y26120 Y86947 | W69333 | Y17023 P91779 | R76988 R73336 | W07241 | W64478 | X16852 | W82429 | R46546 | R59233 | K/006/ W49278 | R99964 | X41907 | Y42029 Y51905 | | ALIGN | | AA. | |
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| 4.5 Compugen Ltd. | | Search time 107.12 Seconds (without alignments) 2.873 Million cell updates/sec | | | Ø | ers: 61695 | | | | eseqp/AA1980.DAT:* eseqp/AA1981.DAT:* esequ/AA1982.DAT:* | eseqp/AA1983.DAT:* eseqp/AA1984.DAT:* | eseqp/AA1985.DAT:* eseqp/AA1986.DAT:* | eseqp/AA198/.DAT:* eseqp/AA1988.DAT:* | neseqp/AA1990.DAT:* | neseqp/AA1991.DAT:* neseqp/AA1992.DAT:* | neseqp/AA1993.DAT:* neseqp/AA1994.DAT:* | /geneseqp/AA1995.DAT:* /geneseqp/AA1996.DAT:* | /geneseqp/AA1997.DAT:* /geneseqp/AA1998.DAT:* | /geneseqp/AA1999.DAT:* | cted by chance to have a | н | | | Description | | Carcinoembryonic a Carcinoembryonic a | Carcinoembryonic a Human carcina-embr | CEA Synthetic pept CEA derived HLA-A2 | Immunogenic peptid Carcinoembryonic a | HLA binding peptid Carcinoembryonic a Peptide comprising | Rheumatoid arthrit |
| GenCore version 4 Copyright (c) 1993 - 2000 Co | protein search, using sw model | December 16, 2000, 03:07:18 ; | US-09-529-121-3 45 1 YLSGADINL 9 | BLOSUM62 Gapop 10.0 , Gapext 0.5 | | hits satisfying chosen parameters | th: 0 th: 9 | Minimum Match 0% Maximum Match 100% Listing first 75 summaries | | A_Geneseq_36:* 1: /SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:* 2: /SIDS6/gcgdata/geneseq/geneseqp/AA1981.DAT:* 3: /SIDS6/gcgdata/geneseq/geneseqp/AA1982.DAT:* | /SIDS6/gcgdata/geneseg/gene/SIDS6/gcgdata/geneseg/gene | /SIDS6/gcgdata/geneseq/geneseq/geneseq/geneseq/geneseq/geneseg/geneseq/geneseq/geneseq/geneseq/geneseg | /SIDS6/gcgdata/geneseq/gene/SIDS6/gcgdata/geneseq/gene/SIDS6/gcgdata/geneseq/gene | /SIDS6/gcgdata/geneseq/gen | /SIDS6/gcgdata/geneseq/geneseqp/AA1991.DAT /SIDS6/gcgdata/geneseq/geneseqp/AA1992.DAT | /SIDS6/gcgdata/geneseg/geneseqp/AA1993.DAT /SIDS6/gcgdata/geneseg/geneseqp/AA1994.DAT | /SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT /SIDS6/gcgdata/geneseq/geneseqp/AA1996.DAT | /gcgdata/geneseg/ | /gcgdata/geneseq./acgdata/geneseq. | the number of results predic | qual to the score | COLORANGIA | | Query Match Lepath DB ID | 3 : | 0.00 | 4 9 9 20 | 4 4 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 | 4 9 20 | .8 9 21 Y54173 .6 9 20 Y09529 .9 9 17 W00680 | .6 7 20 |
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                                                                                                                                                                                                                                                                                                                                                                   The present invention describes peptides (A) that comprise agonists (Ia)
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                                                                   immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                        Carcinoembryonic antigen; CEA; human; agonist; antagonist;
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                                  Carcinoembryonic antigen peptide agonist SEQ ID NO:3.
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or antagonists (TD) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                             present invention describes peptides (A) that comprise agonists (Ia)
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Peptide agonists and antagonists of carcinoembryonal antigen
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Pred. No. 2.1e+05;
1; Mismatches 0;
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                                                                 Claim 5; Page 53; 72pp; English.
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immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and WHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEA synthetic peptide epitope 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W77134 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                    84.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 84.4
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YLSGADINL 9
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| ylsganlnl
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cytotoxic T
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                                                                                                                                                                                                                The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method of selecting T cell peptide epitope(s) - by measuring the stability of HLA class I-peptide complexes on intact B cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                           Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
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(SCIS-) SCI SEED CAPITAL INVESTMENTS BV
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                                                                                                                                                                        Claim 5; Page 53; 72pp; English.
                                Zaremba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W39723 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.9%;
88.9%;
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96EP-0201145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                             WPI; 1999-326544/27
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YLSGADINL 9
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                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disease specific immunogen \cdot comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response
                                                                              ;
Length 9;
Score 38; DB 18; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tyrosinase cytotoxic lymphocyte response; lymphocyte; cysteine-depleted; melanoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYVI-) UNIV VIRGINIA PATENT FOUND.
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Length 9;

Query Match

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carcinoembryonic antigen (CEA). The peptides can bind to a human leukocyte antigen (LEA). The peptides can bind to a human leukocyte antigen (LEA). The peptides can bind to a human leukocyte antigen (LHA), HHA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLS) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCS) pretreated with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing trarget cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCs pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLS can be used for treating cancers, immune disorders, viral infections, AIDS, hepatitis, bacterial infection, fungal infection, malaria or
                                                      ö
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                         Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immuno disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                      ö
                                                                                                                                                                                                                                                                                                                         HLA-A2.1 binding peptide 2 (residues 605-613).
                  Length 9;
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tsai V;
                  DB 19; Le
2.1e+05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood S,
                                                      Mismatches
                    Score 38;
                                       Pred. No.
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                                                      2;
                                                                                                                                                                                                                 W70045 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sidney J,
                  84.4%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US01959.
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                                                                                                                                                                                                                                                                                      (first entry)
                                                      Conservative
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Query Match
Best Local Similarity
'hns 7; Conserve
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                                                                                       1 YLSGADINL 9
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| ylsganlnl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JAN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                                                                                                                                                    W70045;
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                                                                                                                                                                               RESULT
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Table 10 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human neukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) corpusorate cancer, hepatitis B and C, ALDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunogenic peptide having a human leukocyte antigen binding motif #2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activatio; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunogenic peptides with HLA binding motif, useful in treatment
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                                                                    Indels
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   Score 38; DB 19;
Pred. No. 2.1e+05;
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                                                                        2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 118; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   Y47655 standard; Peptide; 9 AA.
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84.4%;
77.8%;
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          raccine; immunisation.
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                                    Best Local Similarity
Matches 7; Conserv
                                                                                                                                     1 YLSGADINL 9
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1 ylsganlnl
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                                                                                                                                                                                                                                                                                                                     RESULT
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Length 9;

DB 20;

Score 38;

84.48;

Query Match

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Allele-specific binding motif; major histocompatibility complex; MHC; HLA; HLA-A2.1; cytotoxic T cell response; antigen; microbial infection; hepatitis; AIDS; malaria; condyloma acuminatum; cancer; prostate cancer; renal carcinoma; cervical carcinoma; lymphoma; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel HLA binding immunogenic peptides used to induce {\tt T} cell activation and to induce an immune response -
                                                                                                                 HLA binding peptide 1233.11 derived from source CEA.605v9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 32; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US13789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0098584
                                                                     06-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-106018/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
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1 ylsganlnv
                                                                                                                                                                                                                                                                                                                           W09965522-A1.
                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y09529;
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Y09529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or antigonists (Tb) of human carefuncembryonal antigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to prollferate T cells, e.g. from vaccinated subjects; for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but GEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes peptides (A) that comprise agonists (Ia)
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                        Indels
Pred. No. 2.1e+05;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         Carcinoembryonic antigen peptide agonist CAP-1.
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                                                                                                                                                                                                                                  Y09525 standard; peptide; 9 AA.
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77.8%;
77.8%;
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                                                                                                                                                                                                                                                                                                                           20-JUL-1999 (first entry)
Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
                                                                   1 YLSGADINL 9
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| ylsganln|
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| ylsganlnl
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Y54173
ID Y5
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Peptides Y54171-Y54236 represent immunogenic peptides comprising an allele-specific binding motif for the major histocompatibility complex (MHC) molecule HLA, e.g. HLA-A2.1. The peptides have conserved residues at certain positions such as positions 2 and 9. Also, the peptides do not comprise negative binding residues at other positions, such as positions 1, 3, 6 and/or 7 (peptides 9 amino acids long) and at poisons 1, 3, 4, 5, 7, 8 and/or 9 (peptides 10 amino acids long). The peptides are used to induce a cytotoxic 7 cell response to a preselected antigen. The method comprises contacting cytotoxic 7 cells from a patient (optionally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vivo. The resulting CTLS can be used to treat chronic infections (viral or bacterial) or tumours in patients that do not respond to conventional forms of therapy. The peptides may also be used to produce monoclonal antibodies, which are useful as potential diagnostic or therapeutic agents. The peptides may also be used as diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing a specific MIC class I allele) with the present peptides. The peptides are used to treat and prevent microbial infection (e.g. in viral hepatitis B and C. human papilomavirus (HPV) infection AIDS, cytomegalovirus (CMV), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Patients in the acute phase of infection can be treated with the peptides in conjunction with other treatments. The antigenic peptides may be used to elicit cytotoxic T lymphocytes (CTLs) ex vivo and in
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Pred. No. 2.1e+05;
3; Mismatches 0; Indels
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W09947925-A2
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                                                     22-FEB-1995;
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         29-AUG-1996
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                                                                        (THER-)
                                                                                       ( HSSN)
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                                                                                                                                                                                                                                                                                                                                                 or antagonists (ID) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA response. Cytotoxic T sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                         The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                   Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide comprising residues 571-579 of Carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                              Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 20; Length 9; Pred. No. 2.1e+05; l; Mismatches 1; Indels
                               Carcinoembryonic antigen peptide agonist SEQ ID NO:5.
                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                  Claim 5; Page 53; 72pp; English.
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77.8%;
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          20-JUL-1999 (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
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| ylsgacini 9
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                                                                                                           Homo sapiens
                                                                                                                                         W09919478-A1
                                                                                                                                                                                     22-SEP-1998;
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                                                                                                                      Synthetic.
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cells (CTC), comprises introducing a 1st pox virus vector, having at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC production, and at least 1 periodic interval after that, contacting the host with an additional antigen. The CEA specific CTC can be used to determine the CTC eliciting epitope of CEA, and to screen for compounds which enhance the ability of the antigen to create a CTC response. A host with a CEA expressing tumour can be treated by introducing the CTC to the host, and at least 1 periodic interval after that introducing a CEA peptide, i.e. the present peptide. The present peptide is positive for binding to HIA-A2, and scored 561 and 806 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HIA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HIA-A2 antibody (background 280 and 300).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation of human cytotoxic T-cells specific for CEA - useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoembryonic antigen (CEA) specific human cytotoxic
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Pred. No. 2.1e+05;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy, epitope mapping and drug screening
                                                                                                                                              THERION BIOLOGICS CORP.
US DEPT HEALTH & HUMAN SERVICES.
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75.0%;
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96WO-US02156
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Best Local Similarity
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Parekh RB, Patel TP,
                         WPI; 1998-480383/41.
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Matches 4; Conserv
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Lee SH,
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| yltgtd 6
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  Kim S,
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Y41847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                      feature whose relative abundance correlates with the presence or absence of RA; and (C) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy protocols. Y41844 to Y42100 represent RPI peptides y42101 to Y42103 represent expression reference protein isoform peptides and 225066 to 225068 represent dependent or protein isoform peptides and 225066 to 225068 represent dependent or protein isoform peptides and 225066 to 225068 represent PRID to WHIS, which are all used in
                                                                                                                                            A method has been developed for the diagnosis of human rheumatoid arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features: (b) identifying at least one chosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis; mycobacterial; methionyl-tRNA synthetase; enzyme; antibiotic; tuberculosis; Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
0
                                                                              Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 25; DB 20; Length 7; Pred. No. 2.1e+05; 1; Mismatches 0; Indels

    B. stearothermophilus methionyl-tRNA synthetase fragment.

                                                                                                                                                                                                                                                                                                                                                                                                                                                  the exemplification of the present invention.
 (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                    Claim 20; Page 150; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W70078
ID W70078 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus stearothermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0305766.
96US-0584226.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CUBI-) CUBIST PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                    WPI; 1999-571871/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                             electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 SGADIN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JAN-1996;
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11-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W70078;
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Sequences shown in W70077 to W70086 represent methionyl-tRNA (Met-tRNA)

Synthetase fragments from different bacterial species. These are used
for designing degenerate primers (W4887 to W43800) used for isolating
Met-tRNA synthetase gene fragment by PCR from M. tuberculosis and M.

Kansasii. The invention provides an expression vector comprising a
nucleic acid encoding a mycobacterial aminoacyl-tRNAs (atRNA) (sepecially
Met-tRNA) synthetase under control of transcriptional signals that can be
used to transform suitable host cells. The nucleict acids and host cells
are used for the recombinant production of mycobacterial amino acyl tRNA
synthetases, especially of methionyl tRNA synthetase. The recombinant
classed by the organism in protein synthesis, and as such, the recombinant
enzyme can be used to identify candidate drugs for use as antiblotics
towards mycobacteria, especially M. tuberculosis, which is responsible
to tuberculosis. Antisense constructs of the nucleic acids can also be
used in antisense inhibition of the synthetase gene. The recombinant
enzyme allows quick assays in screening of antiblotics. Present testing
protocols involve exposing whole mycobacteria to candidate drugs and
seeing their effect. This is time consuming as the bacteria are generally
slow growing to the enzyme also prevents researchers from having to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                               Recombinant genes encoding mycobacterial amino acyl tRNA synthetases - useful for recombinant production of the enzyme for use in screening of antibiotics against Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; rheumatoid arthritis; RA; dlagnosis; RPI; RADF; detection; Theumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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Pred. No. 2.1e+05;
1; Mismatches 1; Indels
    Schimmel PR;
Sassanfar M,
                                                                                                                                                                                                                                                                                                                                                                         Example 1; Columns 33-34; 32pp; English.
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Martinis SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.3%;
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19-MAR-1996;
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                                                                                                                                                                                                                                                                                                                                                           4 ylxggd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COX AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  W38383;
                                                                                                                                                                                                                                                                                                                                                                                                RESULT 16
                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Turnitis (RA) using two-dimensional electrophoresis to generate a trivitis (RA) using two-dimensional electrophoresis to generate a diagnosis and prognosis of RA in a subject or for monitoring the effect diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally syno-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature of features in the sample indicates the presence or subsence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA-diagnostic acid encoding RADFs can be used in gene therapy concludes and expression reference protein isoforms peptides and 225066 to be concluded by the property of RPIS, which are all used in feature the processor the property of RPIS, which are all used in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                          has been developed for the diagnosis of human rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human N-lipocortin; placenta; inflammation reduction; arthritis; phospholipase A2 inhibitor; tryptic fragment T32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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           Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23; DB 20; Length 7; Pred. No. 2.1e+05; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pepinsky RB, Garwin JL, Schindler DG,
                                                                                                                                                                                                                                                                                                                                                           the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tryptic fragment T32 of human N-lipocortin.
                                               Claim 20; Page 150; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R07966 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                        51.18;
66.78;
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85US-0712376.
85US-0690146.
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85US-0772892.
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Best Local Similarity
Matches 4; Conserv
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                          electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 SGADIN 8
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2 sgadls 7
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15-MAR-1985;
10-JAN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JAN-1986;
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05-SEP-1985;
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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T32 corresponds to a peak from the tryptic map of N-lipocortin, isolated from human placenta, on a Speed Vac Concentration. Amino acids 1 can also be G. Based on the similarity in the phospholipase A2 inhibitory activity of lipocortin and N-lipocortin and the similarity in the protein and sequences, it was concluded that the two proteins represent a family of related proteins. There is ca. 60% homology. The protein can be used for reducing inflammation or treating arthritic, allergic, dermatologic, opthalmic and collagen diseases and other diseases involving inflammation processes. See also Q05805-25, Q06581, R07926-37 and R07956-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         novel melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human leukocyte antigen-A1; HLA-A1; human leukocyte antigen-A3; HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present peptide was used in the preparation of a novel melan specific immunogen, comprising at least 1 melanoma specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the epitopes is substantially homologous to a human leukocyte antigen-Al (HLA-Al) and HLA-A3 restricted epitope of a melanoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23; DB 11; Length 9;
Pred. No. 2.1e+05;
Arnhae 2; Indels
Pure fragment of human lipocortin - useful for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Melanoma; immunogen; cytotoxic T lymphocyte; CTL;
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                           inflammation or for treating arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                    51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W38383 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.1%;
66.7%;
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96US-0013972.
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                                                                                                    Disclosure; Fig 25;
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Best Local Similarity
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therapeutically and for immunisation as above.
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31-JUL-1992;
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                                              Sequence
                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                              RESULT 18
R67605
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Cytotoxic T lymphocytes (CTLs) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) critical susceptible or otherwise at risk of viral infection or individuals susceptible or otherwise at risk of viral infection or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic peptide having a human leukocyte antigen binding motif #1673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                Gaps
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antigen, either pWEL-17 or tyrosinase. The immunogen can be used in vaccines for protection against melanoma in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Southwood S;
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                                                                                                               DB 18; Lens
2.1e+05; Indels
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                                                                                                                                  Score 23; DB 1
Pred. No. 2.1e<sup>4</sup>
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New immunogenic peptides with HLA binding more and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 92; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Y47062 standard; Peptide; 9 AA.
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                                                                                                                                  51.1%;
50.0%;
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                                                                                                                                                                                Conservative
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                                                                                                                                  Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                 9 AA;
                                                                                                                                                                                                                          1 YLSGADIN 8
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                                                                 Sequence
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                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               size exclusion chromatography, these bands probably represented two related forms of the enzyme instead of two different subunits of the enzyme. This sequence is a peptide fragment from the 56 kD protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New recombinant constructs for transforming plants of E. coli contg. nucleic acid encoding jojoba embryo long chain fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jojoba; fatty acyl CoA reductase; fatty acyl; fatty alcohol.
Score 23; DB 20; Length 9;
Pred. No. 2.1e+05;
3; Mismatches 1; Indels
     Length 9;
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                                                           3,
                                                                                                                                                                                                                                                                                                                      R67605 standard; Protein; 9 AA.
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91US-0796256.
92US-0920430.
                                50.0%;
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Best Local Similarity
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                                Best Local Similarity
Matches 4; Conserv
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RESULT 19

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NCA analogue of residues 571-579 of carcinoembryonic antigen
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                                                                                                                                                                                                                                                                                                                                       Example 2; Page 60; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BH3 domain of mouse BAK protein.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
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                                                           Homo sapiens
                                                                                                                                           13-FEB-1996;
                                                                                    WO9626271-A1
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                                                                                                                                                                                                                                           Panicali D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                              Jojoba; fatty acyl CoA reductase; fatty acyl; fatty alcohol
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                                                                                                                                                  Jojoba fatty acyl-CoA reductase 54kd protein fragment.
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                                                                  R67613 standard; Protein; 9 AA.
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91US-0767251.
91US-0796256.
92US-0920430.
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ilarity 66.7%;
Conservative
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Best Local Similarity
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27-SEP-1991;
20-NOV-1991;
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2 gldinv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997
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RESULT 20

AXXXIX

Matches

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Mouse; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma; neuron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death; BH3 domain; BCL-2 homology domain; BAK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present peptide is negative for binding to HLA-A2, and scored 252 and 225 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HLA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HLA-A2 antibody (background 280 and 300).
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Carcinoembryonic; antigen; epitope; NCA; analogue
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trehalose content
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trehalose;
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                                                                                 Sequence
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                                                                                                The parent largerouse's specific tunneated by trophic factor deprivation.

The anti-apoptotic tBAX proteins include tBAX70, tBAX78

and thair mituants. These proteins contain the N-terminal region and at least a portion of the BH3 domain of BAX alpha and lack the BH1, BH2 and C-terminal transmembrane domains. The tBAX protein lacking only the craminal transmembrane domains. The tBAX protein lacking only the craminal transmembrane domain has been shown to have anti-apoptotic activity.

The tBAX proteins are used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke. tBAX proteins

truncating at amino acid 68 of the BH3 domain of BAX alpha also have anti-apoptotic activity and is conserved in all BCL-2 family members.

The present sequence is a BH3 domain of mouse BAX protein, a pro-apoptotic protein belonging to BCL-2 family that is involved in creating the formal programmed cell death. The present sequence
                                                                                                                                                                                                                                                                                                                                                                       ó
                                 Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The alpha-subunit (a-SU), contg. al least one of the polypeptides given in R09404-417, can bind to ICAM-1 (or other natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lymphocyte function associated antigen; inflammation; metastasis.
                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pure alpha subunit of lymphocyte function associated antigen and encoding DNA sequences, useful eg for suppressing inflammation or metastasis
                                                                                           patent discloses specific truncated BAX (tBAX) proteins
                                                                                                                                                                                                                                                                                                                                                 Length 9;
                                                                                                                                                                                                                                                                                                                                             Score 22; DB 21; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFA-1 alpha subunit polypeptide (k).
                                                                                                                                                                                                                                                                                      contains the conserved Asp residue.
                                                                     Disclosure; Fig 3; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 19; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R09414 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 71.4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88US-0235227
89US-0321017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89EP-0115160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DANA-) DANA FARBER CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larson R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-108985/15.
                                                                                                                                                                                                                                                                                                             9 AA;
                                                                                                                                                                                                                                                                                                                                                                                             2 LSGADIN 8
                                                                                                                                                                                                                                                                                                                                                                                                             3 ligddin 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Springer TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1990
                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R09414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 22
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derived from trehalose-6-phosphate (Tre6P) synthase from M. smegnatis. Tre6P is the key enzyme in the synthasis of trehalose via Tre6P. The aim of the invention is to produce a transgenic plant with increase trehalose content. Tre6P in M. smegnatis is heparin-activated and was isolated and purified. These peptides were derived from a protein which was purified with a mol. Wt. of 55 kb which shared antigenic determinants with the yeast Tre6P synthase protein. Using these peptides probes may be designed for the isolation of the Tre6P gene (TSP1) for the production of the transgenic plants. The trehalose may be isolated from the transgenic plants and used in bulk preparation including the preservation of the flavour and structure of food stuffs during drying. Fruits and berries form the transformed plants may be processed into purees, fallies and is and rich have a fresher and richer flavour due to the increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New transgenic plants with increase trehalose contents - prepd. by transforming plants with a trehalose-6-phosphate synthase gene fused to a non-constitutive promoter
ligands) on the surface of cells, and can associate with the beta-SU to form a heterodimer (also able to bind to ICAM-I). a-SU, and its derivs., are useful in suppressing inflammation, metastasis and growth of a-SU expressing tumour cells and is used in the treatment of viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tryptic peptide; trehalose-6-phosphate synthase; M. smegmatis; probe trehalose; transgenic plant; heparin-activated; preservation; food; antigenic determinant; yeast; TSP1; fruit; berry; puree; jelly; jam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequences given in R88473-80 are internal tryptic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Internal tryptic peptide from Tre6P synthase (peak 29) #2.
                                                                                                                                                                                                                                                                                                                                                                                              Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ü
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                                                                                                                                                                                                                                                                                                                                                                                      46.7%; Score 21; DB 11; L
100.0%; Pred. No. 2.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mandal A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 36; 55pp; English.
                                                                                                                                                                                             The pref. dose is 1 pg - 10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R88476 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        i, Londesborough J,
Tunnela O, Welin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95WO-FI00377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94FI-0003133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium smegmatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ALKO-) ALKO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-077499/08
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                         6 AA;
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2 LSGADIN 8 |||| :| | lsggrvn 7

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Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection, rheumatoid arthritis diagnostic feature; ERPI; symovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                   Rheumatoid arthritis diagnostic protein isoform peptide #113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                  Y41962 standard; Peptide; 7 AA.
                                                                                                                                                                                                  09-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-571871/48.
                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09947925-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parekh RB,
                                                                                                                                                                 Y41962;
                                                                                                 RESULT
Y41962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is a randomised AB loop encoded by clone 7 (see V26501) of a large peptide library (2 million clones) of synthetic Pleckstrin homology (PH) domains with randomised discontinuous surface epitopes. The progenitor AB sequence comprises amino acid residues of 16-21 of a stabilised synthetic PH domain (see W54310) of human cytohesin 1. The peptide library was generated by randomisation of AB and CD loop regions using randomised oligonucleotide primers (see W24929-399) of the peptide library are provided. Randomisation did not compromise the structural integrity and folding stability of the prodention of PH domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, which can be of use in research or therapy, or as vaccines, Novel synthetic protein structural templates for the generation, screening and coultion of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vectors used to produce PH domain-like peptide libraries - which are screened for therapeutically useful peptide(s), e.g. to produce
                                                                                   Gaps
                                                                                 ó;
                                                                                                                                                                                                                                                                                                                                                                  Pleckstrin homology domain; PH domain; peptide library; functional molecular surface; protein structural template; vaccine; gene therapy; cytohesin 1; human.
                                              Length 6;
                                                                                                                                                                                                                                                                                                                                   Human cytohesin-1 PH domain randomised AB loop (clone 7).
                                                                               1; Indels
                                              Score 21; DB 17;
Pred. No. 2.1e+05;
                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steipe B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 12; 137pp; English.
                                                                                                                                                                                                                                 W54298 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Funk M, Henkel T,
                                              46.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-EP02840.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96EP-0108776
                                                                                                                                                                                                                                                                                                  28-AUG-1998 (first entry)
                                                                                   4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MEDI-) MEDIGENE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230215/20.
                                                  Query Match
Best Local Similarity
 6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V26501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-MAY-1996;
                                                                                                                1 YLSGA 5
                                                                                                                                                l ylega 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09745538-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruhn H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccines
                                                                                                                                                                                                                                                                 W54298;
                                                                                                                                                                                                  RESULT 24
W54298
                                                                                   Matches
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Townsend RR;

Patel TP,

Location/Qualifiers

/label= Ile, Leu

99WO-GB00763 98GB-0005477

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The first (RA) using two-dimensional electrophoresis to an extending and prognosis of Rain a subject or for monitoring the effect diagnosis and prognosis of Rain a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance of each chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the come or more persons without RA, where the relative abundance of the chosen feature in the sample come or more persons without RA, where the relative abundance of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method on also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy compounds that expression reference protein isoform peptides and 22566 to 225068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention.
                                                                                                                        A method has been developed for the diagnosis of human rheumatoid
Disclosure; Page 20; 157pp; English.
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7 AA; Sequence

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Gaps

. 0

Score 21; DB 19; Length 9; Pred. No. 2.1e+05; 1; Mismatches 2; Indels

46.7%; ilarity 57.1%; Conservative 1

Query Match Best Local Similarity Matches 4; Conserv

7 AA;

Sequence

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tribules (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method.

Comprises: (a) analysing a sample of serum or plasma and optionally syno-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in the cone or more persons without RA, where the relative abundance of the chosen feature in the sample with the abundance of that chosen feature in the sample indicates the presence or chosen feature or features in the sample indicates the presence or studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins on the used in clinical studies for testing drugs for therapy of RA, for purification of antibodies to compounds that promote or inhibit their activity, which are then used as Protein succods. Yal 844 to Yal 840 to 
                                                             ö
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          has been developed for the diagnosis of human rheumatoid
                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                          Rheumatoid arthritis diagnostic protein isoform peptide #179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis of human rheumatoid arthritis by two-dimensional
                  Length 7;
                                                             Indels
                DB 20; L
2.1e+05;
                                                             ö
                Score 20; DB 2; Pred. No. 2.1e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 21; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend RR;
44.4%; Scc.
100.0%; Pre
0; '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Ile, Leu
                                                                                                                                                                                                                                                       Y42028 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB00763
                                                                                                                                                                                                                                                                                                                                              09-DEC-1999 (first entry)
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patel TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-571871/48.
                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9947925-A2
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                                                                                                         9
                                                                                                                                                  sgad 5
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                                                                                                       SGAD
                                                                                                                                                                                                                                                                                                     Y42028;
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                                                             Matches
                                                                                                                                                                                                                  RESULT
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Sequences shown in W70077 to W70086 represent methionyl-tRNA (Wet-tRNA)

Synthetase fragments from different bacterial species. These are used

for designing degenerate primers (V43887 to V43890) used for isolating

Met-tRNA synthetase gene fragment by PCR from M. tuberculosis and M.

Kansasii. The invention provides an expression vector comprising a

nucleic acid encoding a mycobacterial aminoacyl-tRNAs (atRNA) (especially

Met-tRNA) synthetase under control of transcriptional signals that can be

CC used to transform suitable host cells. The nucleict acids and host cells

are used for the recombinant production of mycobacterial amino acyl tRNA

Synthetases, especially of methionyl tRNA synthetase. The enzymes are

used by the organism in protein synthesis, and as such, the recombinant

c anzyme can be used to identify candidate drugs for use as antibiotics

towards mycobacteria, especially M. tuberculosis, which is responsible

CC towards mycobacteria, especially M. tuberculosis, which is responsible

CC towards mycobacteria constructs of the nucleic acids can also be

Cused in antisense inhibition of the synthetase gene. The recombinant

c arzyme allows quick assays in screening of antibiotics. Present testing
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seeing their effect. This is time consuming as the bacteria are generally slow growing. Use of the enzyme also prevents researchers from having to
                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis; mycobacterial; methlonyl-tRNA synthetase; enzyme; antiblotic; tuberculosis; Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant genes encoding mycobacterial amino acyl tRNA synthetases - useful for recombinant production of the enzyme for use in screening of antibiotics against Mycobacterium tuberculosis
                                                       Gaps
                                                       ö
                 Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schimmel PR;
                                                     Indels
                                                                                                                                                                                                                                                                                                                               Thermus thermophilus methionyl-tRNA synthetase fragment.
DB 20; Leu., 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sassanfar M,
               44.4%; Score 20; DB 100.0%; Pred. No. 2.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Columns 33-34; 32pp; English.
                                                                                                                                                                                                                 W70077 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinis SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             slow growing. Use of the enzy work with pathogenic strains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94US-0305766.
96US-0584226.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0584226
                                                                                                                                                                                                                                                                                             (first entry)
                                                    4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                            Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-480383/41.
               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lee SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CUBI-) CUBIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-SEP-1994;
11-JAN-1996;
                                                                                                                                                                                                                                                                                           28-OCT-1998
                                                                                    3 SGAD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5798240-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1998
                                                                                                                       2 sgad
                                                                                                                                                                                                                                                        W70077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kim S,
                                                                                                                                                                                 RESULT 27
                                                    Matches
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Length 9;

44.4%; Score 20; DB 19;

9 AA;

Sequence

Query Match

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New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
                                                                                                                                                                        Human, cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
                                                                                                                                                                                                                                                                                                                                                                                             (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Fig 12; 173pp; English.
                                                       Y55587 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                  98GB-0005877
                                                                                                                  (first entry)
                                                                                                                                             HLA binding plu-1 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor-papadimitriou J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                  17-JAN-2000
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                                                                                                                                                                                                                                 Synthetic
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                                                                                    Y55587;
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                              RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a human cancer-associated polypeptide plu-1. The plu-1 polypeptide can be recombinantly expressed by standard recombinant methodology. Detection of the plu-1 nucleic acid or the polypeptide is used for the following: (1) diagnosis (including imaging) and prognosis of, and determination of susceptibility to, cancer, specifically ovarian or breast cancer; and il) treating cancer (by inducing an immune response against cancer cells, e.g. as a vaccine, or by antisense inhibition). Antigens derived from the polypeptide are used to generate activated cytocoxic T lymphocytes, or dendritic cells, for subsequent return to the patient for treatment of cancer. The polypeptide may also be used to identify inhibitors of plu-1 activity. Fragments of the polypeptide, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (to induce an anti-idiotype response or where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conjugated to cytotóxic agents). The plu-1 antigen is expressed more commonly in breast tumors than some known tumor antigens. Sequences Y55320-629 represent predicted peptides from the plu-1 polypetide which may bind to the human class I alleles B27, A2, A3 and All.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
                                                                                                                                                                                                                                                          Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
               Gaps
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               Indels
Pred. No. 2.1e+05;
; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                          Y55545 standard; peptide; 9 AA.
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    98GB-0005877
                                                                                                                                                                                                    17-JAN-2000 (first entry)
                                                                                                                                                                                                                                 HLA binding plu-1 peptide.
               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taylor-papadimitriou J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 4; Conservai
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Best Local Similarity
Matches 3; Conserv
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                                          1 YLSGAD
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                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                  RESULT
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The invention relates to a human cancer-associated polypeptide plu-1. The plu-1 polypeptide can be recombinantly expressed by standard recombinant methodology. Detection of the plu-1 nucleic acid or the polypeptide is used for the following: (i) diagnosis (including imaging) and prognosis used for the following: (i) diagnosis (including imaging) and prognosis of, and determination of susceptibility to, cancer, specifically ovarian or breast cancer; and ii) treating cancer (by inducing an immune response against cancer cells, e.g. as a vaccine, or by antisense inhibition).

Contoxic I lymphocytes, or dendritic cells, for subsequent return to the patient for treatment of cancer. The polypeptide may also be used to dentify inhibitors of plu-1 activity. Fragments of the polypeptide, and antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (to induce an anti-idiotype response or where conjugated to cytocoxic agents). The plu-1 antigen is expressed more commonly in breast tunnors than some known tunnor antigens. Sequences x 55320-629 represent predicted peptides from the plu-1 polypetide which may bind to the human class I alleles B27, A2, A3 and A11.
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Best Local Similarity
Matches 4; Conserva
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02-JUL-1999 (first entry)
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                                                                                                                                                        WO9916787-A1.
                                                                                                                               Homo sapiens.
                                                                                                                                                                                                          22-SEP-1998;
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                                                                                                                                                                                                                                                 26-SEP-1997;
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5 gddin
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                                                                                                                                                                                                                                                                                                                                                                                                                                       having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also having a human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen -bearing cells are normally induced by an antigen from of a peptide fragment bound are particularly important in the form of a peptide fragment bound are particularly important in tumour rejection and in fighthing viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) are prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also the used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The period of the immungentic particular and also the used to the immungent paperides are also useful
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                                                  Immunogenic peptide having a human leukocyte antigen binding motif #2429
                                                                         Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                             New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \cdot
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Pred. No. 2.1e+05;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                            Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                            Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 124; 150pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y05407 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                            Sette A, Kubo RT, Sidney J,
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57.18;
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                        01-DEC-1999 (first entry)
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                                                                                                                               vaccine; immunisation.
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Best Local Similarity
Matches 4; Conserv
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| ylsegdm 7
                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                        Synthetic
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Y47818;
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Human; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma; neuron; anti-apoptotic; cerebroprotective; neuroprotective; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death; BH3 domain; BCL-2 homology domain; BAK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a bcl homology domain 3 (BH3 domain) of the invention, derived from a proapoptotic member of the BCL-2 family. The BH3 polypeptide can be used in a method for promoting apoptosis in a target cell, especially where the cell is a cancer cell a virus infected cell or an autoantibody producing cell. The BH3 polypeptide can be used in therapeutic compositions for freating disease including cancer, other lymphoproliferative conditions, arthritis, inflammation, and autoimmune diseases, which may result from the down regulation of cell death
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                                                                   BH3 domain; cell death agonist; bcl homology domain; BCL-2 family; apoptosis promoter; cancer cell; virus infected cell; inflammation; autoantibody producing cell; cancer; lymphoproliferative condition; arthritis; autoimmune disease; therapy.
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Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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80.08;
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Human BAK BH3 domain.
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Best Local Similarity
Matches 4; Conserv
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WPI; 2000-106018/09.
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                                                                                                                                                                                                                                                                                                                                                                            9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine.
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  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The patent discloses specific truncated BAX (tBAX) proteins
which inhibit neuronal apoptosis induced by trophic factor deprivation.
The anti-apoptotic tBAX proteins include tBAX70, tBAX78
and their mutants. These proteins contain the N-terminal region and at
least a portion of the BH3 domain of BAX alpha and lacking only the
transmembrane domain. The tBAX protein lacking only the
transmembrane domain has been shown to have anti-apoptotic activity.
The tBAX proteins are used to treat diseases associated with neuronal
apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury,
spinal cord injury, head trauma and stroke. tBAX proteins
truncating at amino acid 68 of the BH3 domain of BAX alpha also have
anti-apoptotic activity because Asp at position 68 is shown to be
important for BAX activity and is conserved in all BCL-2 family members.
The present sequence is a BH3 domain of human BAK protein, a
propopolic protein belonging to BCL-2 family that is involved in
regulation of neuronal programmed cell death. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Allele-specific binding motif; major histocompatibility complex; MHC; HLA; HLAA-A2.1; cytocoxic T cell response; antigen; microbial infection; hepatitis; AIDS; malaria; condyloma acuminatum; cancer; prostate cancer; renal carcinoma; cervical carcinoma; lymphoma; tumour.
                                                                                                                                     Truncated BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                                                                                                                                        Disclosure; Flg 3; 43pp; English.
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80.08;
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                      99WO-US24747.
                                            98US-0177315
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Best Local Similarity 80.0
Matches 4; Conservative
                                                                  (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIM-) EPIMMUNE INC.
                                                                                          Easton
                                                                                                               WPI; 2000-339513/29.
                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
                        22-0CT-1999;
                                            22-OCT-1998;
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5 gddin 9
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27-APR-2000
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                                                                                           Johnson EM,
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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Peptides Y54171-Y54236 represent immunogenic peptides comprising an allele-specific binding motif for the major histocompatibility complex callele-specific binding motif for the major histocompatibility complex common modecule HiA, e.g. HiA-A21. The peptides have conserved residues at certain positions such as positions 2 and 9 Also, the peptides do not comprise negative binding residues at other positions, such as positions (2 1, 3, 6 and/or 7 (peptides 9 amino acids long) and at polsons 1, 3, 4, 5, 7, 8 and/or 9 (peptides 9 amino acids long). The peptides are used to induce a cytocoxic T cell response to a preselected antigen. The method comprises contacting cytotoxic T cells from a patient (optionally expressing a specific MMC class I allele) with the present peptides. Cromprises contacting cytotoxic T cells from a patient (optionally expressing a specific MMC class I allele) with the present peptides. Crital hepatitis B and C, human papilomavirus (HPV) infection, AIDS, cytomagalovirus (CM), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Crital hepatitis B and C, human papilomavirus (RPV) infection and in peptides in conjunction with other treatments. The antigenic peptides can be used to elicit cytotoxic T lymphocytes (CTLS) ex vivo and in cytor. The resulting CTLS can be used to treat chronic infections (viral conventional corns of therapy. The peptides may also be used to produce monoclonal antibodies, which are useful as potential diagnostic or therapeutic can expend to conventional corns of the peptides may also be used as diagnostic reagents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                 Novel HLA binding immunogenic peptides used to induce T cell activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20; DB 21; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sojar HT;
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Southwood S;
                                                                                                                                                                                                            and to induce an immune response
                                                                                                                                                                                                                                                                                               Claim 1; Page 33; 42pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enzyme Inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active; latent; substrate subtraction phage display peptide library; identification; kinase; phosphatase; serpin.
                                                                                                                    The present peptide was prepd. by chemical synthesis, on the basis of an amino acid sequence deduced from the DNA sequence of the cloned P. gingivalis fimbrillin gene described in J. Bacteriol, 170, 1658, 1988. The peptide inhibits the adhesion of P. gingivalis to saliva coated surfaces, and is therefore useful for preventing periodontitis by application to teeth and gums, esp. in dentifices, mouthwashes or topical formulations, or by admin. as a vaccine. In an assay to determine the effect of the peptide on Peptide resulted in a percentage binding inhibition of approx. 30 %.
                           Peptide inhibitor of Porphyromonas gingivalis adhesion to saliva coated surface - useful for preventing periodontitis by application to the teeth and gums esp. in dentifrices, mouth:washes or topical formulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substrate subtraction phage display peptide libraries – used to distinguish between active and latent forms of enzyme, e.g. serine
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                                                                                                                                                                                                                                                                                                                                   42.2%; Score 19; DB 17; Length 6; 60.0%; Pred. No. 2.1e+05; Live 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enzyme inhibitor peptide SEQ ID NO:80.
                                                                                               Claim 1; Columns 17-18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; Page 67; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W56879 standard; peptide; 6 AA.
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WPI; 1996-341445/34.
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                                                                                                           6 AA;
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1 ngadl
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                                                                                                                                                                                                  P93755 arabidopsis
Q83100 unidentifie
Q06708 saccharomyc
                                                                                                                                                                                                                              Q9sa76 arabidopsis
Q9uvj5 botrytis ci
 borrelia bu
          schizosacch
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=S85;
MEDLINE, 97017599.

REDLINE, 97017599.

"Endoglucanase G from Fibrobacter succinogenes S85 belongs to a class of enzymes characterized by a basic C-terminal domain.";
of mixpmes characterized by a basic C-terminal domain.";
EMBL; U33887; AAB38548.1;
EMBL; U33887; AAB38548.1;
EMBL; U33887; AAB38548.1;
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INTERPRO; IPRO01547; -.
PFAM; PF00150; collulase; 1.
SEQUENCE 519 AA; 56848 MW; B06D2113B10FF27E CRC64;
                                                                                                                                                                                                                                                                                                               047916 PRELIMINARY; PRT; 519 AA.
047916;
01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY - 2000 (TrEMBLrel. 13, Last annotation update)
ENDOGLUCANASE CELG.
                                                                                                                                                                                                                                                                                                                                                                         Fibrobacter succinogenes (Bacteroides succinogenes).
Bacteria; Fibrobacteria; Fibrobacter.
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Last sequence update)
Last annotation update).
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050747
014167
Q99521
Q9QRQ7
Q9QRQ8
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P93755
Q83100
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09UVJ5
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P94599
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031716;
01-738-1998 (TrEMBLrel. 05, C;
01-738-1998 (TrEMBLrel. 05, Li
01-JUN-2000 (TrEMBLrel. 14, Li
YKPA PROTEIN.
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Matches 7; Conserv
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030217 archaeoglob
091u0 listeria mo
074798 schizosacch
051274 borrella bu
Q1679 homo saplen
0999v6 drosophila
099v16 thermotoga
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Q20618 caenorhabdi
                                                               Search time 113.2 Seconds (without alignments)
7.424 Million cell updates/sec
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                                                                                                                                                                                        297973
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                      297973 seqs, 93374136 residues
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Q92VIO
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1: sp_archea:*
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394 YFEGSDLNL 402

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TISSUE-BRAIN;
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SEQUENCE
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RA AZEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA AZEVEGO V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA AZEVEGO V., Burschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Brouillet S., Brischi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Fabret C., Furilich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Farilich S.D., Emmerson P.T.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Alibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Rosahara Y., Klaerr-Blanchard M., Klein C.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kutia K., Lapidus A., Lardhols S., Lauber J., Lazarevic V.,
RA Kutia K., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Roche B., Rose M., Sadale Y.,
RA Sexiguchi J., Sekowska A., Seror S.J., Serror F., Shin B.S., Soldo B.,
RA Seto T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannen K., Vassanctti A.,
A Viari A., Wambutt K., Wedler E., Voshikawa H.F., Zoshikawa H.F., Zoshikawa H.F., Zoshikawa H., Zoshikawa H., Zoshikawa H., Zoshikawa H.F., Zoshikawa H., Zoshikawa H., Zoshikawa H.F., Zoshikawa H.F., Zoshikawa H.F., Zoshikawa H.S., Zoshikawa H., Zoshikawa H.F., Zoshikawa H.S., Z
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Hemila H., Palva A., Paulin L., Arvidson S., Palva I.;

Hemila H., Palva A. Bacillus subtilis: sequence analysis and identity to pyruvate dehydrogenase.";

J. Bacteriol. 172:5052-5063(1990).
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EMBL: 299111; CAB1316.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.6%; Score 34; DB 2; Length 540; 66.7%; Pred. No. 63; Live 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61055 MW; F5588EDF1B948109 CRC64;
                           Firmicutes; Bacillus/Clostridium group;
                                                       Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF012285; AAC24918.1; -. INTERPRO; IPR001617; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00005; ABC_tran;
SEQUENCE 540 AA; 6105
                                                                                                                                                STRAIN=168;
MEDLINE; 98044033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                 SEQUENCE FROM N.A.
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Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-1168
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                                 Bacteria;
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Gaps

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1 YLSGADLNL 9

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                                                                                                              Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Length 763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ003123; CAA05878.1; -.
HSSP; P14604; 2DUB.
                                                                                                                                                                                                                                                                             Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJ222637; CAA10897.1; -. HSSP; P14604; 2DUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83291 MW; 81E72BA3222D7FF2 CRC64;
                                                         01-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) GASTRIN BINDING PROTEIN-LIKE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AMA-2000 (TrEMBLrel. 13, Last annotation update)
FGF-2 BINDING PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00067; 3HCDH; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 34; DB
Pred. No. 95;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                   01-AUG-1998 (TrEMBLrel. 07, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO, IPRO02135; -. PFAM; PF00378; ECH; 1. PFAM; PF00725; 3HCDH; 1. PROSITE; PS00067; 3HCDH; 1.
                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR001128; -
INTERPRO; IPR001753; -
INTERPRO; IPR001753; -
PFAM; PF00378; ECH; 1.
PFAM; PF00725; 3HCDH; 1.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                       01-AUG-1998 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001128; -. INTERPRO; IPR001753; -.
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>763
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                                                                                                                                                                       Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       763 AA;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Equus caballus (Horse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
  Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rieder S., Checa-Cortes M.L., Joerg H., Stranzinger G.;
"An equine sequence homologous to melanocyte protein 17 (PMEL17)
                                            SEQUENCE FROM N.A.
Federagala N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.
Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Llu S.
Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AC060695, AAD30730.1;
INTERPO. IPRO02290;
INTERPO. IPRO02290;
                                                                                                                                                                                                                                                                                     73.3%; Score 33; DB 10; Length 404; 66.7%; Pred. No. 73; 2; Indels ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Length 461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mapped to chromosome 6q23.";
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases
EMBL, AF075708, AAC97108.1;
INTERPRO; IPR000601;
                                                                                                                                                                                 PROSTIE; PEO0009; pkinase; 1.
PROSTIE; PEO0107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSTIE; PS00108; PROTEIN_KINASE_ST; 1.
PROSTIE; PS0011; PROTEIN_KINASE_ST; 1.
SEQUENCE 404 AA; 45664 MW; 17BD70E18A25B063 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               461 AA; 49334 MW; 12752AF6C1EC373D CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
MELANOCYTE PROTEIN 17 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                461 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%; Score 33; DB
75.0%; Pred. No. 85;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 66./۳
احد 6; Conservative
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Matches 6; Conser
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59 YLAGADLS 66
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NON_TER
SEQUENCE
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097884
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
FILMIS. 3 PROTEIN
FILMIS. 3. PROTEIN (Mouse-ear cress).
Eukaldopesis thallana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dixon L.K., Twigg S.R.F., Baylis S.A., Vydelingum S., Bristow C., Hammond J.M., Smith G.L.; Wulledelide sequence of a 55 kbp region from the right end of the genome of a pathogenic African swine fever virus isolate (Malawi LIL20/1)."
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-MALAWI LIL20 /1;
MEDLINE; 94014996.
Vydelingum S., Baylis S.A., Bristow C., Smith G.L., Dixon L.K.;
"Duplicated genes within the variable right end of the genome of pathogenic isolate of African swine fever virus.";
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                                                                                                                 Length 773;
                                                                                                                                             Indels
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                                         1 46 POTENTIAL.
47 773 POTENTIAL.
773 AA: 84815 MW; 53B860715681445C CRC64;
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                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                 .
9
PS00086; CYTOCHROME_P450; UNKNOWN_1.
PS00166; ENOYL_COA_HYDRATASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1
Pred. No. 62;
1; Mismatches
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                                                                                                                                                                                                                                                                        352 AA
                                                                                                               DB
96;
                                                                                                                                           4; Mismatches
                                                                                                               Score 34;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                          ORF L3R.
African swine fever virus (ASFV).
Viruses; dsDNA viruses, no RNA stage;
African swine fever-like viruses.
                                                                                                                                                                                                                                                                        PRT;
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J. Gen. VILTOL. 7:1655-1684(1994).
EMBL; X71992; CAA50855.1;
INTERPRO; IPR002595;
PRAM; PF01671; ASFV_360; 1.
PRODOM; PD003462; -1.
SEQUENCE 352 AA; 40682 MW; 6156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gen. Virol. 74:2125-2130(1993).
                                                                                                               75.6%;
55.6%;
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75.0%;
                                                                                                                                             5; Conservative
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STRAIN-MALAWI LIL20 /1;
MEDLINE; 94292916.
                                                                                                              Query Match
Best Local Similarity
Matches 5; Conserv
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108 FIAGADLNM 116
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                       1 YLSGADLNL 9
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                                                                      SEQUENCE
PROSITE;
PROSITE;
                             Signal.
SIGNAL
CHAIN
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Gaps

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Indels

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Kawarabayaal Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakal M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Rushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyper-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                 Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
EMBL; AP000005; BAA30312.1; -.
HSSP; P00644; 1SNQ.
INTERPRO; IPR000080; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%; Score 32; DB 1; Length 176; 62.5%; Pred. No. 45; 1: Indels 1: ve 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE, PEO0555; SNASE, 1.
PROSITE, PSO1123; TNASE_1; 1.
PRODOM; PD002274; -; 1.
SEQUENCE 176 AA; 20010 MW; CB802A467B17E29E CRC64;
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Last sequence update)
Last annotation update)
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Last annotation update)
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        Mismatches
                                                                                                                                                                                                                                                                                                      176AA LONG HYPOTHETICAL THERMONUCLEASE
                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                              PRT;
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      2,
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01-NOV-1996 (TrEMBLrel. 01, L
01-MAY-2000 (TrEMBLrel. 13, L
F49E12.5 PROTEIN.
F49E12.5.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 62.5
Matches 5; Conservative
    6; Conservative
                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JUN-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                             Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=OT3;
MEDLINE; 98344137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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751 ISGSDLNL 758
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128 YLNGTDIN 135
                                              2 LSGADLNL 9
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Q20618;
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      Matches
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Q20618
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                                                                                                                                                                                                       Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaudhan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Embryophyta, Tracheophyta; Spermatophyta,
Magnoliophyta, eudicotyledons, Rosidae, eurosids II; Brassicales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%; Score 33; DB 5; Length 596; 87.5%; Pred. No. 1.2e+02; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. Beavan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.W. Mayer K.F.X., Lemcke K., Schueller C.; Chr. T.X., Lemcke K., Schueller C.; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                           Matthews L.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ALO80253; CAB45809.1;
INTERRO; IPR002099;
INTERPRO; IPR002465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z78545; CAB01766.1; -.
INTERPRO; IPR002897; -.
PFAM; PF01587; MCT; 1.
SEQUENCE 596 AA; 63884 MW; 4EEFB6CB56CBC7B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0723; SUBTILIEIN.
PROSITE; PSO0136; SUBTILASE_ASP; UNKNOWN_1.
PROSITE; PSO0138; SUBTILASE_SER; 1.
PROSITE; PS00140; RECEPTOR_CYTOKIRES_2; UNKNOWN_1.
SEQUENCE 856 AA; 91814 MW; OC9FD624F5DF81E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       856 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY 2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14, PUTATIVE SERINE PROTEINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.5%,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                          MEDLINE; 94150718.
                                                                                   SEQUENCE FROM N.A.
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09SUN6; 9NNS60 0

ACC DDT ACC DD

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Gaps

RA RA RA RE RE DR DR DR DR SQ

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STRAIN-VC-16 / DSM 4304 / ATCC 49558;
MEDLINE; 98049343.
Rienk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
Peterson S., Reich C.I., Weidman J.F., McDonald L., Utterback T.,
Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
Sadow P.M., D'Andrea K.P., Bowman C., Fujil C., Garland S.A.,
Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NCTC 7973;
Morse R., O'Hanlon K., Virji M., Collins M.D.;
"Isolation of rifampin-resistant mutants of Listeria monocytogenes and
                                                                                                                                                                                                                                                                     "The complete genome sequence of the hyperthermophilic, sulphate-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          their characterization by rpoB gene sequencing, temperature sensitivity for growth, and interaction with an epithelial cell
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Pred. No. 1.1e+02;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32; DB 1; Length 391
Pred. No. 1.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                391 AA; 43065 MW; F26932FA3A20E8C0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Clin. Microbiol. 37:2913-2919(1999).
EMBL. X16468; CAB56705.1; -.
Hypothetical protein.
SEQUENCE 392 AA; 43566 WW; 398B953F0B668D9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update) HYPOTHETICAL 43.6 KDA PROTEIN. Listeria monocytogenes. Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Listeria.
                                                                                                                                                                                                                                                                                    reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL; AE001105; AAB91208.1; -.
TIGR: AF0018; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 AA.
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                                                                                                                                                                                                                                                                                                                                                            INTERPRO: IPRO02155; -. PFAM; PF00108; thiolase; 1. PROSITE; PS00737; THIOLASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
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01-NOV-1998 (TrEMBLrel. 08, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.18;
66.78;
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62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.1
Best Local Similarity 66.7
Matches 6; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 YVSGAELGL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |::|:||
221 YVTGSDLN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YLSGADLNL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RLUO;
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Q9RLU0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaudahan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FULL CE FROM N.A.
STRAIN-CV. COLUMBIA;
ROUNSIEY S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
STRAIN-CV. COLUMBIA;
Rounsiey C.M., Fraser C.M., Somerville C.K., Venter J.C.;
Shen M., Konning C.M., Fraser C.M., Somerville C.K., Venter J.C.;
Arabidopsis thallana chromosome II BAC T6A23 genomic sequence.";
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005A99; AAC67360.1;
SEQUENCE 377 AA; 41905 MW; 0D066A25C9A02930 CRC64;
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Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                             Length 350;
                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                        PFAN; PF02117; Sra; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SEQUENCE 350 AA; 40044 WW; F92F03B3C7347B68 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
3-KETOACYL-COA THIOLASE (ACAB-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 10;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                           DB 5;
1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    377 AA.
                                                                                                                                                                                                                                                                                                                                           Score 32; DB 9
Pred. No. 1e+03
1; Mismatches
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                                                                                                                                                                Nature 368:32-38(1994).
EMBL; Z66520, CAA91390.1; -.
INTERPRO: IPRO02144; -.
INTERPRO: IPRO02106; -.
                                                                                                                                                                                                                                                                                                                                             71.18;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.1%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10,
                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 66./۰
استاهه 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| || || 1|
286 YMSSADYNL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T6A23.22 PROTEIN.
T6A23.22.
                                                                                                                                                                                                                                                                                                                                                                                                                         1 YLSGADLNL 9
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367 YVSGADL 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGADL 7
                                                                                                                                              elegans."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 13
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Matches

ô qq ö

Gaps

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Gaps

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T 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
T 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HYPOTHETICAL 57.9 KDA PROTEIN.
SPEC2D10.04.
Schizosaccharomyces pombe (Fission yeast).
C Edwaryota: Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
N [1]
SQUENCE FROM N.A.
STRAIN-972H-;
A WOOd V., Rajandream M.A., Barrell B.G., Taylor K., Harris D.;
L Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
R EMBL; AL031788; CAA2116.2.1; ---
O SEQUENCE 658 AA; 72731 MW; 40EB066BB970B4F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                          Query Match 71.1%; Score 32; DB 3; Length 658; Best Local Similarity 75.0%; Pred. No. 2.1e+02; Matches 6; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          ||:| |||
159 YLAGFDLN 166
                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGADLN 8
     Qγ
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Search completed: December 16, 2000, 02:00:57 Job time: 5931 sec

625 T

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2000, 01:51:13; Search time 91.14 Seconds

(without alignments)
6.267 Million cell updates/sec
Ferfect score: 45
Sequence: 1 YLSCADLNL 9
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 182106 seqs, 63460219 residues
Total number of hits satisfying chosen parameters: 182106
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database: PIR_65:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | , | | | SUMMARIES | |
|---------------|-------|---------------------|--------|-----|-----------|--------------------|
| Result No. | Score | * Query Match | Length | DB | ID | Description |
| - | | 0 00 | | ; ; | 01636x | • |
| ۱, | 7 | • | 100 | ۹ (| 100 | Carcinempt yourc a |
| 7 (| * * | • | 000 | ۷ (| COT/O4 | oxygenase-rer |
| ν, . | 34 | | 540 | ~ (| ESSES | |
| 4 | 33 | m. | 491 | ~ | A49179 | melanoma antigen h |
| Ŋ | 33 | œ. | 596 | 7 | T23685 | hypothetical prote |
| ø | 33 | 73.3 | 856 | 7 | T10585 | serine proteinase |
| 7 | 32 | 71.1 | 108 | 7 | 537313 | hlyU protein - Vib |
| æ | 32 | 71.1 | 167 | 7 | S29515 | lktC protein - Pas |
| 6 | 32 | 71.1 | 167 | 7 | A30169 | 19 |
| 10 | 32 | 71.1 | 176 | 7 | F71064 | micrococcal nuclea |
| 11 | 32 | 71.1 | 275 | ~ | PN0511 | gastrin-binding pr |
| 12 | 32 | 71.1 | 350 | ~ | T22450 | hypothetical prote |
| 13 | 32 | 71.1 | 391 | ~ | B69252 | 0 |
| 14 | . 32 | 71.1 | 502 | ~ | S50519 | hypothetical prote |
| 15 | 32 | 71.1 | 658 | ~ | T40107 | hypothetical 57.9 |
| 16 | 32 | 71.1 | 661 | Н | KFHU13 | coagulation factor |
| 17 | 32 | 71.1 | 668 | 7 | A46013 | coagulation factor |
| 18 | 32 | 71.1 | 714 | ~ | C65007 | ~ |
| 19 | 32 | 71.1 | 737 | ~ | C70132 | |
| 20 | 32 | 71.1 | 763 | 7 | JC2108 | Ø |
| 21 | 32 | 71.1 | 860 | 7 | C72338 | hypothetical prote |
| 22 | 32 | 71.1 | 896 | 7 | H70233 | |
| 23 | 32 | 71.1 | 1473 | 7 | 138791 | cal |
| 24 | 32 | 71.1 | 1986 | | S28353 | probable polyketid |
| 25 | 31 | 68.8 | 184 | - | 847020 | |
| 26 | 31 | 68.9 | 265 | ~ | T14645 | hypothetical prote |
| 27 | 31 | 68.8 | 295 | ~ | T44541 | hypothetical prote |
| 28 | 31 | 6.89 | 311 | ~ | 3 | □ |
| 59 | 31 | 68.8 | 324 | ~ | F71243 | probable translati |

| MAP kinase (EC 2.7 | cell division cycl | protein kinase (EC | protein kinase Mpk | beta-N-acetylgluco | hypothetical prote | hypothetical prote | ribulose-bisphosph | hypothetical prote | hypothetical prote | | hypothetical prote | cell division prot | sublancin 168 lant | long-chain-fatty-a | transcription init |
|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|
| S53536 | 149066 | S52419 | A54805 | A33396 | T24929 | T24930 | A45507 | T20840 | T21262 | T21261 | T22188 | G75582 | T12784 | A49681 | A23308 |
| 7 | 7 | ~ | 7 | 7 | 7 | 7 | 7 | ~ | ~ | ~ | ~ | 7 | 7 | ٦ | 7 |
| 360 | 360 | 360 | 361 | 399 | 401 | 402 | 408 | 441 | 445 | 454 | 472 | 655 | 705 | 763 | 778 |
| 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.8 | 68.89 | 68.8 | 68.8 | 68.8 | 68.8 | 68.89 | 68.9 |
| 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 |
| 30 | 31 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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C;Accession: B69861
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berr C; Bron, S.; Brouillet, S.; Buschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Brid, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, Nature 390, 249-256, 1997
A;Authors: Foulgar, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galich, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Forono, S.; Hullo, M. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Laphdus, A.; Lardino A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Seklguchi, J.; Sekowska, A.; Se akeuchi, M.; Tamakoshi, A.; Taranaka, T.; Terpstra, P.; Tognoni, A.; Tara, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tara, K.; Yasumoto, K.; Yata, K.; Yoshida A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; Tara, K.; Yasumoto, M.; Mallie, The complete genome sequence of the Gram-positive bacterium Bacillus subtill A;Reference number: A69580; MID:98044033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Gene: ykpA
C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog
C; Keywords: ATP; P-loop
F;17-228/Domain: ATP-binding cassette homology <ABCl>
F;34-41/Region: nucleotide-binding motif A (P-loop)
F;35-512/Domain: ATP-binding cassette homology <ABC2>
                                                                                                                                                                                                                                                                                                                                                            R; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A; Reference number: A81500; MUID:20150255
A; Accession: C81704
A; Status: preliminary
A; Modelule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:299111; GB:AL009126; NID:92633699; PIDN:CAB13316.1; PID:e11850
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF39281.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
                                                                                                                                                                                                                       - Chlamydia muridarum (strain Nigg)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-540 <KUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                           C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
C;Accession: C81704
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABC transporter (ATP-binding protein) homolog ykpA - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.6%; Score 34; DB 2; Length 540; larity 66.7%; Pred. No. 44; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 41;
                                                                                                                                                                                                                   monooxygenase-related protein TC0425 [imported]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.68;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Residues: 1-506 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 YLSGVNLNI 298
    605 YLSGANLNL 613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YLSGADLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: TC0425
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    g
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A; Accession: 159098
A; Molecule type: maka
A; Residues: 31.702 kE2.
A; Crossreferences: GB:M16234; NID: 9180240; PIDN: AAA51972.1; PID: 9180241
B; Sispen, D: Paxton, R.J.; Neumaler, M.; Shively, J.E.; Wagener, C.
B; Accession: A26831
A; Molecule type: Res. Commun. 147, 212-218, 1987
A; Molecule type: protein
A; Residues: 35-46 kIE
B; Thomas, P: 70th, C.
B; Commer: A26831; MUID: 87326349
A; Molecule type: Res. Commun. 170, 391-396, 1990
A; Title: Carcinocembryonic antigen binding to kupffer cells is via a peptide located at the A; Residues: 35-46 kIE
B; Thomas, P: 70th, C.
B; Accession: A3490
A; Title: Carcinocembryonic antigen binding to kupffer cells is via a peptide located at the A; Residues: X, 140-151, X, 153-156 kTHO
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: GB:CBA
A; Residues: GB:CBA
A; Residues: X, 140-151, X, 153-159 (X, 153-156 kTHO)
A; Residues: X, 140-151, X, 153-139 (X, 1413-14)
A; Residues: X, 140-151, X, 140
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F;678/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Gly) (in mature form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA

**Residues: 1-7 < RES->

**Residues: 1-7 < RES->

**Residues: 1-7 < RES->

**Residues: 1-8 < RES->

**Simmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.

**Riximmermann, W.; Ortlieb, B.; Friedrich, R.; von Kleist, S.

**Proc. Natl. Acad. Sci. U.S. A. 84, 2960-2964, 1987

**A; Title: Isolation and characterization of cDNA clones encoding the human carcinoembryon A; Reference number: 159098; MUID: 87204247
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 35-141 <KRN>
R;Willococks, T.C.; Craig, I.W.
Genomics 8, 492-500, 1990
A;Title: Characterization of the genomic organization of human carcinoembryonic antigen
A;Reference number: 154224; MUID:91139118
                                                                                                                                                                                                                                                                                                       and estimation of the size of the carcinoemb
A;Accession: S31737
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-141 CAB2>
A;Cross-references: EMBL:X62151
A;Cross-references: EMBL:X62151
A;Cross-references: EMBL:X62151
A;Title: Identification of three new genes and estimation of the size of the carcinoe
A;Reference number: A44476; MUID:93052339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: 154224
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.9%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Gaps

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Length 506; Indels ö

Gaps

m

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Gaps

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RESULT 7
S37313
http protein - Vibrio cholerae
C; Species: Vibrio cholerae
C; Species: Vibrio cholerae
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 26-Aug-1999
C; Accession: S37313
R; Williams, S:G.; Attridge, S:R.; Manning, P.A.
Mol. Microbiol. 9, 751-760, 1993
A; Title: The transcriptional activator HlyU of Vibrio cholerae: nucleotide sequence a A; Reference number: S37312; MUID: 94049116
A; Reference conneber: S37312; MUID: 94049116
A; Residues: 1-108
A; Residues: 1-108
A; Residues: 1-108
A; Cross-references: EMBL: X66866; NID: 9403330; PIDN: CAA47336.1; PID: 9403332
C; Genetics:
A; Gene: hlyU
C; Superfamily: arsenical resistance operon repressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Pasteurella haemolytica
C.Species: Pasteurella haemolytica
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C.Accession: S29515
E.Lo. R.Y.C.; Strathdee, C.A.; Shewen, P.E.
Infect. Immun. 55, 1987-1996, 1987
A.Fitle: Nucleotide sequence of the leukotoxin genes of Pasteurella haemolytica Al.
A.Reference number: S29515; MUID:87306837
A.Accession: S29515
A.Molecule type: DNA
A.Residues: 1-167 <LOR>
A.Residues: 1-167 <LOR>
A.Residues: 1-167 <LOR>
A.Residues: 1-167 <LOR>
C.Genetics:
A; Reference number: 216991
A; Accession: T10885
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-856 < GEV>
A; Cross-references: EMED: ALO80253; GSPDB: GN00062; ATSP:F9F13.80
A; Experimental source: cultivar Columbia; BAC clone F9F13
C; Genetics: ATSP: F9F13.80
A; Map position: AMED: AMED
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Pred. No. 20;
1; Mismatches
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Pred. No. 32;
0; Mismatches
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66.78;
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77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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C;Superfamily: hemolysin C
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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                                                                                                                                                                                                                                                         melanoma antigen homolog rpel - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Nov-1996
C;Accession: A49179; 145861
R;Kim, R.Y.; Wistow, G.J.
R;Kim, R.Y.; Wistow, G.J.
A;Title: The CDNA RPE1 and monoclonal antibody HMB-50 define gene products preferentiall A;Reference number: A49179; MUID:93122163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serine proteinase homolog F9F13.80 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: G-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999 (C.Accession: T10585 R.Sevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein M03B6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T23685
R;Matthews, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Experimental source: retinal pigment epithelium A:Note: sequence extracted from NCBI backbone (NCBIN:122438, NCBIP:122439) C:Genetics: A:Gene: RPE1
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79;
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A;Molecule type: DNA
A;Residues: 1-596 <WIL>
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Pred. No. 64;
2; Mismatches
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A; Reference number: 219782
A; Accession: T23685
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87.5%;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-491 <KIM>
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Best Local Similarity
Matches 6; Conserv
                                                                            394 YFEGSDLNL 402
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Best Local Similarity
Matches 7; Conserv
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| YLAGADLS 100
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                                    1 YLSGADLNL 9
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A;Map position: X
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Gaps

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Gaps

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gastrin-binding protein precursor - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999
C;Accession: PNO511
R;Baldwin, G.S.; Casey, A.; Weinstock, J.
Bjochem. Biochem. Biophys. Res. Commun. 193, 560-564, 1993
A;Title: Partial structure of the gene encoding the 78KDa gastrin binding protein enc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 23/1; 37/1; 60/3; 105/2; 151/3; 191/3; 226/1
C; Superfamily: enoyl-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase; 3-hydroxyacyl-CoA
F; 1-36/Domain: signal sequence #status predicted <SIG>
F; 57-276/Product: gastrin-binding protein #status predicted <MAT>
F; 62-218/Domain: enoyl-CoA hydratase homology <ECH>
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C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: B69252
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, W.F.; McDonald, L.
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A;Experimental source: clone F49E12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F49E12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R; Thomas, K.
Submitted to the EMBL Data Library, October 1995
A; Accession: T22450
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71;
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A;Map position: 2
A;Introns: 97/3; 171/3; 238/2; 300/3
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Best Local Similarity 66.7%;
Matches 6; Conservative
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A; Residues: 1-275 <BAL>
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98 FIAGADINM 106
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286 YMSSADYNL 294
      128 YLNGTDIN 135
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B69252
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A; Residues: 1-167 <HIG>
A; Residues: 1-167 <HIG>
A; Residues: 1-167 <HIG>
A; Cross-references: GB:M24197; GB:M34943; GB:M34944; NID:g150511; PIDN:AAA25542.1; PID:g
B; Highlander, S.K.; Englar, M.J.; Weinstock, G.M.
J; Bacteriol 172, 2343-2350, 1990
A; Title: Secretion and expression of the Pasteurella haemolytica leukotoxin.
A; Reference number: A35254; MUID:90236888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           micrococcal nuclease (EC 3.1.31.1) PH1212 precursor - Pyrococcus horikoshii
N;Alternate names: thermonuclease homolog
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: F71064
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
DNA Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137
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A;Reference number: A30169; MUID:89210283
A;Accession: A30169
                                                                                                                                                                                                                                            C;Species: Pasteurella haemolytica
C;Date: 12-Oct_1989 #sequence_revision 12-Oct-1989 #text_change 16-Jul-1999
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                                                                                                                                                                                                               hypothetical 19.9K protein (lktA 5' region) - Pasteurella haemolytica
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R; Highlander, S.K.; Chidambaram, M.; Engler, M.J.; Weinstock, G.M.
DNA 8, 15-28, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; not compared with conceptual translation
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C;Superfamily: micrococcal nuclease
C;Keywords: hydrolase
F;1-27/Domain: signal sequence #status predicted <SIG>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-20 <HI2>
A; Residues: 1-20 <HI2>
A; Cross-references: GB:M24197; GB:M34943; GB:M34944
C; Superfamily: hemolysin C
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Pred. No. 32;
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77.88;
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Best Local Similarity 77.8
Matches 7; Conservative
                                   55 YCSWADLNL 63
1 YLSGADLNL 9
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A;Cross-references: EMBL:X86790
A;Genetics: C14
C;Genetics: CC05>
A;Gene : MIPS:YELO70w
A:Map position: 5L
C;Genetics: <C14>
A;Gene: MIPS:YRN073c
A;Gene: MIPS:YRN073c
A;Map position: 14R
C;Superfamily: conserved hypothetical protein YEL070w
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159 YLAGFDLN 166
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A;Molecule type: DNA
A;Residues: 1-438 <LEV)
A;Residues: 1-438 <LEV)
A;CESSION: S63411
A;CESSION: S6
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A;Residues: 1-502 <AND>
A;Cross-references: EMBL:Z71688; GSPDB:GN00014; MIPS:YNR073c; NID:g1302609; PIDN:CAA9635
Nature 390, 364-370, 1997

A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed A:Reference number: A69250; MUID:98049343
                                                                                                                                                                                                                                                                                                                  A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: DNA A:Molecule type: DNA A:Molecule type: DNA A:Residues: 1-391 CKLE> A:Cross-references: GB:AE001105; GB:AE000782; NID:g2689428; PIDN:AAB91208.1; PID:g265063 C; Superfamily: probable 3-ketoacyl-CoA thiolase MTH1177
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N;Alternate names: hypothetical protein N3810; hypothetical protein YNR073c
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 20-Jun-2000
C;Accession: S50519; S63406; S63411; S54055; S63890
E;Dietrich, R.S.
Submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae cosmids 9669, 8334, 8199, and lambda clone
A;Reference number: S50428
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A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-502 CDIE>
A; Genetics: C05
A; Genetics: C05
B; Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.; Vissers, S.
Bubmitted to the Protein Sequence Database, April 1996
A; Reference number: S62920
A; Accession: S63406
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A; Accession: S63890
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R;Levesque, H.; Lepingle, A.; Nicaud, J.M.; Gaillardin, C. Yeast 12, 289-295, 1996
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A; Genetics: C14
R; Levesque, H:; Lepingle, A.; Nicaud, J.M.; Gaillardin,
submitted to the Protein Sequence Database, April 1996
A; Reference number: $63411
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A;Molecule type: DNA
A;Residues: 1-438 <LEF>
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A; Molecule type: DNA
A: Residues: 1-438 < LEW>
A; Cross-references: EMBL: X86790
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Best Local Similarity 66.75
Matches 6; Conservative
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A; Residues: 1.658 <WOO>
A; Rossidues: 1.658 <WOO>
A; Cross-references: EMBL:AL031788; PIDN:CAA21162.1; GSPDB:GN00067; SPDB:SPBC2D10.04
A; Experimental source: strain 972h-; cosmid c2D10
C; Genetics:
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Cibate: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
Ciscossion: T40107
Swood, V.; Rajandream, M.A.; Barrell, B.G.; Taylor, K.; Harris, D.
submitted to the EMBL Data Library, September 1998
A;Reference number: 221906
A;Accession: T40107
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Andcoule type: DMAA
                                                      Gaps
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Length 502;
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Pred. No. 1.4e+02;
1; Mismatches 1; Indels
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  Ouery Match 71.1%; Score 32; DB 2; Best Local Similarity 62.5%; Pred. No. 1e+02; Matches 5; Conservative 2; Mismatches
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                            hypothetical 57.9 kd protein
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A;Map position: 2
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423 YLTGVDMN 430
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006186 mus musculu 02913 archaeoglob 027495 methanobact 000446 colletotric 060290 methanococc P46502 caenorhabdi P43686 homo sapien P54775 mus musculu
                      vesicular s
mus musculu
    neurospora
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                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDITHE; 90258861.
SCHICHE; 90258861.
SCHICHEH, Thompson J., Bona M., Hefta L.J.F., Maruya A.,
Hassauer M., Shively J.E., von Kleist S., Zimmermann W.;
"Cloning of the complete gene for carcinoembryonic antigen: analysis
of its promoter indicates a region conveying cell type-specific
expression.";
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-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
-!- TISSUB SPECIFICITY: FOUND IN ADDIOCATIONARS OF ENDOBERMALLY
DERIVED DIGESTIVE SYSTEM EPITHELIUM AND FETAL COLON.
-!- PTM: COMPLEX IMMUNOREACTIVE GLYCOPROTEIN WITH A MW OF 180 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE; 89122014.
Barnett T., Goebel S.J., Nothdurft M.A., Elting J.J.;
"Carcinoembryonic antigen family: characterization of cDNAs coding for NCA and CEA and suggestion of nonrandom sequence variation in their conserved loop-domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Olkawa S., Nakazato H., Kosaki G.;
"Primary structure of human carcinoembryonic antigen (CEA) deduced
from cDNA sequence.";
                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immermann W., Ortlieb B., Friedrich R., von Kleist S.;
"Isolation and characterization of cDNA clones encoding the human carcinoembryonic antigen reveal a highly conserved repeating
                                                                                                                                                                                                        P06731;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100)
(CD66E ANTIGEN).
           042632
P13615
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                                                                                                                                              ALIGNMENTS
                              HBGF_MOUSE
PYRD_ARCFU
OTC_METTH
YF44_METTH
          KPC1_COCHE
RRPL_VSVJH
                                                                      PGL1_COLLN
YZ33_METJA
PRS6_CAEEL
                                                                                                      PRS6_HUMAN
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11142
11174
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363
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ID CCEM_HUMAN
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Q99014 trichoderma
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Q07968
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         GenCore version
Copyright (c) 1993 - 2000
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GPC5_HUMAN
F13B_HUMAN
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ECHA_HUMAN
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MK14_CANFA
MK14_HUMAN
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RS13_SULAC
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KPC1_TRIRE
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MK14_XENLA
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YL86_YEAST
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Listing first 45 summaries
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Match Length DB
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COMPRISING 60% CARBOHYDRATE.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
7 IG-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC ANTIGEN
SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00047; ig; 7.
Immunoglobulin domain; Glycoprotein; GPI-anchor; Membrane; Signal.
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REMOVED IN MATURE FORM.
IG-LIKE DOMAIN 1.
IG-LIKE DOMAIN 2.
IG-LIKE DOMAIN 4.
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IG-LIKE DOMAIN 5.
IG-LIKE DOMAIN 5.
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                                                                  DATABASE: NAME-PROW; NOTE-CD guide CD66e entry; WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD66E.HTM"
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                                                                                                                                                                                                                                                                                                                                                                                            M59709; -; NOT_ANNOTATED_CDS.
M59710; -; NOT_ANNOTATED_CDS.
M29540; AAA51967.1; -.
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EMBL, M59259, AAA62835.1;
EMBL, M59260, AAA62835.1;
EMBL, M59260, AAA62835.1;
EMBL, M59260, AAA62835.1;
EMBL, M59709; NOT_ANNOTEMBL, M597109; NOT_ANNOTEMBL, M297100; NAT_ANNOTEMBL, M297100; NAT_ANNOTEMBL, M2642, AAA51967.1;
EMBL, M16542, AAA51967.1;
PIR, A36319; A36319.
INTERPRO; IPR003006; NATEMPRO; IPR003006; NATEMBLA, PF00047; 19; N
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                           Pichia pastoris (Yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Protein translocation into peroxisomes.";
blol. Chem. 271:32483-32486(1996).
-!- FUNCTION: INVOLVED IN PEROXISOME BLOSYNTHESIS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PMIT_BOOUN STANDARD; PRT; 491 AA.
006154;
001.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
MELANOCYTE PROTEIN PMEL 17 (RETINAL PIGMENT EPITHELIAL-SPECIFIC PROTEIN) (FRAGMENT).
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CYTOPLASMIC (POTENTIAL).
6853C5EA5C67EC34 CRC64;
MISSING (IN REF. 4).
6299AE26CDDBDB5C CRC64;
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                                                              Score 40; DB 1;
Pred. No. 1.2:
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01-NOV-1997 (Rel. 35, Last annotation update)
PEROXISOMAL MEMBRANE PROTEIN PAS2 (PEROXIN-3)
                                                                                                                                                                                                                                               455 AA.
                                                                               Pred. No. 1.2;
1; Mismatches
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Pred. No. 14;
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01-NOV-1997 (Rel. 35, Last sequ
01-NOV-1997 (Rel. 35, Last anno
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DOMAIN

1 15 M

TRANSMEM 16 33 PC

DOMAIN

34 455 CS

SEQUENCE 455 AA; 51973 MW;
320 M.
76795 MW;
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                                                              88.9%;
88.9%;
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                                                              Query Match 88.9
Best Local Similarity 88.9
Matches 8; Conservative
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320
702 AA;
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353 YLNNADINL 361
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CONFLICT
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PM17_BOVIN
AC Q06154;
DT 01-NOV.
DT 15-UUV.
DE MELANOV
DG PRELIA
OS BOS TAI
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OC BURALY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=KIDNEY;
MEDLINE; 96305376.
Hjaelm G., Murray E., Crumley G., Harazim W., Lundgren S., Onyango I.,
Ek B., Larsson M., Juhlin C., Hellman P., Davis H., Aekerstroem G.,
Rask L., Morse B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          LRP2_HUMAN STANDARD, PRT: 4655 AA.
P98164: 000711; Q16215;
01-0CT-1996 (Rel. 34, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 PRECURSOR (MEGALIN)
                                                                                                                                                                                                                                                                                                                                                                       Gaps
                             X 13 AA APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                             8:
CXS-RICH.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
W; 2BBFE5DFBD397D6D CRC64;
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                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 1; Length 491;
                                                                                                                                                                                  Transmembrane; Glycoprotein; Melanin biosynthesis; Repeat.
                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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75.08;
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199
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                                                                                                                                                                                                                                                                                                                              491 AA;
                       MEDLINE; 93122163.
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A Rounnas M. Z., Loukinova E. B., Stefansson S., Harmony J.A.K.,
Brewer B.H., Strickland D.K., Argraves W.S.;
Indentification of glycoprotein 330 as an endocytic receptor for
"Identification of glycoprotein 330 as an endocytic receptor for
"Identification of glycoprotein 330 as an endocytic receptor for
"Identification of glycoprotein 330 as an endocytic receptor for
"Identification of glycoprotein 350 as an endocytic receptor for
"Identification of glycoprotein 1000 as an endocytic receptor for
"Identification of glycoprotein 1000 as an endocytic receptor for
"Identification of glycoprotein 1000 as an endocytic receptor for
"Identification of glycoprotein 1000 as an endocytic receptor in the glycoprotein 1000 as an endocytic struction and 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Chromosomal localization of human genes for the LDL receptor family member glycoprotein 330 (LRP2) and its associated protein RAP (LRPAP1).";
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"Cloning and sequencing of human gp330, a Ca(2+)-binding receptor with potential intracellular signaling properties."; Eur. J. Biochem. 239:132-137(1996).
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-i- TISSUE SPECIFICITY: ABSORPTIVE EPITHELIA, INCLUDING RENAL
PROXIMAL TUBULES.
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-!- SIMILARITY: CONTAINS 37 LDL-RECEPTOR CLASS B DOMAINS.
-!- SIMILARITY: CONTAINS 17 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 4 SH3-BINDING DOMAINS.
-!- SIMILARITY: CONTAINS 1 SH2-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                  Knaak C., Argraves W.S.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Korenberg J.R., Argraves K.M., Chen X.N., Tran H., Strickland D.K., Argraves W.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Exp. Cell Res. 212:344-350(1994).
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SEQUENCE OF 2705-4453 FROM N.A.
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INTERPRO; IPR001881;
INTERPRO; IPR002172;
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INTERPRO; IPR000152;
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P01130; 1AJJ.
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MEDLINE; 95048397.
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                                                                                                                                                                                                                       CALCIUM-BINDING (POTENTIAL).
R CLASS B 30.
R CLASS B 31.
R CLASS B 33.
R CLASS B 33.
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STRAIN-CLASSICAL 01 / 217561;

MEDLINE; 94049116.

Williams S.G., Attridge S.R., Manning P.A.;

"The transcriptional activator HlyU of Vibrio cholerae: nucleotide sequence and role in Virulence gene expression.";

Mol. Microbiol. 9:751-760(1993).

--- FUNCTION: UPREGULATES THE EXPRESSION OF THE HEMOLYSIN GENE, HLYA, AND MAY PROMOTE EXPRESSION OF OTHER VIRULENCE DETERMINANTS IN VIVO. IT MAY HAVE BOTH POSITIVE AND NEGATIVE REGULATOR ACTIVITIES.
--- SIMILARITY: BELONGS TO THE ARSR FAMILY OF TRANSCRIPTIONAL
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Pred. No. 2.8e+02;
; Mismatches 1; Indels
LDL-RECEPTOR CLASS A 17.

LDL-RECEPTOR CLASS A 19.

LDL-RECEPTOR CLASS A 20.

LDL-RECEPTOR CLASS A 21.

LDL-RECEPTOR CLASS A 22.

LDL-RECEPTOR CLASS A 23.

LDL-RECEPTOR CLASS A 24.

LDL-RECEPTOR CLASS A 24.

LDL-RECEPTOR CLASS A 25.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

CALCIUM-BIND)

LDL-RECEPTOR CLASS B 31.

LDL-RECEPTOR CLASS B 31.

LDL-RECEPTOR CLASS B 32.

LDL-RECEPTOR CLASS B 32.

LDL-RECEPTOR CLASS B 34.

EGF-LIKE 13.

LDL-RECEPTOR CLASS A 29.

LDL-RECEPTOR CLASS A 29.

LDL-RECEPTOR CLASS A 30.

LDL-RECEPTOR CLASS A 31.

LDL-RECEPTOR CLASS A 35.

LDL-RECEPTOR CLASS B 35.

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01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
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66.7%;
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6; Conserv
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P52695;
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LUL-RECEPTOR CLASS A 1.

LUL-RECEPTOR CLASS A 3.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 4.

LUL-RECEPTOR CLASS A 5.

LUL-RECEPTOR CLASS A 5.

LUL-RECEPTOR CLASS A 6.

LUL-RECEPTOR CLASS A 7.

EGF-LIKE 1.

EGF-LIKE 2.

LUL-RECEPTOR CLASS B 1.

LUL-RECEPTOR CLASS B 1.

LUL-RECEPTOR CLASS B 3.

LUL-RECEPTOR CLASS B 4.

LUL-RECEPTOR CLASS B 4.

LUL-RECEPTOR CLASS B 9.

EGF-LIKE 3.

LUL-RECEPTOR CLASS B 9.

EGF-LIKE 3.

LUL-RECEPTOR CLASS B 9.

LUL-RECEPTOR CLASS B 11.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS A 12.

LUL-RECEPTOR CLASS A 13.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS A 11.

LUL-RECEPTOR CLASS B 12.

LUL-RECEPTOR CLASS B 22.

LUL-RECEPTOR CLASS B 22.

LUL-RECEPTOR CLASS B 23.

LUL-RECEPTOR CLASS B 24.

EGF-LIKE 9.

LUL-RECEPTOR CLASS B 25.

LUL-RECEPTOR CLASS B 26.

LUL-RECEPTOR CLASS B 27.

LUL-RECEPTOR CLASS B 
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                    R PFAM; PF00057; 1d1_recept_a; 36.

R PRINTS; PR00057; 1d1_recept_b; 37.

R PRINTS; PR00021; LDLRECEPTOR.

R PROSITE; PS00012; EGF_1; 1.

R PROSITE; PS01186; EGF_2; 9.

R PROSITE; PS011209; LDLRA_1; 31.

R PROSITE; PS01068; LDLRA_1; 31.

R PROSITE; PS01069; LDLRA_2; 36.

M Glycoprotein; Repeat; Endocytosis; Coated pits; Transmembrane; M Receptor; EGF-like domain; Signal; Polymorphism.

I SIGNAL

Z GLAIN

Z GHAIN

Z CHAIN

Z CHAIN

Z CHAIN

R PECEPTOR-RELP
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EGF-LIKE 10.
LDL-RECEPTOR CLASS
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01-AUG-1990 (Rel. 15, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
LEUKOTOXIN-ACTIVATING LYSINE-ACTIVATINSFERASE LKTC SEROTYPE A1 (EC 2.3.1.-) (TOXIN-ACTIVATING PROTEIN C) (LEUKOTOXIN C).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasteurella haemolytica.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Infect. Immun. 61:5431-5431(1993).
                                                                                                                                                                                                                                                                                                                                                                          Length 108
                                                                                                                                                                                                                                                                                          H-T-H MOTIF (BY SIMILARITY).
4FC1BE6DA960F217 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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DNA_BIND 47 66 H-T-H MOTIF (BY SIMI
SEQUENCE 108 AA; 12293 MW; 4FC1BE6DA960F217 C
                                                                                                                                                                                                                                                                                                                                                                          DB 1;
7.7;
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Pred. No. 7.7;
1; Mismatches
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                                                                                                                                                   EMBL; X66866; CAA47336.1; -. HSSP; P30340; LSMT.
INTERPRO; IPRO01865; -. PFAM: PFO1022; HTH_5; 1. PRINTS; PRO0778; HTHARSR.
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66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                     6; Conservative
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Best Local Similarity
Matches 6; Conserv
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3 YLKGAPMNL 11
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P1.6533;
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      S T X D D R R D D R T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X S T X 
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- FUNCTION: INVOLVED IN EATTY ACYLATION OF THE PROTOXIN (LKTA) AT TWO INTERNAL LYSINE RESIDUES, THEREBY CONVERTING IT TO THE ACTIVE TOXIN. THE ACYL DONOR IS ACP (BY SIMILARITY).
- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTAL).
- SIMILARITY: BELONGS TO THE RTX TOXIN ACYLTRANSFERASE FAMILY.
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 39, Last annotation update)
LEUKOTOXIN-ACTIVATING LYSINE-ACYLTRANSFERASE LKTC SEROTYPE T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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Pred. No. 12;
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OD2ED2CBF2D7F1C5 CRC64;
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77.88;
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Best Local Similarity 77.0
درم 7; Conservative
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STRAIN-SEROTYPE T3;
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P55120;
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Saccharomycetaceae; Saccharomyces.
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GPC5_HUMAN
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MEDLINE; 94041617.

STRAIN-SEROTYPE All;
BUTTOWS L.L., Olah Winfield E., Lo R.Y.C.;
BUTTOWS L.L., Olah Winfield E., Lo R.Y.C.;
"Molecular analysis of the leukotoxin determinants from Pasteurella haemolytica serotypes 1 to 16.";
Infect. Immun. 61:5001-5007(1993).

-! FUNCTION: INVOLVED IN FATTY ACYLATION OF THE PROTOXIN (LKTA) AT TWO INTERNAL LYSINE RESIDUES, THEREDY CONVERTING IT TO THE ACTIVE TOXIN. THE ACYL DONOR IS ACP (BY SIMILARITY).

-! SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

-! SIMILARITY: BELONGS TO THE RIX TOXIN ACYLTRANSFERASE FAMILY.
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL 56.5 KDA PROTEIN IN HXTB 5'REGION AND IN HXT17-COSIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERCENIC REGION.
(YELO70W) AND (YNR073C OR N3810).
Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetales;
                                             ;
                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
LEUGOTOXIN -ACTIVATING LYSINE-ACYLTRANSFERASE LKTC SEROTYPE All
(EC. 2.3.1.-) (TOXIN-ACTIVATING PROTEIN C) (LEUKOTOXIN C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                    Length 167;
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Pred. No. 12;
0; Mismatches 2; Indels
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                    Score 32; DB 1;
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                                           0; Mismatches
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CT_SITE 22 22 PROBABLE.
EQUENCE 167 AA; 19753 MW; 0F4FA5D4E(
                                 Pred. No.
                                                                                                                                                          PRT;
                   71.18;
77.88;
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77.88;
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     Ouery Match
Best Local Similarity 7/...
                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                       Pasteurella haemolytica
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Best Local Similarity
Matches 7; Conserv
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                                                                   1 YLSGADLNL
                                                                                                                                                                                                                                                                                Pasteurella.
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YEIO_YEAST
TO YEIO_YEAST
AC P39941;
DT 01-FEB-1995
DT 01-FEB-1995
DT 01-OCT-2000
DE HYPOTHETICAL
DE INTERGENIC R
GN (YELO70W) AN
COC SACCHATOMYCE
OC EUNARYOLA;
                                                                                                                                                         LKCB_PASHA
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SEQUENCE
                                                                                                                               RESULT 8
LKCB_PASHA
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SEQUENCE FROM N.A. (YEL070W).

STRAIN-S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Rayser A., Komp C., Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Schl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levesque H., Nicaud J.-M., Lepingle A., Gaillardin C.; Sequencing of a 9.2 kb telomeric fragment from the right arm of Saccharomyces cerevisiae chromosome XIV."; Yeast 12:289-295(1996).
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (YNR073C).
Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers S.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 32; DB 1; Length 502;
Pred. No. 40;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPC5_HUWAN STANDARD; PRT; 572 AA. P7833; 060436; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) GLYPICAN-5 PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1-439 FROM N.A. (YNR073C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U18795; AAB65017.1; -
EMBL; Z71688; CAA96356.1; -
EMBL; Z71689; CAA96358.1; -
EMBL; X86790; CAA60486.1; -
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62.5%;
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SGD; S0005356; YNR073C.
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Best Local Similarity
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MEDLINE; 97224481.
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sapiens (Human).
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GLYPICAN-5.

REMOVED IN MATURE FORM (POTENTIAL).

POLY-LEU.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

O-LINKED (GLCNAC. . .) (POTENTIAL).

O-LINKED (GLYCOSAMINOGLYCAN) (POTENTIAL).

S -> F (IN REF. 2).
                                                                                                                                                                               -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (BY
                         "Characterization of glypican-5 and chromosomal localization of human GPC5, a new member of the glypican gene family."; Genomics 40:24-30(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                     -!- TISSUE SPECIFICITY: IN ADULT, PRIMARILY EXPRESSED IN THE BRAIN. ALSO DETECTED IN FETAL BRAIN, LUNG, AND LIVER.
-!- SIMILARITY: BELONGS TO THE GLYPICAN FAMILY.
Veugelers M., Vermeesch J., Reekmans G., Steinfeld R., Marynen P.,
David G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUC-1987 (Rel. 05, Created)
01-AUC-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 18, Last annotetation update)
COAGULATION FACTOR XII B CHAIN PRECURSOR (C. 2.3.2.13) (PROTEIN-GLUTAMINE GAMMA-GLUTAMNZERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                                                                                                                                                                                                                                                                      INTERPRO: IPR001863; -.
INTERPRO: IPR001863; -.
PRAM: PF01153; G1ypican; 1.
PROSITE: PS01207; GLYPICAN; 1.
PROSEQTYCAN; Heparan sulfate; Glycoprotein; Signal; GPI-anchor.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                           MEDLINE: 97470873.
Saunders S., Paine-Saunders S., Lander A.D.;
Saunders S., Paine-Saunders S., Lander A.D.;
Expression of the cell surface proteoglycan glypican-5 is developmentally regulated in kidney, limb, and brain.";
Dev. Biol. 190:78-93(1997).
-: FUNCTION: HEPARAN SULFATE CELL SURFACE PROTEOGLYCAN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 1; Length 572;
Pred. No. 46;
L; Mismatches 1; Indels
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75.0%;
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MIM; 602446; -.
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205
245
572 AA;
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Best Local Similarity
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                                                                                                                                                                                           SIMILARITY).
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                                                                                                                                                                     SIMILARITY)
                                                                                     TISSUE-BRAIN
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P05160;
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F13B.
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grundmann U., Nerlich C., Rein T., Zettlmeissl G.; "Complete cDNA sequence encoding the B subunit of human factor XIII."; Nucleic Acids Res. 18:2817-2817(1990).
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EMBL; M14057; AAA88042.1; -.
EMBL; M14057; AAA88042.1; -.
PIR; A23830; A23830.
PIR; A36397; A36397.
PIR; S09980; S09980.
HSP; P08603; IHFI.
MIM; 134580; -.
INTERPRO; IPRO00436; -.
INTERPRO; IPRO0044; Sushi; 8.
Transferase; Plasma; Blood coagulation; Repeat; Glycoprotein; Signal; Sushi; Disease mutation.
                                                                                                                                                                                                                                                                                                                                                                        Ichinose A., McMullen B.A., Fujikawa K., Davie E.W.;
"Annino acid sequence of the b subunit of human factor XIII, a protein
Composed of ten repetitive segments.";
Blochemistry 25:4633-4638(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 3313189.

Hashiguchi T., Saito M., Morishita E., Matsuda T., Ichinose A.;

Two genetic defects in a patient with complete deficiency of the b-
subunit for coagulation factor XIII.";

Blood 82:145-150(1993).

-I. FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALYTICALLY ACTIVE,

BUT IS THOUGHT TO STABLIZE THE A SUBUNITS AND REGULATE THE RATE

OF TRANSGLUTAMINASE FORMATION BY THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.
-!- DISBASE: A DEFICIENCY IN FAI3 CAN RESULT IN A LIFELONG BLEEDING.
TENDENCY, DEFECTIVE WOUND HEALING, AND HABITUAL ABORTION.
-!- SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS.
                                                                                                                                                         Bottenus R.E., Ichinose A., Davie E.W.; "Nucleotide sequence of the gene for the b subunit of human factor
   Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COAGULATION FACTOR XIII B CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (FEB-1987) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                     Biochemistry 29:11195-11209(1990).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                SEQUENCE OF 2-661 FROM N.A. MEDLINE; 87026535.
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88
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451
                                                                                     SEQUENCE FROM N.A. MEDLINE; 91105054.
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           There are no restrictions on
                                                                                                                                                                                 INTERPRO) IPRO00436; -.
PFAM; PF00084; sushi; 8.
Transferase; Plasma; Blood coagulation; Repeat; Glycoprotein; Signal; Sushi.
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P77399,
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
PUTATIVE FATTY OXIDATION COMPLEX ALPHA SUBUNIT [INCLUDES: ENOYL-COA HYDRATASE (EC 4.2.1.17); 3-HYDRAYASCHOON DELYBROGENASE (EC 11.1.35); 3-HYDROXYBUTYRYL-COA EPIMERASE (EC 5.1.2.3)].
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SUSHI 3.
SUSHI 4.
SUSHI 4.
SUSHI 4.
SUSHI 6.
SUSHI 7.
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SUSHI 7.
SUSHI 9.
SUSHI 10.
BY SIMILARITY.
BY SIMILARI
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COAGULATION FACTOR XIII B CHAIN.
10 X SUSHI (SCR) REPEATS.
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           the European Bioinformatics Institute. Thuse by non-profit institutions as long
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HSSP; P10998; 1VVC.
MGD; MGI:88379; F13B.
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Escherichia coli.
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246 YLSGSDL 252
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01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
COAGULATION PACYOR XII B CHAIN PRECURSOR (EC 2.3.2.13) (PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Natsuume-Sakai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 661;
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57A2FB46560857F2 CRC64;
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1; Mismatches
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246 YLSGSDL 252
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STANDARD;

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01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MX-2000 (Rel. 39, Last annotation update)
MITOCHONDRIAL FIRFUNCTIONAL BAZZME ALPHA SUBUNIT PRECURSOR (TP-ALPHA)
INCLUDES: LONG-CHAIN ENOYL-COA HYDRATASE (EC 4.2.1.17); LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE (EC 1.1.1.35)].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 92:841-845(1995).
-!- FUNCTION: BIFUNCTIONAL SUBUNIT.
-!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COA + H(2)0.
-!- CATALYIIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dehydrogenase deficiency associated with maternal acute fatty liver
                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                Sins H.F., Brackett J.C., Powell C.K., Treem W.R., Hale D.E., Bennett M.J., Gibson B., Shapiro S., Strauss A.W.; The molecular basis of pediatric long chain 3-hydroxyacyl-CoA
                                                                                                                                                                                                                                                                                             Kamijo T., Aoyama T., Miyazaki J.I., Hashimoto T.;
Structural analysis of CDNAs for subunits of human
fatty acid beta-oxidation trifunctional protein.";
Biochem. Biophys. Res. Commun. 199:818-825(1994).
                                                                                                                                                                                                                                                                                                                                                                                    VARIANT AFLP GLN-510.
                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pregnancy.";
                                                                                                                                                                                  HADHA OR HADH.
                                              ECHA_HUMAN
P40939;
                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                           MEDLINE: 97349980.

Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S.,
Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
Yamagata S., Horiuchi T.;
"Construction of a contiguous 874-kb sequence of the Escherichia coli
- K12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).

--- CATALYIX. ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-
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PROSITE; PS00067; 3HCDH; 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; FALSE_NEG.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; FALSE_NEG.
OXIGOTEQUETIS: Table acid metabolism; Multifunctional enzyme; Oxidoreductase; NAD; Lyase; Isomerase.
ACIIVATES A WATER MOLECULE (BY ACIIVATES A WATER MOLECULE (BY ACIIVATES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (R)-3-HYDROXYBUTANOYL-COA.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ENOYL-COA
HYDRATASE/ISOMBRASE FAMILY.
SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE 3-
HYDROXYACYL-COA DEHYDROGENASE FAMILY.
                                             SEQUENCE FROM N.A.
STRIN-K12 / MG1655;
MEDLINE; 97426611,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 714;
                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROVIDES THE ALPHA-PROTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
F4E0A75680039A0D CRC64;
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Pred. No.
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INTERPRO, IPR001753; -.
INTERPRO, IPR002135; -.
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PROSITE; PS00067; 3HCDH: 1.
PROSITE; PS00166; ENOYL_COA_HYDRATASE; 1.
Fatty acid metabolism: Multifunctional enzyme; Oxidoreductase; NAD;
Fatty acid metabolism: Multifunctional enzyme; Oxidoreductase; NAD;
Lyase; Mitochondrion; Transit peptide; Disease mutation.
TRANSIT 1 36 MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA
                                                            -!-SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
-!-SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX
-!-DISEASE: DEFECTS IN HADHA ARE A CAUSE OF MATERNAL ACUTE FATTY
LIVER OF PRECNANCY (AFLP), A SEVERE MATERNAL ILLNESS OCCURING
DURING PRECNANCIES WITH AFFECTED FETUSES: THIS DISEASE IS
CHARACTERIZED BY SUDDEN UNEXPLAINED INFANT DEATH OR HYPOGLYCEMIA
AND ABNORMAL LIVER ENTYMES (REYE-LIKE SYNDROME).
-!-SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE ENOYL-COA
HYDROXYACYL-COA DEHYDROGENASE FAMILY.
-!- PATHWAY: CATALYZES TWO STEPS OF THE FATTY ACID BETA-OXIDATION
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INTERPRO; IPR002135; -.
PFAM; PF00725; 3HCDH; 1.
PFAM; PF00378; ECH; 1.
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HSSP; P14604; 2DUB.
MIM; 600890;
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Gaps

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Indels

Mismatches

ilarity 44.48; Conservative

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ENOYL-COA

SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE HYDRATASE/ISOMERASE FAMILY.

SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.

PATHWAY: CATALYZES TWO STEPS OF THE FATTY ACID BETA-OXIDATION

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oxidation complex is a long-chain enoyl-CoA hydratase: 3-hydroxyacyl-
CoA dehydrogenase bifunctional enzyme."

Comp. Biochem. Physiol. 10981:557-566[1994).

-!- FUNCTION: BIFUNCTIONAL SUBUNIT; CANNOT USE CROTONYL-COA OR 3-
HYDROXYBUTYRYL-COA AS SUBSTRATE.

-!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-
COA + H(12)O.

-!- CATALYTIC ACTIVITY: L-3-HYDROXYACYL-COA + NAD(+) = 3-OXOACYL-COA +
                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
MITOCHONDRIAL TRIFUCTIONAL ENTYME ALBHA SUBUNIT PRECURSOR (TP-ALPHA)
(78 KDA GASTRIN-BINDING PROTEIN) [INCLUDES: LONG-CHAIN ENOYL-COA
HYDRATASE (EC 4.2.1.17); LONG CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE
(EC 11.1.35)].
HADHA OR LCHYD-HAD.
SUS SCTOFE. "
                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yang S.-Y., He X.-Y., Styles J., Luo M.J., Schulz H., Elzinga M.; Primary Structure of the large subunit of trifunctional beta-oxidation complex from pig heart mitochondria."; Biochem. Biophys. Res. Commun. 198:431-437(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
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ACTIVATES A WATER MOLECULE (BY SIMILARITY).
PROVIDES THE ALPHA-PROTON (BY
                                                                                                                                     DB 1; Length 763;
                                                                                                                                                                    Indels
                                        SIMILARITY).
E -> Q (IN AFLP).
/FIId=VAR 002273.
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                                                                                                                                                                  5; Mismatches
                                                                                                                                                    Pred. No. 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hydratase/dehydrogenase family.";
Biochim. Biophys. Acta 1170:211-215(1993).
                                                                                                                                     Score 32;
                                                                                       82959 MW;
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44.48;
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                                                                                       763 AA;
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Best Local Similarity
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98 FIAGADINM 106
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MEDLINE; 94002212.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRIAL TRIFUNCTIONAL ENZYME ALPHA
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Transit peptide.

MITOCHONDRION (POTENTIAL).

MITOCHONDRION (POTENTIAL).
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                                                                                           -!- SIMILARITY: IN THE CENTRAL SECTION; BELONGS TO THE 3-HYDROXYACYL-COA DEHYDROGENASE FAMILY.
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ACTIVATES A WATER MOLECULE
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HSSP; P14604; 2DUB.
INTERPRO; IPR001753; --
INTERPRO; IPR001355; --
PFAM; PF00725; 3HCDH; 1.
PFAM; PF00378; ECH; 1.
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Search completed: December 16, 2000, 03:05:19 Job time: 8039 sec

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Carcinoembryonic antigen; CEA; human; agonist; antagonist; minimune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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Listing first 45 summaries

    protein search, using sw model

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                                                              or antagonists (ID) of human carcinomaryonal antigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (ID) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but GEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA responses. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and
                                    The present invention describes peptides (A) that comprise agonists (Ia)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 5; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y09527 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-326544/27.
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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Y09527
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generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatability complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides W39430-W39734 are used in a novel method for the selection of
                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method of selecting T cell peptide epitope(s) - by measuring stability of HLA class I-peptide complexes on intact B cells
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                                                                                                                                                                                                         Length 9;
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                                                                                                                                                                                                      Score 43; DB 20; L
Pred. No. 2.1e+05;
L; Mismatches 0;
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Pred. No. 2.1e+05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W39723 standard; peptide; 9 AA.
                                                                                                                                                                                                      95.6%;
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96EP-0201145.
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                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
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                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                    1 YLSGADLNL
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26-APR-1996;
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                                                                                                                      Sequence
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Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human carcinoembryonic antigen (CEA). The peptides can bind to a human cleaked bear and are used to exemplify the method of luvention of producing antigen-specific cytotoxic T cells (CTLs) in vir. The method comprises contacting immunogenic peptides from an contecules with antigen presenting cells (APCs) pretreated with antigen presenting cells (APCs) pretreated with purified CDE cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytoxic T cells with APCs pretreated with pre-treatend APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contexted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLS can be used for treating cancers, immune disorders, viral infections, malaria or the context or the patient. The activated or the context or the composition or the context or the patient. The activated context or the composition or the patient or the patient or the context or the composition or the context or the patient or the context or the composition or the context or the patient or the context or the contex
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Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antiqen; HLA; tumour associated antiqen; cancer; antiqen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antiqen.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 9;
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                                                                                                                                                                                                                                                                                                                                                               Southwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 6; Page 75; 104pp; English.
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                 Sette A,
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                                                                                                                                     Homo sapiens.
                                                                                                                                                                      WO9833888-A1.
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                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                               Celis E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytotoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific fimunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptide epitope W77119-W77138 were created for human tumour-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disease specific immunogen - comprises disease specific cytotoxic T lymphocyte epitope used to elicit melanoma specific CTL response
     Gaps
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Pred. No. 2.1e+05;
1; Mismatches 0; Indels
   Indels
                                                                                                                                                                                                                                                                                                                          tyrosinase cytotoxic lymphocyte response; lymphocyte; cysteine-depleted; melanoma.
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 ö
   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYVI-) UNIV VIRGINIA PATENT FOUND.
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                                                                                                                                                                                                                                                                                   CEA synthetic peptide epitope 1.
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 1;
                                                                                                                                                                   W77134 standard; peptide; 9 AA
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88.9%;
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 Conservative
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Best Local Similarity
Matches 8; Conser
                                     1 YLSGADLNL 9
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                                                                                                                                                                                                                                                                                                                                            cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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 Matches
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W70045
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Gaps

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Synthetic.
                                                                                      W09919478-A1
                                                                                                                                      22-SEP-1998;
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                                                                                                                                                                                                            Barzaga E,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Table 10 to 148214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLAA subtypes CE HLAA2.1, Al, A3.2 or A24.1 or HLAA B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or pervent viral infections and cancers in mammals (especially humans) crop prevent viral infections and cancers in mammals (especially humans).

They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLEs x vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful chapturedly and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó;
Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                            New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                 Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen; CEA; human; agonist; antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%; Score 40; DB 20; Length 9; 88.9%; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carcinoembryonic antigen peptide agonist CAP-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                Celis E,
                                                                                                                                                                                                                                                                                                               Claim 1; Page 118; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y09525 standard; peptide; 9 AA.
                                                                                                                                                                                                                                Sidney J,
                                                                                                                                                          98WO-US05039.
                                                                                                                                                                                 98WO-US05039
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                                                immunisation
                                                                                                                                                                                                        (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                     WPI; 1999-551214/46.
                                                                                                                                                                                                                                Kubo RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGADLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 AA;
                                                                                    Homo sapiens
                                                                                                           W09945954-A1
                                                                                                                                                                                 13-MAR-1998;
                                                                                                                                   16-SEP-1999
                                                                        Synthetic
                                                                                                                                                                                                                                Sette A,
                                                vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific fummune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immuno response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zaremba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunisation.
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Best Local Similarity
Thes 8; Conserve
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Sette A,

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proteins. The method comprises determining at least part of the analysis acid sequence of the protein; (b) identifying in the analysis acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunogenic presents is also provided. The products can be used for diagnosis and therapy. The present sequence represents the protein sequence of vaccine 2 708 VI.
                                                                                                                                                                                                                                                                                                                                      The invention relates to a method for the production of non-immunogenic
                                                                                                                                                                                                         Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 20; Length 107;
Pred. No. 0.39;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                             Example 4; Fig 19; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="domain B"
97GB-0016197.
97GB-0025270.
97US-0067235.
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88.9%;
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Best Local Similarity 88.97
                                                                                    (BIOV-) BIOVATION LTD
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                                                                                                                                                                WPI; 1999-045301/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGADLNL 9
31-JUL-1997;
28-NOV-1997;
02-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-MAY-1989;
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                                                                                                                           Carr FJ;
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P93499
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                                                                                                                                                                                                                                                                                                                                             having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic comparatides can bind to a specific HLA allele (i.e. HLA-A subtypes that A21, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) c.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in Individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                                                                                                                                                                                          New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases \dot{}
                                                                                                                                                                                                                                                                                                                                Y45390 to Y48214 represent specifically claimed immunogenic peptides
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                                                                                                                                              Southwood S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.024;
1; Mismatches 0; Indels
                                                                                                                                              Grey HM,
                                                                                                                                              Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein sequence of vaccine 2 708 Vl.
                                                                                                                                                                                                                                                                                       Claim 1; Page 76; 150pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W86133 standard; Protein; 107 AA.
                                                                                                                                            Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.9%;
88.9%;
                   98WO-US05039
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                                                            98WO-US05039
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97GB-0010480
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                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                   WPI; 1999-551214/46.
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Best Local Similarity
Matches 8; Conserv
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                   13-MAR-1998;
                                                          13-MAR-1998;
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21-MAY-1997;
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Sequence

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Gaps

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Mismatches

DB 16; Length 468; 0; Indels

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indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membranebound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           biliary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BGP (1-314)/CEA (490-C-terminal) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CEA (490-C-terminal)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Primer; amplify; polymerse chain reaction;
                                                                                                                                                                                                                                Score 40;
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                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "BGP (1-314)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        R77435 standard; Protein; 493 AA.
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                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                 Local Similarity
nes 8; Conserv
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396 ylsganini 404
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and purifications
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                                                                                                                                       molecules
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                              Query Match
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Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R77435;
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                                                                                                                                   of
                                   fragments - used in assays to determine the antigen in samples also contg. related antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GFI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer, amplify; polymerse chain reaction; PCR; human;
biliary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimaeric protein; PR1A3 epitope; anti-PR1A3 antibody;
                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecules which bind carcinoembryonic antigen - used for the gnosis and treatment of colorectal carcinoma and for isolation
                                                                                                                           CEA fragments can be used in assays to determine the presence and CEA in samples which also may contain related antigens including normal cross-reacting antigen or the 128 kD antigen.
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                                                                                                                                                                                                                                                                 DB 10; Length 178;
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                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                               Score 40; DB 10
Pred. No. 0.71;
L; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colorectal carcinoma; monoclonal antibody
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.+≏= "CEA (490-643)"
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315..468
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                                                                                            Disclosure; page 4; 15pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R77436 standard; Protein; 468 AA
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                                                                                                                                                                                                                                                               88.9%;
88.9%;
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                                   Carcinoembryonic antigen
presence and amt. of the
                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                        178 AA;
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Protein Protein

R77436;

RESULT 11

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PCR; human;

Stewart LMD;

Snary D,

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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
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bound carcinoembryonic antigen (CEA). These chimaeric proteins were
used to identify the PRIA3 epitope. The PRIA3 epitope was found to be
an epitope of CEA within the B3-GPI ragion. Chimaeras in which the CEA
is no longer membrane bound did not react with anti-PRIA3 antibodies
indicating that the PRIA3 epitope is not present in non-membrane bound
hybrid proteins. Antibodies which recognise the PRIA3 epitope are used
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                                                                                                         Score 40; DB 16; Length 493;
Pred. No. 2.3;
1; Mismatches 0; Indels
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/note= "CEA (490-644)"
470..509
/note= "BGP (391-430)"
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/note= "BGP (1-314)"
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                                                                                                                                                                                                                            R77437 standard; Protein; 509 AA.
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88.9%;
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                                                                                                          Query Match 88.9
Best Local Similarity 88.9
Matches 8; Conservative
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396 ylsganini 404
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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
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                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                      Length 509;
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Pred. No. 2.4;
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468..511
/note= "BGP (387-430)"
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                                                                                                                                                                                                                                                                                88.9%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q01567 is the DNA sequence which encodes carcinoembryonic antigen (CEA) R60619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine. R60619 can be used in a reagent composition for detecting neoplastic diseases in biological samples, or in an immunoassay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood.
                                                                                                                                                                                          Gaps
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                                                                                                                                                         DB 16; Length 511;
                                                                                                                                                                                       0; Indels
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                                                                                                                                                         Score 40;
Pred. No.
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ID R60619 standard; Protein; 642 AA.
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                                                                                                                                                       88.9%;
88.9%;
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                                                                                                                                                                                         Conservative
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N-PSDB; Q71567.
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Best Local Similarity
Matches 8; Conserv
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396 ylsganlnl 404
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Score 40; DB 15; Length 642; Pred. No. 3.2;

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015897 homo sapien

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092169 neisseria m

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09149 homo sapien

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038185 ratus norv

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080081 limnodynast
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Q9rq57 buchnera ap
Q9rq49 buchnera ap
Q15889 homo sapien
Q9ucn4 homo sapien
Q9xsy1 canis famil
Q3s792 saccharomyc
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09r7e8 escherichia
09r5m1 staphylococ
P78484 homo sapien
09x810 capra hircu
092009 gallus gall
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044001 aeromonas e
044377 aeromonas t
044468 aeromonas v
04328 aeromonas v
091635 chlamydia t
09ucn5 homo sapien
096417 drosophila
027396 babosia bov
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090498 erythrura 9
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homo sapien
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalía; Eutheria; Rodentia; Sciurognathi; Murídae; Murinae; Rattus.
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
TR4-NS ORPHAN RECEPTOR (FRAGMENT).
                                                      044468
043928
098635
099CN5
096417
027396
028112
098057
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0921E9
0987T2
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0908B9
0916428
0914433
090024
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Q015889
Q015889
Q05821
Q035792
Q090874
Q083332
Q087789
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Q08868
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1D 0663480
DT 001
DT 011
DT 011
DT TF
CGN TF
CGN RESULT
Opps69 gallus gall
050812 methanococc
01620 homo sapien
095953 homo sapien
095953 mus musculu
035953 mus musculu
055184 rattus norv
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P82079 limnodynast
P82003 bombyx mori
P87225 saccharomyc
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9 gallus gall
methanococc
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Q9trw2 oryctolagus
P77556 escherichia
Q15901 homo sapien
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homo sapien
prochloroco
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7.553 Million cell updates/sec
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Copyright (c) 1993 - 2000
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Listing first 75 summaries

    protein search, using sw model

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sp_fung::*
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TISSUE-TIBIAL GLAND;
Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilli and
                                                                                                                                                                                                                                                                                                                                   Limnodynastes interioris (Giant banjo frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
Limnodynastes.
                            Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M., Detera-Wadleigh S.D., "Splice variants of rat TR4 orphan receptor: differential expression of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;

Bombycoidea; Bombycidae; Bombyx.
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Pred. No. 3e+05;
1; Mismatches 2; Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
PROTHORACICOSTATIC PEPTIDE (PTSP).
                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                                                                                                                                           8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Limnodynastes terraereginae.";
Aust. J. Chem. 46:833-842(1993).
-!- MASS SPECTROMETRY: WW=729; METHOD=FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE.
STRAIN=C145 X N140; TISSUE=BRAIN;
Hua Y.-J., Tanaka Y., Nakamura K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                    Endocrinology 137:1562-1571(1996).
EMBL; U59125; AAB02827.1; -.
                                                                                                                                                   37.8%;
50.0%;
                                                                                                                     7 AA; 758 MW;
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Best Local Similarity 50.0
Matches 3; Conservative
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Matches 4; Conserv
           SEQUENCE FROM N.A. MEDLINE; 96198747.
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2 IRGGDL 7
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"Identification of a prothoracicostatic peptide (PTSP) from the larval brain of the S1Lkworm, Bombyx mori."; J. Biol. Chem. 0:0-011999; Lio. chem. 0:0-011999; Lio. chem. 0:0-011899.
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Chave K.J., Snell K., Sanders P.G.;
Chave K.J., Snell K., Sanders P.G.;
"Isolation and characterisation of human genomic sequences encoding cytosolic serine hydroxymethyltransferase.";
Biochem. Soc. Trans. 25:35(1997).
EMBL; Y14492; CAB54844.1; -.
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Eukaryota: Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z73169; CAA97518.2; -.
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(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 12, Last annotation update)
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3878C5B4472AB6C3 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last seq
01-WAY-2000 (TrEMBLrel. 13, Last ann
SHWT PROTEIN (FRAGMENT).
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9 AA; 1090 MW;
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Matches 3; Conserv
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SEQUENCE FROM N.A.
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Conservative
 Best Local Similarity
Matches 3; Conserv
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Urbach E., Chisholm S.W.;
Urbach E., Chisholm S.W.;
Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";
Limnol. Oceanog. 43:1615-1630(1998).
EMBL; AF070193; AAD23233.1; -.
SEQUENCE 8 AA; 799 MW; 10376865B72866D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                   Gaps
                                                                                                                                                                                                                                                                        Fukumaki I., Higasa K.;
"Two novel mutations in Thai patients with hereditary
methemoglobinemia types I and II: a subtle amino acid change causes
instability of NADH-cytochrome b5 reductase.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF061830; AAF06818.1;
Oxidoreductase.
                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Prochlorococcus.
                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                         33.3%; Score 15; DB 4; Length 8; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
                                                Score 15; DB 4; Length 8; Pred. No. 3e+05;
                                                                   Indels
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Last annotation update)
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MW; 76C5B73B5051F6D8 CRC64;
                    7C205721E44AB5B8 CRC64;
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                                                                                                                                                          8 AA.
                                                                   2; Mismatches
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                                                33.3%;
50.0%;
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                                                                   3; Conservative
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Matches 3; Conserv
                                                       Best Local Similarity
Matches 3; Conserv
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8 AA;
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8
8 AA;
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1 GSDNHL 6
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VARIANT
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5 YLS 7
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Q9X3K1;
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Q9UL56;
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DB 2; Length

31.1%; Score 14;

Query Match

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MEDLINE; 92011685.
Stifanl S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J., Schneider W.J.;
The laying hen expresses two different low density lipoprotein receptor related proteins.";
J. Biol. Chem. 266:19079-19987(1991).
SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Gallus.
                                     Gaps
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Benard M., Lagnel C., Pallotta D., Pierron G.;
"Mapping of a replication origin within the promoter region of two unlinked, abundantly transcribed actin genes of Physarum
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Pred. No. 3e+05;
2; Mismatches 2; Indels
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(TrEMBLrel. 02, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LOW DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN
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3e+05;
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                                                                                                                                                                                                                                                                                                                                                        Physarum polycephalum (Slime mold).
Eukaryota; Myxogastria; Physarida; Physarum
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llarity 100.0%; Pred. No. 3e4
Conservative 0; Mismatches
                                   Mismatches
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EMBL; M73459; AAB03706.1; -.
NON_TER 8
100.0%; Pre-
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31.1%;
Best Local Similarity 33.3%;
Matches 2; Conservative
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RESULT 10

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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALCYCLIN-ASSOCIATED PROTEIN, CAP50=CA2+/PHOSPHOLIPID-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tokumitsu H., Mizutani A., Minami H., Kobayashi R., Hidaka H.;
"A calcyclin-associated protein is a newly identified member of the caz+'phospholipid-binding proteins, annexin family.";
J. Biol. Chem. 267:8919-8924(1992).
SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-ONV-1999 (TrEMBLrel. 12, Last annotation update)
SODIUM CHANNEL, VOLTAGE-GATED, TYPE VIII, ALPHA POLYPEPTIDE
(TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT) (FRAGMENT).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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llarity 100.0%; Pred. No. 3e+05;
Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                  31.1%; Score 14; DB 4; Length 9; 100.0%; Pred. No. 3e+05; Live 0; Mismatches 0; Indels
                                                                                                                      Lulli L., Torchiana E., Finocchiaro G.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U77631; AAD15626.1; -.
                                                                                                                                                                                                                9 AA; 1069 MW; 374E2AADC2C699C8 CRC64;
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MEDLINE; 97442476.
Plummer N.W., McBurney M.W., Meisler M.H.;
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Best Local Similarity
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Best Local Similarity
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                                                                                                         TISSUE-BRAIN;
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3 LSG 5
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6 ADL 8
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SEQUENCE
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Bollschweller C., Kuehn R., Klein A.;

Non-repetitive AT-rich sequences are found in intergenic regions of Methanococcus voltae DNA.";

EMBO J. 4:805-809(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Nagalla S.R., Spindel B.R.;
Nagalla S.R., Spindel B.R.;
renetional analysis of the 5'-flanking region of the human gastrin-releasing peptide gene in small cell lung carcinoma cell lines.";
Cancer Res. 54:4461-4467(1994).
BMBL; S73265; AAD14116_1; ...
NON_TER
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
GALACTOCEREBROSIDASE (EC 3.2.1.46) (FRGMENT)
                                                                    01, Created)
01, Last sequence update)
01, Last annotation update)
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Last annotation update)
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Pred. No. 3e+05;
1; Mismatches
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                                   9 AA.
                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NOV-1996 (TrEMBLrel. 01, Last annotation
INTERGENIC AI-RICH DNA SEQUENCE (FRAGMENT).
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ilarity 66.7%;
Conservative
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                                                                                                                                             Methanococcus voltae.
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1 MRGRELPL 8
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"Alternative splicing of the sodium channel SCNBA predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
by 18 tol. Chem. 272:24068-24015(1997).
EMBL: U97672: AABB0914.1;
MGD; MGI:103169; ScnBa.
India channel.
SEQUENCE 9 AA: 898 MW; 22D92865B735B737 CRC64;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 96299786.

Yoshikawa T., Dupont B.R., Leach R.J., Detera-Wadleigh S.D.;
Whew variants of the human and rat nuclear hormone receptor, TR4:

"The sepression and chromosomal localization of the human gene.";
Genomics 35:361-366(1996).

EMBL; U59454; AAB91433.1; -.
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OJTWD6;
OJ-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LED-NPF-1=NEUROPEPTIDE F-RELATED PEPTIDE.
LEDTOCATESA decemilinear (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Chrysomelidae; Chrysomelinae; Leptinotarsa.
                                                                                                                                                                                                                                                                                                                                                                                            Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
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                                                                                                                                        Indels
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                                                                                                                 DB 11; Length
3e+05;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
0RPHAN RECEPTOR TR4-NS (FRAGMENT).
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SEQUENCE 7 AA; 663 MW; 6DDAA8787EB05350 CRC64;
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                                                                                                                                                                                                                                           7 AA.
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Pred. No. 3e+(
0; Mismatches
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100.0%;
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40.0%;
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Best Local Similarity
Matches 2; Conserv
                                                                                                               Ouery Match
Best Local Similarity
Matches 3; Conserv
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5 LSG 7
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SEQUENCE.
MEDLINE; 96245438.

Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B.,
Van Beeumen J., De Loof A.;
Insect neuropeptide F (NPF)-related peptides: isolation from Colorado potato beetle (Leptinotarsa decemlineata) brain.";
Insect Biochem. Mol. Biol. 26:375-382(1996).

SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;
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MEDLINE; 91378498.
MEDLINE; 91378498.
Tikebe M., Hornick T.;
"Determination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C.";
Arch. Biochem. Blophys. 288:538-542(1991).
Arch. Biochem. 9 AA; 1018 MW; 8C901B10533735A5 CRC64;
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MEDLINE; 96400908.
Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;
"Mosaic structure of plasmids from natural populations of Escherichia
                                                                                                                                                                                                                                                                                                                                                  Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALDESMON-PHOSPHORYLATION SITE.
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Last annotation update)
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Pred. No. 3e+05;
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Genetics 143:1091-1100(1996).
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50.0%;
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Best Local Similarity 50.0
Matches 3; Conservative
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01.NOV-1996 (TrEMBLrel. 01, Created)
01.NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 07, Last sequence update)
5.UTR IN IRES SEQUENCES (ISOLATE TH222) (FRAGMENT).
Echovirus 25.
Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
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                                                                                                            MEDLINE; 90349591.
Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P., Hermand P., Salmon C., Cartron J.-P., Colin Y.;
"Molecular cloning and protein structure of a human blood group Rh
    "Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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Last annotation update)
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8 AA: 845 MW; 5CA861B5AB58677B CRC64;
                                                                                                                                                                     polypeptide.";
polypeptide.";
Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990).
EMBL; 297030; CAB09726.1; -..
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Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
Mol. Immunol. 0:0-0(0).
EMBL: U62585; AAB18735.1; -.
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Pred. No. 3e+05;
1; Mismatches
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Pred. No. 3e+05;
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                                      phenotype.";
Am. J. Hum. Genet. 60:808-817(1997).
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Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                   015901,
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 01, Last annotation update)
01-AUG-1998 (TREMBLREL. 07, Last annotation update)
(CLONE XP7B11B) (FRAGMENT).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Matassi G., Cherif-Zahar B., Mouro I., Cartron J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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3e+05;
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EMBL; U50651; AAC44255.1; EMBL; U50653; AAC44236.1; EMBL; U50653; AAC44238.1; EMBL; U50654; AAC44239.1; EMBL; U50656; AAC44240.1; EMBL; U50656; AAC44242.1; EMBL; U50669; AAC44242.1; EMBL; U50669; AAC44242.1; EMBL; U50660; AAC44243.1;
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Hum. Mol. Genet. 0:0-0(0).
EMBL; L32080; AAA73891.1;
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STRAIN-CDC 9179-79;
MEDLINE; 97089747.
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Matches 2; Conserv
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AA;
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MEDLINE: 98208049.
MEDLINE: 98208049.
Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
"Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis.";
Electrophoresis 19:142-151(1998).
EMEL, U40496; AAC60363.1;
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Manorina melanocephala (noisy miner).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                               Erythrura gouldiae (Gouldian finch).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Passeridae; Erythrura.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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       STRAIN-TH222;
Bailly J.L., Borman A.M., Peigue-Lafeuille H., Kean K.M.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, *89074; CAA62259.1; -
NON_TER
SEQUENCE 8 AA; 821 MW; EFC1B5A2D6DDDB76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 12; DB 13; Length 8; Pred. No. 3e+05;
                                                                                        Score 12; DB 12; Length 8;
Pred. No. 3e+05;
2; Mismatches 1; Indels
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
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Last annotation update)
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40.0%;
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                                                                                        Query Match 26.7
Best Local Similarity 40.0
Matches 2; Conservative
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01-NOV-1996 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
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Best Local Similarity
Matches 2; Conserv
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SEQUENCE FROM N.A.
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2 GAQVS 6
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 9179-79) (FRAGMENT).
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Study of the intergenic exer-exeG region and its application as 
simple preliminary test for Aeromonas spp."; 
FEMS Microbiol. Lett. 137:37-44(1996). 
EMBL; X89461; CAA61637.1; -. 
NON_TER 1 SEQUENCE 9 AA; 1059 MM; 785852C69444472B CRC64:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karlyshev A.V., Macintyre S.;
"Study of the intergenic exeF-exeG region and its application as simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; X89466; CAA61647.1; -...
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STRAIN=132, FROM DR M. ALTWEGG UNIV. ZURICH CULTRE COLLECTION.
MEDLINE; 97089747.
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Aeromonas sobria.
Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN 132) (FRAGMENT).
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                                                                                                              Indels
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Pred. No. 3e+05;
1; Mismatches 0; Indels
                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA; 1077 MW; 79E852C6944472B CRC64;
C6C1F2C865B046DE CRC64;
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                                                                DB 13;
3e+05;
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                                                             Score 12; DB
Pred. No. 3e+0
1; Mismatches
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66.7%;
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larity 66.7%;
Conservative
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MEDLINE; 97089747.

Karlyshev A.V., Macintyre S.;

Karlyshev A.V., Macintyre S.;

Study of the intergenic exeF-exeG region and its application as simple preliminary test for Aeromonas spp.";

FEMS Microbiol. Lett. 137:37-44(1996).

FEMS Microbiol. CAA61643.1;

EMBL; X89462; CAA61643.1;

EMBL; X89460; CAA61643.1;

EMBL; X89461;

EMBL; X89461;

EMBL; X89461;

EMBL; X89461;

EMBL; X89461;

EMBL; X89461;
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                                                                                  Q43928 PRELIMINARY; PRT; 9 AA.
Q43928: Q43920; Q43921;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
Q1.NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1.NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                          9 AA; 1059 MW; 785852C69444472B CRC64;
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STRAIN=VARIOUS STRAINS;
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Best Local Similarity
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Matches 2; Conserv
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                                                                                                                                                                      Aeromonas caviae
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2 ELN 4
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2 ELN 4
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN CDC 1306-83) (FRAGMENT).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DNA FOR EXEF-EXEG INTERGENIC REGION (STRAIN ATCC 49659) (FRAGMENT).
                                                                                                                                                                                                                                                                                                       Karlyshev A.V., Macintyre S.;
Study of the intergenic exeF exeG region and its application as a
simple preliminary test for Aeromonas spp.";
FEMS Microbiol. Lett. 137:37-44(1996).
EMBL; x89468; CAA61651.1; -.
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Bacteria; Proteobacteria; gamma subdivision; Aeromonas group;
                                    0; Indels
              Length 9;
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             DB 2;
3e+05;
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             Score 12;
Pred. No.
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66.7%;
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                                                                                                                                           PRELIMINARY;
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Ouery Match
Best Local Similarity
'.^a 2; Conserve
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Best Local Similarity
Lac 2; Conserve
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STRAIN-CDC 1306-83;
MEDLINE; 97089747.
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2 ELN 4
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SEQUENCE
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Length 9;

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Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.;
"Functional and structural mapping of Chlamydia trachomatis species-specific major outer membrane protein epitopes by use of neutralizing monoclonal antibodies.";
Infect. Immun. 59:4147-4153(1991).

SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;
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0
01-MAY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN VARIABLE DOMAIN IV, MOMP VD IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                      Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
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Q9UCN5
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SEQUENCE FROM N.A.
MEDLINE, 99099045.
Izeta A., Smerdou C., Alonso S., Penzes Z., Mendez A., Plana-Duran J.,
Enjuanes L.;
                                                          Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
                                                                                                                                                                                                                                   Gaps
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL FUSION PROTEIN.
HYPOTHETICAL TRANSMISSIBLE GASTROCHIEFITIS VITUS.
Viruses: SSRNA Positive-strand viruses, no DNA stage; Nidovirales; coronavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 93387464.
Vidal H., Crepin K.M., Rider M.H., Hue L., Rousseau G.G.;
Vidal H., orepin G.M., Rider M.H., Hue L., Rousseau G.G.;
"Cloning and expression of novel isoforms of 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase from bovine heart.";
FEBS Lett. 330:329-333(1993).
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                                                                                                             Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; L77326; AAA96415.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 9;
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  01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN 1.
                                                                                                                                             26; AAA96415.1; -.
9 AA; 931 MW; 6D5BD2C865B05044 CRC64;
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NON_TER 9 9 AA; 837 MW; 859CA5BDC7644865 CRC64;
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llarity 66.7%; Pred. No. 3e+05;
Conservative 1; Mismatches (
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Pred. No. 3e+05;
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66.78;
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2: Conserv
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                                                                                      SEQUENCE FROM N.A.
                                            Babesia bovis.
                                                                                                    STRAIN-MO7;
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1 MSG 3
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4 ISG 6
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                   Raboudi N., Julian J., Rohde L.H., Carson D.D.;
"Identification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95).";
J. Blol. Chem. 267:11930-11939(1992).
SEQUENCE 9 AA: 1008 MW: CBS6D0544732C732 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE 2
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Bell M., Cline T'W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF046045; AAC97605.1; -.
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Development 125:3259-3268(1998)
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01-NOV-1996 (TrEMBLREL 01,
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SEQUENCE FROM N.A.
MEDLINE; 95159435.
Elecouet J., Rasschaert D., Lambert P., Levy L., Vende P., Laude H.;
"Complete sequence (20 kilobases) of the polyprotein-encoding gene 1 of transmissible gastroenteritis virus.";
Virology 206:817-822(1995).
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MEDLINE; 88078100.

RASSCHART D., Gelfi J., Laude H.;

"Enteric coronavirus TGEV: partial sequence of the genomic RNA, its organization and expression.",

Biochimie 69:591-600(1987).

EMBL; AJ011482; CAA09625.1; --

SEQUENCE 7 AA; 927 MW; 69D6D7273B5726F0 CRC64;
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"Replication and packaging of transmissible gastroenteritis coronavirus-derived synthetic minigenomes."; J. Virol. 73:1535-1545(1999).
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24.4%; Score 11; DB 12; Length 7;

Best Local Similarity 100.0%; Pred. No. 3e+05;

Matches 2; Conservative 0; Mismatches 0; Indels
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SEX PHEROMONE CPD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
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MEDLINE: 85040388.
MEDLINE: 85040388.
Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Craig R.A., Clewell D.B.;
"Isolation and structure of bacterial sex pheromone, cPDI.";
Science 225:849-8501984).
-i- FUNCTION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF
          P81806
P81807
P81807
P82158
P81675
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P81675
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ACT_CARMA
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GLUR_HUMAN
HTF_TERMO
LCKS_LEUMA
LCKS_LEUMA
RPCMS_STAEP
RPCM_PANBO
UPO6_MOUSE
VGLG_HSV2B
ALIO_CARWA
ALIO_CARWA
FARS_ASCSU
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TRP4_LEUMA
ULAH_HUMAN
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
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Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoidea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley Davey M., East P.D., Thorpe A.;

"Lepidopteran peptides the allatostatin superfamily.";

Peptides 18:1301-13109(1997).

-I. SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA; 1058 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=THORACIC GANGLION;
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAMILI.
PIR; F41978; F41978.
Neuropeptide; Amidation.
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                Query Match
Best Local Similarity
'.has 3; Conserva
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Best Local Similarity
Matches 3; Conserv
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                                                                                                                                                                                                       FAR6_CALVO
P41861;
01-NOV-1995 (
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ID ALLS_CYDPO
AC P82156;
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4 DLN 6
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2 SGQD
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 Gaps
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MEDILNE; 92179466.
Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locustam migratoria."; Regul. Pept. 36:111-119(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBOESOPHAGEAL GANGLION.
PIR; A60065; AKLQIM.
                                                                                                                                                                                                                                                                                                                                   0;
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0
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01-JUL-1993 (Rel. 26, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
LOCUSTANYOINHIBITING PEPTIDE (LOM-MIP).
Locusta migratoria (Migratory locust).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda; Insecta;
Petrygota; Neoptera; Orthopteroida; Orthoptera; Orthoptera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35.6%; Score 16; DB 1; Length 8; 100.0%; Pred. No. 8.8e+04; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMIDATION.
387D7DD4472AB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
736365AB59CAADD8 CRC64;
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0
                                                                                                                                                                       01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
Leucokinin VIII (L-VIII).
Leucophaea maderae (Madeira cockroach).
                                                                                                                                           8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA.
Mismatches
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9 AA; 1060 MW;
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8 AA; 902 MW;
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 Conservative
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Best Local Similarity
-hea 3; Conserve
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3;
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P31799;
                                                                                                                                         LCK8_LEUMA
P19990;
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                                                  FLSG
                                 1 YLSG
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LMIP_LOCMI ID LATE

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Gaps

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MOD_RES

Gaps

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SEQUENCE

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Planta 208:588-598(1999).
-i- FUNCTION: MAY PLAY A STRUCTURAL ROLE IN THE ELAIOPLAST, A TAPETUM-SPECIFIC PLASTIDIAL LIPID ORGANELLE.
-i- TISSUE SPECIFICITY: TAPETUM OF ANTHERS.
NON TER 8
SEQUENCE 8 AA; 989 MW; 9D7B1AA452CAA042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCCIPITAL VENOUS SINUS BLOOD FROM RABBITS KEPT ASLEEP BY ELECTRIC STIMULATION OF THE THALAMUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 77185324.

Monnier M., Dudler L., Gachter R., Maier P.F., Tobler H.J.,
Schoenenberger G.A.:

"The delta sleep inducing peptide (DSIP). Comparative properties of
the original and synthetic nonapeptide.";
Experientia 33:548-552(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                        Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REDUCED MOTOR ACTIVITIES.
-!- MISCELLANEOUS: THIS PEPTIDE WAS OBTAINED FROM DIALYSATES OF
                                                                                                                                   Score 13; DB 1; Length 8; Pred. No. 8.8e+04; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 13; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Panagrellus redivivus.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
U-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last amoniation update)
FMRFAMIDE-LIKE NEUROPEPTIDE PF2 (SADDNFLRF-AMIDE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AA; 849 MW; DDD365BDDAA8787D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Panagrolaimoidea; Panagrolaimidae; Panagrellus
                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA.
                                                                                                                                                                                                                                                                                                                         AA
                                                                                                                                                                                                                                                                                                                                                                                                          DELTA SLEEP-INDUCING PEPTIDE (DSIP).
                                                                                                                                                                                                                                                                                                                         PRT;
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50.0%;
                                                                                                                                     28.9%;
66.7%;
                                                                                                                                     Query Match 28.9
Best Local Similarity 66.7
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FARZ_PANRE
ID FARZ_PANRE
AC P41873;
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P01158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Composition and role of tapetal lipid bodies in the biogenesis of the pollen coat of Brassica napus.";
                                                                                    Gaps
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 39, Last annotation update)
PLAST-2000 (Rel. 39, Last annotation update)
PLASTIDIAL LIPID-ASSOCIATED PROTEIN (FRAGMENT).
Brassica napus (Rape)
Eukaryota, Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Buassicales; Brassicaceae; Brassica.
Brassicales; Rossidae; eurosids II;
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
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MEDLINE; 99349136.
Hernandez-Pinzon I., Ross J.H.E., Barnes K.A., Damant A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 14; DB 1; Length 9;
Pred. No. 8.8e+04;
2; Mismatches 3; Indels
                                                                                    3; Indels
                                                   Length 8;

        MOD_RES
        9
        AMIDATION.

        SEQUENCE
        9 AA;
        969 MW;
        17FF476EB455B04B CRC64;

   922879CABB58640D CRC64;
                                                  Score 14; DB 1; I
Pred. No. 8.8e+04;
0; Mismatches 3;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                      9 AA.
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                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                        Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.18;
Similarity 28.68;
2; Conservative
                                                   31.1%;
50.0%;
   MΜ,
                                                                                    Conservative
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   868
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                                                Query Match
Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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   8 AA;
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                                                                                                                  4 GADLNL 9
                                                                                                                                        GYDFGL 8
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P81707;
15-JUL-1999 (
15-JUL-1999 (
30-MAY-2000 (
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P42993;
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DISULFID

Matches

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SEQUENCE

RESULT 6
1SOT_CYPCA

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STANDARD;
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Best Local Similarity
2; Conservē
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PIR; PQ0012; PQ0012
                                                                                                                                                                                                                                                                                  Hormone; Amidation.
                                                                                                                                        SEQUENCE.
MEDLINE; 66123415.
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                                                                                                                                                                                                                                                                                                                    9 AA;
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                              01-NOV-1995 (
01-NOV-1995 (
01-NOV-1995 (
GLUMITOCIN.
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01-OCT-1996
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        OXYT_RAJCL
P42994;
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SEQUENCE
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2 YIS
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                             Geary T.G., Price D.A., Bowman J.W., Winterrowd C.A., Mackenzie C.D.,
Garrison R.D., Williams J.F., Friedman A.R.;
"Two Embranded-like peptides from the free-living nematode
Panagrellus redivivus.";
Peptides 13:209-214(1992).
-: FUNCTION: MYOACTIVE.
-: FUNCTION: MYOACTIVE.
-: GAUDALLY TO THE BASE OF THE PHARNAX.
-: SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE.
SEQUENCE.
MEDLINE; 73031727.
Acher R., Chauvet J., Chauvet M.-T.;
Acher R., Chauvet J., Chauvet M.-T.;
Phylogeny of the neurohypophysial hormones. Two new active peptides
"Phylogeny of the neurohypophysial hormones. Two new active peptides
"Isolated from a cartillaginous fish, Squalus acanthias.";
Eur. J. Biochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acher R., Chauvet J., Chauvet M.-T., Fontaine M.;
"Identification of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).",
C. R. Acad. Sci., D. Sci. Nat. 274:313-316(1972).
INTERPRO: IPRO00981; ...
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                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  ASPARTOCIN (ASPARGTOCIN).
Squalus accanthias (Spiny dogfish).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Blasmobranchii; Squalea; Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.9%; Score 13; DB 1; Length 9; 28.6%; Pred. No. 8.8e+04; Live 2; Mismatches 3; Indels
                                                                                                                                                                                                            Score 13; DB 1; Length 9;
Pred. No. 8.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                               AMIDATION.
DA0B0729C4576AAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMIDATION.
17F8376EB444404B CRC64;
                                                                                                                                                                                                                                                                                                                                                                            (Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                          9 AA.
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                   (Rel. 32, Created)
                                                                                                                                                                                                          28.9%;
illarity 75.0%;
Conservative 0
                                                                                                                                                                 9 9
9 AA; 1066 MW;
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                                                                                                                                                  Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hormone; Amidation.
DISULFID 1
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Best Local Similarity
Matches 3; Conserv
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Bést Local Similarity
Matches 2; Conserv
                      MEDLINE; 93027659.
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P42999;
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SEQUENCE
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Gaps
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                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajidae; Raja.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides 9:429-431(1988).
-!- FUNCTION: THIS PEPTIDE HORMONE INDUCES GALL BLADDER CONTRACTION AND THE RELEASE OF PANCREATIC ENZYMES IN THE GUT. ITS FUNCTION IN THE BRAIN IS NOT CLEAR.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dasyurus viverrinus (Southeastern quoll).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan Z.W., Eng J., Shaw G., Yalow R.S.; "Cholecystokinin octapeptide purified from brains of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                  Biochim. Nicolary Acta 107:393-396(1965).
-!- FUNCTION: ANTIDIUREIC HORMONE.
-!- SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
INTERPRO; IPRO00981; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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AMIDATION.
DDCAA68378768B5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 13; DB 1; Leng
Pred. No. 8.8e+04;
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17E9C76EB455B04B CRC64;
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(Rel. 25, Last sequence update)
(Rel. 34, Last annotation update)
                                (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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 AA.
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Macropus eugenii (Tammar wallaby), and
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 PRT;
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PROSITE; PS00259; GASTRIN; 1.
                                                                                                    Raja clavata (Thornback ray).
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66.7%;
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8
1064 MW;
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                                                                                                                                                                                                                                                                             the ray (Raia clavata).
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SEQUENCE
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SPECIES-H. AMPHIBIUS;
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P81179;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          CALLIFWRFANIDE 13.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
                                                              Gaps
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MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRFamides) from the blowfly
Calliphora vomitoria.";
Proc. Natl. Acad. Sci. U.S. A. 89:2326-2330(1992).
--- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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"Evolution of neurohypophyseal hormones: isolation of active
principles from rabbits and rats.";
Blochimie 53:1099-1104(1971).
               Score 12; DB 1; Length 8;
Pred. No. 8.8e+04;
!; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
.; Mismatches 1; Indels
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22D10699C87AB6D8 CRC64;
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                         9 AA.
                                                                                                                                                                                                                                                         PRT;
               26.7%;
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50.0%;
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9 AA; 1028 MW;
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MOD_RES 9 9
SEQUENCE 9 AA; 1028 MW
                                                            2; Conservative
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               Query Match
Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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2 YMGWMD 7
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01-NOV-1995
01-NOV-1995
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FARD_CALVO
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Doostdar H., McCollum T.G., Mayer R.T.;
Furtification and characterization of an endo-polygalacturonase from the gut of West Indies sugarcane rootstalk borer weevil (biaprapes
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
ENDO-POLYGALACTURONASE (PC) (EC 3.2.1.15) (FRAGMENT).
Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
EUKARYOLA: Metazoa; Arthropoda; Tracheate, Haxapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cuculiformia; Curculionidae; Entiminae; Entimini; Diaprepes.
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                                                                                                                                                                                                                                                                    SPECIES-A. ACULEATUS;
MEDLINE; 73223515.
Acher R., Chauvet J., Chauvet M.-T.;
"Neurohypophysial hormones and evolution of tetrapods.";
Nature New Biol. 244:124-126(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.7%; Score 12; DB 1; Length 9; 28.6%; Pred. No. 8.8e+04; ive 1; Mismatches 4; Indels
                                                                                                                                            SPECIES-B.PHYSALUS;
Acher R., Chauvet J., Chauvet M.-T.;
"Isolation of finback whale oxytocin and vasopressin.";
Nature 201:191-192(1964).
MEDLINE; 71232719. Ferguagn D.R.; Pickering B.T.; Arginine and lysine vasopressins in the hippopotamus neurohypophysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION.
17F8376EB456D04B CRC64;
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                                                                                Gen. Comp. Endocrinol. 13:425-429(1969)
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PDB; 1XY2; 15-OCT-90.
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Best Local Similarity
Matches 2; Conserv
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Hirata T., Kubota I., Iwasawa N., Takabatake I., Ikeda T., Muneoka Y.; "Structures and actions of Mythlus inhibitory peptides."; Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=P.AMERICANA;
MEDLINE; 81225865.
O'Shea M., Adams M.E.;
"Pentapeptide (proctolin) associated with an identified neuron.";
Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                 "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                  MEDLINE; 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.4%; Score 11; DB 1; Length 100.0%; Pred. No. 8.8e+04; ive 0; Mismatches 0; Inde
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6 AA; 621 MW; 72C9C6876DDB1000 CRC64;
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01-JAN-1990 (Rel. 13, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION INHIBITING PEPTIDE II (MIP II).
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PIR; A01644; HOROHA.
PIR; A60411; A60411.
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                                                 Life Sci. 17:1253-1256(1975).
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                                                                                                                                                                                                       SPECIES=L. POLYPHEMUS;
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Best Local Similarity
Thes 2; Conserva
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                                                                               BIOLOGICAL SOURCE
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                                                                                                                                                                                                                                                                    Shabanowitz J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuropeptide.
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SEQUENCE
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CIP2_MYTED
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   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 92195954.

Brans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;

Identification of RFemide neuropeptides in the medicinal leech.";

Peptides 12:897-908(1991).

-! SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hirudo medicinalis (Medicinal leech).
Eukaryota, Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                     Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
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                                                                                                                                                         9 AA; 1041 MW; 1F49087042DB41BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuropeptide, Amidation.
MOD_RES 4 4 AMIDATION.
SEQUENCE 4 AA; 598 MW; 69D4073B3000000 CRC64;
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0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-1995 (Rel. 32, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                             4 AA.
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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4 YVIG 7
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P42562;
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                                                                                                                                                                                                                                                                  Carnobacterium
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UF03_MOUSE
ID UF03_MOUSE
AC P38641;
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NON_TER
SEQUENCE
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P36960;
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2 YL 3
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                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoldea;
Ascarididae; Ascaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN (P35) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
                               1; Indels
                                                                                                                                                       Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
                                                                                                                                                                                                                                                                                                                                                                                                   Length 7;
              Length 6;
                                                                                                                                                                                                                                                                                                                                                                  MOD_RES 7 7 AMIDATION.
SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  24.4%; Score 11; DB 1; Le
100.0%; Pred. No. 8.8e+04;
ive 0; Mismatches 0;
              Score 11; DB 1; Pred. No. 8.8e+04; 1; Mismatches 1;
                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
                                                                                                       7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 AA.
                                                                                                       PRT;
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              24.4%;
50.0%;
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                        Neuropeptide; Amidation.
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                                                                                                                                                                Panagrellus redivivus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
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Best Local Similarity
Matches 2; Conserv
               Query Match
Best Local Similarity
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MEDLINE; 93324431.
                                                                                                      FAR2_ASCSU
P31890;
                                              4 GADL 7
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P99025;
                                                         1 GAPM
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4 YL 5
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MEDLINE; 92321768.
Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a Carnobacterium sp.";
Appl. Environ. Microbiol. 58:1417-1422(1992).
-!- FUNCTION: LANTHIONINE-CONTAINING PEPTIDE ANTIBLOTIC (LANTIBIOTIC)
ACTIVE ON GRAM POSITIVE BACTERIA.
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
Cowthorne M.;
Submitted (AuG-1998) to the SWISS-PROT data bank.
-1- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
11-NOV-1995 (Rel. 39, PRAGMENT)
Carnobacterium Sp. (Strain U149).
Bacteria: Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P36) (FRAGMENT).
MUS musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 95009907.
Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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                                                                                                                                                                                                                                                                                                         7 AA; 806 MW; 71B5B057273B4700 CRC64;
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                                                                                                                                                    (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
SWISS-2DPAGE; P99025; MOUSE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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PIR; H41978; H41978.
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MEDLINE; 92082847
                                                                                                                                                                          :| |
1 SDRN 4
                                                                                                                                                             5 ADLN 8
                                                                MOD_RES
SEQUENCE
                                                                                                                                                                                                                                            FAR8_CALVO
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                                          FAMILY
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P24816;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
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Best Local S
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D1_NEPNO
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MOTI M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
Craig R.A., Clewell D.B., Suzuki A.;
"Isolation and structure of the bacterial sex pheromone, cADI, that
induces plasmid transfer in Streptococcus faecalis.";
FEBS Lett. 178:97-100(1984).

-i. FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PADI.
"Separation and sequencing of familiar and novel murine proteins using preparative two-dimensional gel electrophoresis."; Electrophoresis 15:735-745(1994).
--- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.1, ITS MW IS: 36 KDA.
                                                                                                                                                                                                                                                                                         SEX PHEROMONE CAD1.
Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trimmer B.A., Kobierski L.A., Kravitz E.A.; "Purification and characterization of FMRFamidelike immunoreactive substances from the lobster nervous system: isolation and sequence analysis of two closely related peptides."; Comp. Neurol. 266:16-26(1987).
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P41486;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
FORTHANIDE-LIKE NEUROPEPTIDE 3 (FLI 3) (F2).
HOMBANIDE-LIKE NEUROPEPTIDE 3 (FLI 3) (F2).
HOMBANIDE AMERICAN (AMERICAN 10bster).
EUKARYOGH; Methacos, Arthropoda; Crustacea; Malacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea; Nephropoidea; Nephropoidee; Homarus.
                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.4%; Score 11; DB 1; Length 8; 66.7%; Pred. No. 8.8e+04; l. Mismatches 0; Indels
                                                                                                           Length 7;
                                                        NON_TER 7 7 7 SEQUENCE 7 AA; 842 MW; 6AA72B1DDB1B1180 CRC64;
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                                                                                                          Score 11; DB 1; I
Pred. No. 8.8e+04;
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(Rel. 13, Last sequence update)
(Rel. 17, Last annotation update)
                                                                                                                                                                                                                                        8 AA.
                                                                                                                                 Mismatches
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                                                                                                       24.4%;
50.0%;
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                                                                                                                              2; Conservative
                                                                                                                                                                                                                                     STANDARD;
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Matches 2; Conserv
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Matches 2; Conserv
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P13268;
01-JAN-1990 (
                                                                                                                                                                   |:|:
4 AELD 7
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                                                                                                                                                                                                                                                                     01-JAN-1990
01-FEB-1991
                                                                                                                                                    5 ADLN 8
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                                                                                                         Query Match
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6 LAG
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CAD1_ENTFA
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
021LIFMRFAMIDE 8.
Calliphora vomitoria (Blue blowfly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
00estroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
MISCELLANEOUS: PERICARDIAL ORGANS RELEASE THIS PEPTIDE WITH 100 POTASSIUM IN THE PRESENCE OF CALCIUM.
SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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MEDLINE; 92196111.
Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFMRRFamides) from the blowfly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last annotation update)
01-MAR-1992 (Rel. 21, Last annotation update)
03-MAR-1992 (Rel. 21, Last annotation update)
04-MAR-1992 (Rel. 21, Last annotation update)
05-MAR-1992 (Rel. 21, Last annotation update)
06-MAR-1992 (Rel. 21, Last annotation u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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66.7%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 8;
                                                                                                                                                                                                                                                                  AMIDATION.
C6D40729C4540AB5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 11; DB 1; I
Pred. No. 8.8e+04;
L; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.48;
50.08;
                                                                                                                                                                                                                                                                                                           8 AA; 1054 MW;
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                                                                                                                                                                                                              Neuropeptide; Amidation.
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Best Local Similarity
'Local 2; Conserv?
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Gaps

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Achatina fulica (Giant African snail).
Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;
Achatinacea; Achatinidae; Achatina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus.";
Zool. Sci. 4:649-656(1987).
-- FINCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
PIR; JN0027; JN0027.
SEQUENCE 9 AA; 924 MW; 93245729CDC5BAB5 CRC64;
      TISSUE-THORACIC GANGLION;

MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

Rehfeld J.E., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2

neuropeptides (designated calliFMRFamides) from the blowfly

Calliphora vomitoria.";

Proc. Natl. Acad. SCI. U.S.A. 89:2326-2330(1992).

-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clypeaster japonicus (Sand dollar).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
Clypeasteridae; Clypeaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIŠSUB=EGG JELLY;
Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
Yamaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.4%; Score 11; DB 1; Length 9; 50.0%; Pred. No. 8.8e+04; ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                      Score 11; DB 1; Length 9;
Pred. No. 8.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                           AMIDATION.
EID10699CAB6D86A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA.
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                                                                                                                                                                                                                                                        24.48;
66.78;
                                                                                                                                                            PIR; G41978, G41978.
Neuropeptide; Amidation.
MOD_RES 9 9 9
SEQUENCE 9 AA; 1081 MW;
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Best Local Similarity
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Best Local Similarity
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P35904;
                                                                                                                                                                                                                                                                                                                                                                                                                            MOSF_CLYJA
P19853;
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6 FLIG
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ACH1_ACHFU
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CALLIFWRFAMIDE 7.

Calliphora vomitoria (Blue blowfly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pteryqota; Neoptera; Endopteryqota; Diptera; Brachycera; Muscomorpha;

Oestroidea; Calliphoridae; Calliphora.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Calliphora vomitoria (Blue blowfly).
Eukaryota: Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota: Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridea; Calliphora.
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                                                                                                                                                                                                           Gaps
Favrel P., Kegel G., Sedlmeler D., Keller R., van Wormhoudt A.; "Structure and biological activity of crustacean gastrointestinal peptides identified with antibodies to gastrin/Cholecystokinin."; Biochimie 73:1233-1239(1991).
-!- FUNCTION: MAY CONTROL DIGESTION PROCESSES IN CRUSTACEANS.
-!- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY. HORMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I., Rehfeld J.F., Thorpe A.;

"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2 neuropeptides (designated calliFMRFamides) from the blowfly calliphora vomitoria.";

Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).

-I. SIMILARITY: BELONGS TO THE PARP (FMRFAMIDE RELATED PEPTIDE)
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Pred. No. 8.8e+04;
0; Mismatches 1; Indels
                                                                                                                                                                                                        1; Indels
                                                                                                                                                                          Score 11; DB 1; Length 9; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMIDATION.
39D10699CAB6D867 CRC64;
                                                                                                                               SEQUENCE 9 AA; 1038 MW; 60EC79CAB6D8787B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAR7_CALVO STANDARD; PRT; 9 AA. P41862; 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                9 AA.
                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                          Query Match 24.4%;
Best Local Similarity 66.7%;
Matches 2; Conservative
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MOD_RES 9 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                   4 GQD 6.
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SEQUENCE
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SEQUENCE.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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01-NOV-1995 (Rel. 32, Last sequence update)
01-RES-1996 (Rel. 33, Last annotation update)
TRYPSIN-MODULATING ODSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neopelera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE INDUCER (INDUCEDELYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
-1- SIMILARITY: BELONGS TO THE LYSR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                            MEDLINE; 94211930.
Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence of the tryptophan synthase genes of Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
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01-JUN-1994 (Rel. 29, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
TRPBA OPERON TRANSCRIPTIONAL ACTIVATOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2%; Score 10; DB 1; L
).0%; Pred. No. 8.8e+04;
                                                                                              6 AA.
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                                                                                                                                                                                                                                                         Oestroidea; Sarcophagidae; Sarcophaga
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPITHELIUM AFTER A BLOOD MEAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.08;
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Biochimie 71:521-531(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                             SEQUENCE, AND SYNTHESIS.
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Best Local Similarity
Thes 2; Conserve
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                                                                                      TMOF_SARBU P41495;
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                                                   RESULT 32
TMOF_SARBU
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                                                                                                                                                                                                                                                                                                                                                                                                           D-amino acid residue. ";
Int. J. Pept. Protein Res. 39:258-264(1992).
-!- FUNCTION: NEUROBXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
-- RUNCTION: NEUROBXCITATORY PEPTIDE; INCREASES THE IMPULSE FREQUENCY
-- AND PRODUCES A SPIKE BRAADBAING OF THE IDENTIFIED HEART EXCITATORY
NEURON (PON); ALSO ENHANCES THE AMPLITUDE AND FREQUENCY OF THE
HEART BEAT HAS ALSO AN EFFECT ON SEVERAL OTHER MUSCLES.
-- PIR; A32480; A32480.
                                                                                                                                                 STRAIN-FERUSSAC; TISSUE-HEART ATRIUM;
MEDLINE; 91264856.
Fujimoto K., Kubota I., Yasuda-Kamatani Y., Minakata H., Nomoto K.,
Yoshida M., Harada A., Muneoka Y., Kobayashi M.;
"Purification of achatin-1 from the atria of the African giant snail,
Achatina fulica, and its possible function.";
Biochem. Biophys. Res. Commun. 177:847-853(1991).
   Kamatani Y., Minakata H., Kenny P.T.M., Iwashita T., Watanabe K., Funase K., Sun X.P., Yongsiri A., Kim K.H., Novales-Li P., Novales E.T., Kanapi C.G., Takeuchi H., Nomoto K.; "Achatin-I, an endogenous neuroexcitatory tetrapeptide from Achatina fulica Ferussac containing a D-amino acid residue."; Blophys. Res. Commun. 160:1015-1020(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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TER 5 5
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Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                   MEDLINE; 93014529.
Ishida T., In Y., Doi M., Inoue M., Yasuda-Kamatani Y., Minakata Ilshida T., Nomoto K.;
Iwashita T., Nomoto K.;
"Crystal structure and molecular conformation of achatin-I (H-Giy-D-Phe-Ala-Asp-OH), an endogenous neuropeptide containing a
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01-OCT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-PHENYLALANINE.
6AADD9C810000000 CRC64;
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100.08; Pi
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SEQUENCE 4 AA; 408 MW;
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Best Local Similarity
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P38005;
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Score 10; DB 1; Length /;
Pred. No. 8.8e+04;

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allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. Biochem. 250:727-734(1997).
-i FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i SIMILARIY: BELLONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide: Multigene family.
SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
                                                                                                                                           Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                       TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
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Job time: 4566 sec
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50.0%;
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@i8b-sib.ch).
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MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
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Carcinus maenas (Common shore crab) (Green crab).
Bukaryota: Metazoa, Arthropoda; Crustacea; Malacostraca;
Bumalacostraca; Bucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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MOD_RES 7 7 7 AMIDATION (POTENTIAL).

SEQUENCE 7 AA; 770 MW; 672879CDCB5DDB70 CRC64;
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SEQUENCE 6 AA: 683 MW; 77672AA1EDD6F000 CRC64;
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100.0%; Pred No.
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US-09-529-121-2 1 YLSGADLNL 9 Title: Perfect score: Sequence:

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182106 seqs, 63460219 residues Searched:

793 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 9

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database :

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1: pir1:*
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3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | probable H+ | T-cell receptor be | leucokinin VIII - | locustamyoinhibiti | neuropeptide Grb-A | neuropeptide Grb-A | hemoqlobin alpha c | T-cell receptor be | T-cell receptor be | T-cell receptor be | | cytochrome oxidase | calliFMRFamide 6 - | Ig heavy chain CRD | T-cell receptor ga | protein-glutamine | T-cell receptor be | T-cell receptor be | T-cell receptor be | elastase - Pseudom | T-cell receptor be | T-cell receptor be | variant surface gl | acetylcholinestera | phosphatidylethano | r-cell receptor be | isotocin - common | neuropeptide Grb-A | Ig mu chain V regi |
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| SUMMARIES | ID | 237 | PT0542 | JS0318 | AKLQIM | A57444 | B57444 | 157650 | PT0540 | PT0726 | PT0526 | PT0676 | T13818 | F41978 | PT0288 | G41946 | A26209 | PT0679 | PT0605 | PT0593 | S20446 | PT0654 | PT0722 | A21440 | A41117 | PN0043 | PT0557 | A61364 | C57444 | 843959 |
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| ø | Query | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 31 | 28 |
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ALIGNMENTS

probable H+-transporting ATP synthase (EC 3.6.1.34) alpha chain [similarity] - Bacill N, Alternate names: unidentified 78k protein (S.Species: Bacillus cereus C;Species: Bacillus cereus C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: PC2370 B;Matsuno, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S. Biosci. Biotechnol. Biotchm. 59, 231-235, 1995 A;Title: Identification of DNA-binding proteins changed after induction of sporulation A;Reference number: PC2370 A;Accession: PC2370 A;Accession: PC2370 A;Accession: protein nary A;Molecule type: protein A;Residues: 1-7 cMaS> C;Keywords: ATP biosynthesis; hydrolase

Gaps ; 0 Indels Query Match 35.6%; Score 16; DB 2; Length 7; Best Local Similarity 100.0%; Pred. No. 1.8e+05; Matches 3; Conservative 0; Mismatches 0; Indels

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"-curupeptide Grb-AST Bl - two-spotted cricket
C:Species: Gryllus bimaculatus (two-spotted cricket)
C:Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C:Accession: A5744
R:Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Recession: A57444; MUID:95403341
A;Accession: A57444; MUID:95403341
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <LOR>
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C;Species: Gryllus binaculatus (two-spotted cricket)
C;Species: Gryllus binaculatus (two-spotted cricket)
C;Date: 26-Jan-1996
C;Accession: B5744
R;Lorenz, M.W.; Kellnor, R.H.
H;Lorenz, M.W.; Kellnor, R.H.
J; Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
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C.Date: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C.Dates: 02-Jul-1996 #sequence_revision 31-Jul-1997 #text_change 20-Apr-2000
C.Datession: 157650
F.Whitelaw, E.; Hogben, P.; Hanscombe, O.; Proudfoot, N.J.
Mol. Cell. Biol. 9, 241-251, 1989
A;Title: Transcriptional promiscuity of the human alpha-globin gene.
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C;Superfamily: locustamyoinhibiting peptide C;Keywords: amidated carboxyl end; hormone F;9/Nodified site: amidated carboxyl end (Trp) #status experimental
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1.8e+05;
hes 0; Indels
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Pred. No. 1.8e+05;
0; Mismatches 0;
                                                                                                                                                                   35.6%; Score 16; DB 100.0%; Pred. No. 1.6:ive 0; Mismatches
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A;Molecule type: protein
A;Residues: 1-9 <LOR>
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Best Local Similarity
Matches 3; Conserv
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C. Accession: A60065
R. Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
R. Schoofs, L.; Holman, G.M.; Hayes, T.K.; Nachman, R.J.; De Loof, A.
A. Title: Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MI A). Reference number: A60065; MUID: 92179466
A. Molecule type: Protein
A. Residues: 1-9 <&CH>
C. Comment: This peptide hormone suppresses spontaneous contractions of the hindgut and o
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C; Comment: Leucokinins, a family of cephalomyotropic peptides, stimulate contractile act
C; Keywords: amidated carboxyl end; cephalomyotropic peptide
F; 8/Modified site: amidated carboxyl end (Gly) #status experimental
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C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: Pr0542
B:Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Accession: Pr0542
A:Accession: P
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R; Holman, G.W.; Cook, B.J.; Nachman, R.J.
Comp. Biochem. Physiol. C 88, 31-34, 1987
A; Title: Isolation, primary structure and synthesis of leucokinins VII and VIII: the A; Reference number: JS0317
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C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Matches 3; Conserv
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RESULT 11
PT0676
T-cell receptor beta chain V-D-J region (140-1AL) - mouse (fragment)
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C.Accession: PT0676
R.Feering A.J.15-124, 1991
A.Fitle: Junctional sequences of fetal T cell receptor beta chains have few N regions A.Reference number: PT0679; MUID:91277601
A.Recession: PT0676
A.Status: translation not shown
A.Status: Lanslation not shown
A.Status: Trenslation of shown
A.Residues: 1-7 <FEE>
A.Status: C.Seywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                     cell receptor beta chains have few N regions
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C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: ulcochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: 10-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13818
R;Delazbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
A;Tille: The main features of the craniate mitochondrial DNA between the NDI and the A;Reference number: Z17775; MUID:97398704
A;Recession: T13818
A;Accession: T13818
A;Accession: T13818
A;Accession: T13818
A;Molecule type: DNA
A;Recial and A;Rec
                                                                                                                          Toell receptor beta chain V-D-J region (100-4E) - mouse (fragment)
T-cell receptor beta chain V-D-J region (100-4E) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: JT-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0526
R;Peeney, A.J.
J; Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N re
A;Reference numbar: PT0509; MUID:91277601
A;Accession: PT0526
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-7 <FEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor
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75.0%; Pred. No. 1.8e+05;
tive 0; Mismatches 1;
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Best Local Similarity
Matches 3; Conserv
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A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A:Reference number: PT0509; MUID:91277601
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                                                                                                                                 A;Residues: 1-9 <WHI>
A;Cross-references: GB:M23454; NID:9340922; PIDN:AAA52629.1; PID:9553329
A;Note: engineered sequence; this sequence was not determined in this report C;Genetics:
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accesslon: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accesslon: PT0726
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: PT0509; MUID:91277601
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0540
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Pred. No. 1.8e+05;
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A;Residues: 1-6 cFEES
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
A;Reference number: 157650; MUID:89181576
A;Accession: 157650
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                  35.6%;
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llarity 75.0%;
Conservative
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A;Cross-references: GDB:119293
A;Map position: 16p13.3-16p13.3
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A,Status: translation not shown
A,Molecule type: mRNA
A,Residues: 1-5 <FEE>
A,Experimental source: day 18 fe
C,Keywords: T-cell receptor
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Best Local Similarity 75.0
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Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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3 LSPAD 7
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R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Titler. Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316
A;Accession: G41946
A;Status: preliminary; not compared with conceptual translation
A;Wolecule type: DNA
A;Residues: 1-9 <a href="https://www.molecule-receptor">whtes://www.molecule-receptor</a>
C;Keywords: T-cell receptor
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Afrittle: Junctional sequences of fetal T cell receptor beta chains have few N regions
A; Accession: PT0679; MUID:91277601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein-glutamine gamma-glutamyltransferase (EC 2.3.2.13) - guinea pig (fragment) c; Species: Cavia porcellus (guinea pig) c; Species: Cavia porcellus (guinea pig) c; Species: Cavia porcellus (guinea pig) diste: 10-8ep-1987 #sequence_revision 10-8ep-1987 #text_change 03-Mar-1995 C; Accession: A26209 R; Connellan, J.M.; Chung, S.I.; Whetzel, N.K.; Bradley, L.M.; Folk, J.E. A; Title: Structural properties of guinea pig liver transglutaminase.

A; Reference number: A26209; MUID: 71111415
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C;Species: Mus musculus (house mouse)
C;Datte: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0679; PT0708
R;Feeney, A.J.
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A;Residues: 1-5 <FE2>
A;Experimental source: newborn thymus, strain BALB/c, 161-2B
C;Keywords: T-cell receptor
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A; Residues: 1-4 < CONN
A; Experimental source: liver
C; Keywords: aminoacyltransferase
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A;Molecule type: DNA
A;Residues: 1-5 <FEE>
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0°
Matches 3; Conservative
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Matches 3; Conserva
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2 ADL 4
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(Species: Calliphora vomttoria
(Species: Calliphora vomttoria)
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C. Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C. Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C. Accession: PT0288
R.Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
J. Exp. Med. 173, 395-407, 1991
A. Reference number: PT0222; MUID: 91108337
A. Accession: PT028
A. Accession: PT028
A. Accession: PT028
A. Residues: 1-9 <Am>
A. Residues: 1-9 <Am>
A. Experimental source: B lymphocyte
C. Keywords: heterotetramer; immunoglobulin
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C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C;Accession: G41946
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A) Molecule type: protein
A) Residues: 1-9 < DUV9 < DUV9 < COV < CO
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                       Length 8;
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                                                                                                                                                                                                                        Query Match 33.3%; Score 15; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.8e+05; Matches 3; Conservative 0; Mismatches 0;
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ilarity 75.0%;
Conservative (
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A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion
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Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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5 YSSG 8
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C. Species: Mus musculus (house mouse)
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C. Accession: Pr0654
B. Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A: Fletence number: Pr0509; MuID: 91277601
A: Reference number: Pr0509; MuID: 91277601
A: Accession: Pr0654
A: Status: translation not shown
A: Molecule type: mRNA
A: Molecule type: mRNA
A: Residues: 1-7 <FEE>
A: Experimental source: day 4 postnatal thymus, strain BALB/C
C: Keywords: T-cell receptor
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A2141
A2141
C. Salat surface glycoprotein pSLc1 - Trypanosoma brucei (fragment)
C. Species: Trypanosoma brucei
C. Species: Trypanosoma brucei
C. Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
C. Accession: A2144
C. Saccession: A2144
C. Saccession: A2146
C. Saccession: A
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Decies: Mus musculus (house mouse)
C;Accession: PT0722
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
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                                                                          Length 7;
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1. 1.8e+05;
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                                                                      31.1%; Score 14; DB 2; Le llarity 100.0%; Pred. No. 1.8e+05; Conservative 0; Mismatches 0;
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A; Residues: 1-7 cFEE>
A; Experimental source: newborn thymus, strain BALB/c
C; Keywords: T-cell receptor
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llarity 100.0%; Pred. No. 1.8
Conservative 0; Mismatches
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Best Local Similarity 75.0
Matches 3; Conservative
                                     Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserv
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elastase - Pseudomonas aeruginosa
cispecies: S20446
Rikesaler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
Rikesaler, E.; Safrin, M.; Peretz, M.; Burstein, Y.
A: Title: Identification of cleavage sites involved in proteolytic processing of Pseudomc A; Reference number: S20446; MUID:92183956
A: Accession: S20446
A: Accession: S20446
A: Accession: Preliminary
A: Molecule type: Protein
A: Residues: 1-7 < KES>
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J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0609.
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A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0593
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0593
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C; Keywords: T-cell receptor
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Best Local Similarity 100.0%; Pred. No. 1.8e+05;
Matches 3; Conservative 0; Mismatches 0;
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A;Residues: 1-6 KFES
A;Experimental source: newborn thymus, strain BALB/c
C;Keywords: T-cell receptor
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A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
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2 SGA 4
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4 SGA 6
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SGDD
SGAD
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C;Species: Cyprinus carpio (common carp)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C;Accession: A61364
R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Blochen. Physiol. A 14, 245-254, 1965
A;Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau do A;Reference number: A61364
                                                                                                                                                        cell receptor beta chains have few N regions
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J. Biol. Chem. 270, 21103-21108, 1995
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the
A;Reference number: A57444; MUID:95403341
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T-cell receptor beta chain V-D-J region (126-1BD) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Bate: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Fitle: Junctional sequences of fetal T cell receptor beta chains have few A;Reference number: Pr0509; MUD:91277601
A;Reference number: Pr0509; MUD:91277601
A;Reference number: Pr0509; MUD:91277601
A;Reference number: ann NA
A;Residues: 1-8 <a href="Mission-Receptor">FEESSARSION-RECEPTOR</a>
C;Reywords: T-cell receptor
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C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan.1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: CS7444
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C.Superfamily: oxytocin-neurophysin
C.Superfamily: oxytocin-neurophysin
C.Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F:9/Modified site: amidated carboxyl end (Gly) #status experimental
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Pred. No. 1.8e+05;
0; Mismatches 1;
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100.0%; Pred. No. 1.8e+05;
live 0; Mismatches 0;
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Best Local Similarity
Matches 3; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-9 <ACH>
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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2 YISNCPI 8
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SGDD 5
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Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neurc
A;Reference number: PN0041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 1-8 CKAT>
A; Residues: 1-8 CART>
A; Experimental source: neuroblastoma cell
C; Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is blocked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rikreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
Aritile: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo A; Reference number: A41117; MUID:91296772
A; Accession: A41117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C;Species: Naja naja oxiana (Asian cobra, Oxus cobra)
C;Date: 27-Mar.1992 #sequence_revision 27-Mar-1992 #text_change 23-Jun-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Mus musculus (house mouse)
C;Date: 29-Oct_1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
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     5' spliced leader sequence.
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                                                                      A;Molecule type: mRNA
A;Residues: 1-8 <PAR>
A;Cross-references: GB:K02195; NID:g162150; PID:g162151
C;Keywords: glycoprotein
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llarity 100.0%; Pred. No. 1.8e+05;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                       3; Mismatches
  A;Title: Trypanosome mRNAs share a common A;Reference number: A90853; MUID:84282716 A;Accession: A21440
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A;Residues: 1-8 <KRE>
C;Keywords: carboxylic ester hydrolase
                                                                                                                                                                                                                          31.1%;
                                                                                                                                                                                                                       Query Match 31.17
Best Local Similarity 33.33
Matches 2; Conservative
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Best Local Similarity
'.haq 2; Conserve
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Best Local Similarity
Matches 3; Conserv
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1 MSGKEV 6
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1 GAEM 4
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5 LSG 7
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Accession: A44873
R.Ikebe, M.: Hornick, T.
Arch Biochem. Blophys. 288, 538-542, 1991
A.Title: Determination of the phosphorylation sites of smooth muscle caldesmon by pro A; Reference number: A44873; MUID:91378498
A.Status: preliminary
A.Status: preliminary
A.Status: preliminary
A.Residues: 1-9 < IKE>
A.Residues: 1-9 < IKE>
C.Superimental source: skeletal myosin
A.Note: sequence extracted from NCBI backbone (NCBIP:63199)
C.Superfamily: caldesmon
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C;Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
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C;Species: Chlamydomonas reinhardtii
C;Date: 05-Jun.1992 #sequence_revision 05-Jun-1992 #text_change 30-Sep-1993
C;Accession: C41170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
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                                                                                                                        Score 13; DB 2; Length 8;
Pred. No. 1.8e+05;
0; Mismatches 1; Indels
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Pred. No. 1.8e+05;
2; Mismatches 2; Indels
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Llarity 50.0%; Pred. No. 1.8e+05;
Conservative 1; Mismatches 1;
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                                                                                                                            28.9%;
75.0%;
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Best Local Similarity 33.3%;
Matches 2; Conservative
                                                                                                                   Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      caldesmon - rabbit (fragment)
        C;Keywords: T·cell receptor
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Best Local Similarity
Matches 2; Conserv
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1 GSSLKI 6
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3 SDAD
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A.Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice.
A.Reference number: $43956; MuID:94248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell receptor beta chain V-D-J region (126-1AI) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: J7-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0547
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Feiter Med. 174, 1991
A;Feiter Med. 174, 1
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                                                                                                                                                                                                                                                                          19 mu chain V region (clone 13) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 20-Oct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C;Accession: S43959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene c-rel protein - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996.#text_change 28-Feb-1997
C;Accession: I50210
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Mol. Cell. Biol. 10, 4788-4794, 1990
A;Title: Characterization of a novel promoter insertion in the c-rel locus.
A;Reference number: 150210; MUID:90355995
A;Recession: 150210
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Pred. No. 1.8e+05;
2; Mismatches 0; Indels
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A;Molecule type: mRNA
A;Residues: 1-8 <FEE>
A;Experimental source: day 18 fetal thymus, strain BALB/c
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C;Genetics:
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Pred. No. 1.8e+05;
1; Mismatches 1;
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A; Residues: 1-4 <WAG>
C; Keywords: immunoglobulin
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Best Local Similarity
Matches 2; Conserv
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A; Residues: 1-7 <KAB;
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R;de Vitry, C.; Diner, B.A.; Popot, J.L.
J. Biol. Chem. 266, 16614-16621, 1991
A;Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91388452
A;Accession: C41170
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 < PDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell receptor beta chain V-D-J region (clone 6) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0935
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergine A;Reference number: PH0891; MUID:92078857
A;Accession: PH0935
A;Accession: PH0935
A;Accession: PH0935
A;Accession: PH0935
A;Residues: 1-9 <GOL>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
C;Keywords: T-cell receptor
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Pred. No. 1.8e+05;
2; Mismatches 0; Indels
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Job time: 5645 sec
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Best Local Similarity 50.0%;
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| Synthetic pwEL17 p Immunogenic peptid NCA analogue of re B. stearchermophi Rheumatoid arthrit Tryptic fragment T LFA-1 alpha subuni Gingivalis adhesio Internal tryptic p K. oxytoca R-speci | Immunogenic peptid Brayme inhibitor p Rheumatoid arthrit Rheumatoid arthrit Rheuman TSH receptor Enzyme inhibitor p Peptide fragment (Control peptide 92 Jojoba fatty acyl- Jojoba fatty acyl- Jojoba fatty acyl- Johetic polypept BH3 domain of meus Amino acids coded Monomeric peptide MAD GAH variable r Human WHC clase II | Human cytohesin-1 HLA binding plu-1 HLA binding plu-1 HLA binding plu-1 Immunogenic peptid Tyrosinase 2 deriv Transcriptional ac Factor Xa inhibiti Peptide specific a Phytase derived pe Haemoglobin mutant Heat shock protein Tumnour antigen ant Trehalose-releasin Synthetic SCM-acti Protease Nexin-1 P CS4-CFA/I family s Heat shock protein VIF-derived HIV pr PVX-2 viral replic Peptide derived ff Jardetzky self pep HIV-derived ff-Jardetzky self hep | Peptide against SH Human leucocyte an SH2 domain binding SH2 domain binding HLA binding plu-1 HLA binding plu-1 Rheumatoid arthrit Rmembrane dipeptida Mycobacterial hsp6 Immunogenic peptid |
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| 9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 | 9 19 W54298 9 20 Y55448 9 20 Y55523 9 20 Y55523 9 21 Y55523 9 21 Y55575 5 19 W31459 6 19 W83899 7 15 W6333 7 20 Y17023 7 20 Y17023 7 20 Y17023 7 20 Y17023 7 20 W84402 8 20 W84402 8 20 W84429 9 13 R22425 9 14 R6546 9 15 Y38246 | 1177 220 220 220 230 24 20 20 20 20 20 20 20 20 20 20 20 20 20 |
| 55.05.05.05.05.05.05.05.05.05.05.05.05.0 | | 900 900 900 900 900 900 900 900 | 18 40. 18 40. |
| 13 14 16 16 17 18 19 20 22 | 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3 3 3 3 | 601 601 601 601 601 601 601 601 601 601 | 99 5 |
| 4.5 Compugen Ltd. ; Search time 107.12 Seconds (without alignments) 2.873 Million cell updates/sec | . 61695 | Immaries | predicted by chance to have a score of the result being printed, otal score distribution. RIES Description Carcinoembryonic a Carcinoembryonic a Human carcina-embr CEA synthetic pept CEA derived HLA-A2 Immunogenic peptid Carcinoembryonic a Carcinoembryonic a Carcinoembryonic a HLA binding peptid Carcinoembryonic a HLA binding peptid Carcinoembryonic a Peptide comprising Rheumatoid arthrit |
| GenCore version 4. Copyright (c) 1993 - 2000 Cc protein search, using sw model December 16, 2000, 03:07:17; | US-09-529-121-2 45 1 YLSGADLNL 9 BLOSUM62 Gapop 10.0 , Gapext 0.5 268485 seqs, 34193795 residues f hits satisfying chosen parameters length: 0 length: 0 length: 9 3: Minimum Match 0% Maximum Match 100% | /5 su a ata/g a ta/g a ta/g a ta/g da ta/g da ta/g da ta/g da ta/g da ta/g da ta/g da ta/g da ta/g | Score greater than or equal to the score of and is derived by analysis of the total score and is derived by analysis of the total score of a query score Match Length DB ID Score Match Length DB ID 45 100.0 9 20 Y09526 43 95.6 9 18 W39723 40 88.9 9 19 W70455 40 88.9 9 19 W70455 40 88.9 9 20 Y09528 |
| OM protein - pro Run on: | Title: Perfect score: Sequence: Scoring table: Searched: Total number of I Minimum DB seq I | Database : | Result No. Score grea and 1s der No. Score 1 1 45 2 44 4 40 5 40 6 40 7 40 8 8 38 110 33 112 25 |

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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating astrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatability complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                    Peptide agonists and antagonists of carcinoembryonal antigen
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Pred. No. 2.1e+05;
1; Mismatches 0; Indels
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(SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
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                                                                                                                                                                                                                                                         Zaremba
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88.9%;
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96EP-0201145.
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Matches 8; Conservative
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                                                                                                                         22-SEP-1998;
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26-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or antigonists (ID) of human carcinoembryonal antigon (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (ID) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune cearcinon to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes peptides (A) that comprise agonists (Ia)
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                                                                                      Carcinoembryonic antiqen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                 Carcinoembryonic antigen peptide agonist SEQ ID NO:2.
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          20-JUL-1999 (first entry)
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Best Local Similarity 100.
Matches 9; Conservative
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Synthetic.
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Seguence

Y09527;

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Barzaga E,

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Gaps

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Length 9;

Gaps

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Length 9; 0; Indels

DB 19; 2.1e+05;

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Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human carcinoembryonic antigen (CEA). The peptides can bind to a human of inwortien (HLA), HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CTLs) in vitro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCs) pretreated with prefreatment growth factors, and incubating the APCs with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLs. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCs pretreated with pre-treatment growth factors,
depleted mutants of a native disease-specific CTL epitope. The cysteine-depleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immuno disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Production of antigen-specific cytotoxic T cells - by incubating fimunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen presenting cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood S,
                                                                                                                                                                                      Score 40; DB 1
Pred. No. 2.1e+
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                W70045 standard; peptide; 9 AA.
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                                                                                                                                                                                        88.9%;
88.9%;
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                                                                                                                                                                      Query Match
Best Local Similarity
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| ylsganini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
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                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                  W70045;
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                                                                                                                                                                                                                                                                                                                                               RESULT
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                                                                                                                                                                                Immunogenic T-cell peptide epitopes present in polypetide entigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral immune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC Class I allele HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The peptide epitope W77119-W77138 were created for human tumour-specific cytotoxic T lymphocyte response. These peptides are are cysteine-
                                                                                                                                                                      used in a novel method for the selection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disease specific immunogen · comprises disease specific cytotoxic lymphocyte epitope used to elicit melanoma specific CTL response
                 Van Der Burg SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                  Method of selecting T cell peptide epitope(s) - by measuring stability of HLA class I-peptide complexes on intact B cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tyrosinase cytotoxic lymphocyte response; lymphocyte; cysteine-depleted; melanoma.
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2.1e+05;
0;
                 Toes REM,
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Pred. No. 2.1e+
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 27; 93pp; English.
                                                                                                                                    Example 3; Page 85; 109pp; English.
                Offringa R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEA synthetic peptide epitope 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.9%;
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                Melief CJM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1998-437388/37.
                                                WPI; 1997-549891/50
                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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cytotoxic T
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                                                                                Method of
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                                                                                                                                                                  Peptides
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              Kast WM,
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Tsai V;

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RESULT
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where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CILs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CILs can be used for treating cancers, immune disorders, viral infections, AIDS, hepatilts, bacterial infection, fungal infection, malaria or
                                                                                                                                                                                                                                                                                                                                                            Immunogenic peptide having a human leukocyte antigen binding motif #2266.
                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                                                                                                                              Length 9;
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                                                                                                                                            Score 40; DB 19; L
Pred. No. 2.1e+05;
.; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 118; 150pp; English.
                                                                                                                                                                                                                                                                                Y47655 standard; Peptide; 9 AA.
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                                                                                                                                            88.9%;
88.9%;
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                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immunisation.
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Best Local Similarity
Thes 8; Conserve
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                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                            1 YLSGADLNL 9
                                                                              cuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
Homo sapiens.
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                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS ex vivo for infusion back into a patient. The polynuclectides encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                     Score 40; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carcinoembryonic antigen peptide agonist CAP-1.
                                                                                                                                                                        therapeutically and for immunisation as above.
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                                                                                                                                                                                                                                                                                                                                     88.9%;
88.9%;
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Matches 8; Conservative
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                                                                                                                                                                                                                                     9 AA;
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1 ylsganini
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                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                         Query Match
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Length 9;

DB 20;

88.9%; Score 40;

Query Match

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Allele-specific binding motif; major histocompatibility complex; MHC; HLA; HLA-A2.1; cytotoxic T cell response; antigen; microbial infection; hepatitis; AIDS; malaria; condyloma acuminatum; cancer; prostate cancer; renal carcinoma; cervical carcinoma; lymphoma; tumour.
                                                                                                                                                                                                                                                                                                                                                                    Novel HLA binding immunogenic peptides used to induce T cell activation
                                                                 HLA binding peptide 1233.11 derived from source CEA.605V9.
                                                                                                                                                                                                                                                                                                                                                                                    and to induce an immune response
                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 32; 42pp; English.
                                                                                                                                                                                                                                                                                                                  Sidney J, Southwood
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                                        06-APR-2000 (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                          (EPIM-) EPIMMUNE INC.
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| ylsganlnv 9
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                                                                                                                                                          Unidentified
                                                                                                                                                                                    WO9965522-A1
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                Gaps
                                                                                                                                                                                                                                   Carcinoembryonic antigen; CEA; human; agonist; antagonist; fimune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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Pred. No. 2.1e+05;
Mismatches 0; Indels
              Indels
                                                                                                                                                                                                            Carcinoembryonic antigen peptide agonist SEQ ID NO:4.
 Pred. No. 2.1e+05;
l; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zaremba S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Page 53; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y54173 standard; peptide; 9 AA.
                                                                                                                               Y09528 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.4%;
77.8%;
 88.98;
                                                                                                                                                                                                                                                                                                                                                                                                                        97US-0061589
                                                                                                                                                                                                                                                                                                                                                                                              98WO-US19794
                                                                                                                                                                                  (first entry)
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-326544/27.
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 7; Conserv
                                       1 YLSCADLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YLSGADLNL 9
                                                              1 ylsganini 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||||||::||
| ylsganinl
                                                                                                                                                                                  20-JUL-1999
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                      10-OCT-1997;
                                                                                                                                                                                                                                                                                                                                          WO9919478-A1
                                                                                                                                                                                                                                                                                                                                                                    22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barzaga E,
                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                         Y09528;
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ID Y
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Peptides Y54171-Y54236 represent immunogenic peptides comprising an allele-specific binding motif for the major histocompatibility complex conflowed residues at cartain positions such as positions 2 and 9. Also, the peptides do not comprise negative binding residues at other positions, such as positions 1, 3, 6 and/or 7 (peptides 9 mino acids long) and at poisons 1, 3, 4, 5, 7, 8 and/or 9 (peptides 10 amino acids long). The peptides are used to induce a cytotoxic T cell response to a preselected antigen. The method comprises contacting cytotoxic T cells from a patient (optionally expressing a specific MHC class I allele) with the present peptides. The peptides are used to treat and prevent microbial infection (e.g. treat peptides are used to treat and prevent microbial infection (e.g. treat peptides are used to treat and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Cytomegalovirus (CWV), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Comprises in the acute phase of infection can be treated with the comprise phase of infection can be treated with the compression of the conventions of the respond to conventional corbacterial) or tumours in patients that do not respond to conventional corbacterial) or tumours in patients that do not respond to conventional corporations and an antibuted are useful as potential diagnostic or therapeutic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agents. The peptides may also be used as diagnostic reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 21; Length 9; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y09529 standard; peptide; 9 AA.
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Producing carcinoembryonic antigen (CEA) specific human cytotoxic rels (CTC), comprises introducing a 1st pox virus vector, having at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC production, and at least 1 periodic interval after that, contacting production, and at least 1 periodic interval after that, contacting the host with an additional antigen. The CEA specific CTC can be used to determine the CTC eliciting epitope of CEB, and to screen for compounds which enhance the ability of the antigen to create a introducing the CTC to the host, and at least 1 periodic interval after that introducing a CEA peptide, i.e. the present peptide is positive for binding to HiA-A2, and scored appropriate peptide results in the upresulation of surface HIA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HIA-A2 antibody (background 280 and 300).
                                                                                                                                                                                                                                                                                          Generation of human cytotoxic T-cells specific for CEA - useful in therapy, epitope mapping and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rheumatoid arthritis diagnostic protein isoform 17 peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%; Score 33; DB 17;
87.5%; Pred. No. 2.1e+05;
                                                                                                                                                              (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                               Tsang KY;
                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 57; 76pp; English.
                                                                                                                                          (THER-) THERION BIOLOGICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y41847 standard; Peptide; 7 AA.
                                                             96WO-US02156.
                                                                                                     95US-0396385
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Best Local Similarity 8/....
7; Conservative
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                                                                                                                                                                                                          Schlom J,
                                                                                                                                                                                                                                                  WPI; 1996-402364/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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2 lsganlnl
                                                                                                   22-FEB-1995;
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                   29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or antagonists (Tb) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific firmune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA expressing cells). (Ia) are more active than native sequence (I) and generated recognize both (Ia) and native CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA express. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                        Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide comprising residues 571-579 of Carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carcinoembryonic; antigen; human; cytotoxic T cell; pox virus vector; epitope; determination; screening; tumour; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                  Carcinoembryonic antigen peptide agonist SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 20; L. Pred. No. 2.1e+05; ); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 53; 72pp; English.
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88.9%;
                                                                                                                                                                                                                                                                                                                                                   98WO-US19794
                                                                                                                                                                                                                                                                                                                                                                                           97US-0061589
           (first entry)
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Best Local Similarity 88.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-326544/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-1997;
                                                                                                                                                                                                 Homo sapiens
Synthetic.
                                                                                                                                                                                                                                                           WO9919478-A1
                                                                                                                                                                                                                                                                                                                                                 22-SEP-1998;
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Sequence

W00680;

RESULT 11 M00680

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Immunogenic peptide having a human leukocyte antigen binding motif #1673
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cance; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                         The present peptide was used in the preparation of a novel melanoma specific immunogen, comprising at least 1 melanoma specific cytocoxic T lymphocyte (CTL) epitope, where at least 1 of the epitopes is substantially homologous to a human leukocyte antigen-Al (HLA Al) and HLA A3 restricted epitope of a melanoma antigen, either pMEL-17 or tyrosinase. The immunogen can be used in vaccines for protection against melanoma in mammals.
                                                                                                                                      Melanoma-specific immunogens of pMel-17 and tyrosinase - useful in vaccination for producing melanoma-specific cytotoxic T lymphocytes
                         Hunt DF, Kittlesen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 25; DB 18; Length 9;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grey HM,
                       Engelhard VH, Hendrikson RC, H. Lz J, Skipper J, Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Celis E,
                                                                                                                                                                                                      Example 9; Page 65; 106pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55.6%;
62.5%;
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Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIM-) EPIMMUNE INC.
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                                                                                         WPI; 1997-479982/44.
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                                               Shabanowitz J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||: |||:
| ylaeadls
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                       archod has been developed for the diagnosis of human rheumatoid archifits (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features: (b) identifying at least one chosen clamens whose relative abundance correlates with the presence or absence of RA; and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature of features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy proteonically and second in special and second in compounds that expensent expressent expressent expressent expressent expressent invention. RPIS, which are all used in class the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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human leukocyte antigen-Al; HLA-Al; human leukocyte antigen-A3;
HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                               Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 20; Length 7; Pred. No. 2.1e+05; 1; Mismatches 0; Indels
(OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                            Townsend RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYVI-) UNIV VIRGINIA PATENT FOUND.
                                                                                                                                                                                                      Claim 20; Page 150; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W38383 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96us-0027627.
96us-0013972.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 55.6
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic pMEL17 peptide.
                                            Patel TP,
                                                                                       WPI; 1999-571871/48.
                                                                                                                                                              electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 SGADLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-MAR-1997;
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19-MAR-1996;
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                                          Parekh RB,
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Sequence

W38383;

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cancer;

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Southwood

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Gaps

Query Match

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HIA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are cormally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapetuically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell conditions and account or concerns to the peptide e.g. to concerns the conditions of the conditions or content or content or concerns the conditions of the conditions or concerns the conditions of the conditions or concerns the conditions or concerns the conditions or concerns the conditions of the conditions of the conditions of the conditions of the conditions or concerns the conditions of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present peptide is negative for binding to HLA-A2, and scored 2.52 and 2.25 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HLA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HLA-A2 antibody (background 280 and 300).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCA analogue of residues 571-579 of carcinoembryonic antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 20; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carcinoembryonic; antigen; epitope; NCA; analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 60; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsang KY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W00690 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (THER-) THERION BIOLOGICS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0396385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-402364/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
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| ylaeadis 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YLSGADLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9626271-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-FEB-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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W00690
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Sequences shown in W70077 to W70086 represent methionyl-tRNA (Met-tRNA) synthetase fragments from different bacterial species. These are used for designing degenerate primers (W43887) to W48800) used for isolating Met-tRNA sythetase gene fragment by PCR from M. tuberculosis and M. whereten a special manioacyl-tRNAS (atRNA) and M. which can be annotacyl-tRNAS (atRNA) (especially Met-tRNA) synthetase under control of transcriptional signals that can be used for the recombinant production of mycobacterial amino acyl tRNA synthetases, especially of methionyl tRNA synthetase. The enzymes are used by the organism in protein synthesis, and as such, the recombinant enzyme can be used to ofdentify candidate drugs for use as antibitotics towards mycobacteria, especially M. tuberculosis, which is responsible towards mycobacteria, especially M. tuberculosis, which is responsible used in antisense inhibition of the synthetase gene. The recombinant enzyme allows quick assays in screening of antibiotics. Present testing sections their enzyme allows quick assays in screening of antibiotics. Present testing seeing their effect. This is time consuming as the bacteria are generally solve with pathogenic strains.
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                                           Gaps
                                                                                                                                                                                                                                                                                                                                       synthetase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant genes encoding mycobacterial amino acyl tRNA synthetases - useful for recombinant production of the enzyme for use in screening of antibiotics against Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis; mycobacterial; methionyl-tRNA synienzyme; antiblotic; tuberculosis; Bacillus stearothermophilus
Score 24; DB 17; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 3; Indels

    B. stearothermophilus methionyl-tRNA synthetase fragment.

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Pred. No. 2.1e+05;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schimmel PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sassanfar M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Columns 33-34; 32pp; English.
                                                                                                                                                                                          W70078 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lee SH, Martinis SA,
 53.3%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53.3%;
66.7%;
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96US-0584226.
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                                                                                                                                                                                                                                                                                                                                                                                  Bacillus stearothermophilus
                                                                                                                                                                                                                                                                (first entry)
                                   5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CUBI-) CUBIST PHARM INC
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                Best_Local Similarity
Matches 5; Conserv
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Best Local Similarity
Matches 4; Conserv
                                                                     1 YLSGADLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 AA;
                                                                                       | | :|||
1 yrpgenlnl
                                                                                                                                                                                                                                                              28-OCT-1998
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11-JAN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                     US5798240-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim S,
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                                                                                                                                                          RESULT
W70078
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(BIOJ ) BIOGEN NV.
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4 ylxggd 9
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2 sgadis 7
                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           10-JAN-1986;
                                                                                                                                                                                   14-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wallner BP,
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                                                                                                                                                                                                                                                                                                                                                    US4950646-A.
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                                                                                                                                                                                                                                                                                                                                                                                         21-AUG-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JAN-1986;
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14-AUG-1985;
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                                                                                                                                               R07966;
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R09414
                                                                          RESULT
R07966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Activities (RA) using two-dimensional electrophoresis to generate a arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comparises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features (b) identifying at least one chosen (c) comparing the abundance of each chosen feature in the sample with the abundance of each chosen feature in the sample with the abundance of each chosen feature in the cone or more persons without RA, where the relative abundance of the chosen feature of features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic protein isoforms (RPIS), and for production of antibodies to RPIS. The RA-diagnostic feature (RADF) proteins can be used in clinical compounds that promote or inhibit their activity, which are then used as CR A drugs. Nucleic acid encoding RADFs can be used in gene therapy corporations for the present RPI peptides and 225066 to protocols. Y41804 to Y42101 represent expression reference protein isoform peptides and 225066 to the exemplification of the present invention.
                                                                                                                                                                                                                                                                          RA; diagnosis; RPI; RADF; detection;
                                                                                                                                                                                                                                       Rheumatoid arthritis diagnostic protein isoform 17 peptide #1.
                                                                                                                                                                                                                                                                                           rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 20; Length 7; Pred. No. 2.1e+05; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Townsend RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 150; 157pp; English
                                                                                                                        Y41846 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                            Human; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB00763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0005477
                                                                                                                                                                                                   09-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patel TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-571871/48.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        electrophoresis
               1 YLSGAD 6
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                              Y41846;
                                                                                         RESULT 17
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Gaps

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Conservative

3 SGADLN 8

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Based on the similarity in the phospholipase A2 inhibitory activity of lipocortin and N-lipocortin and the similarity in the protein and the similarity in the protein and the similarity in the protein and the protein and the protein and the similarity in the protein and sequences, it was concluded that the two proteins represent a family of related proteins. There is ca. 60% homology.

The protein can be used for reducing inflammation or treating antituitic, allergic, dermatologic, opthalmic and collagen diseases and other diseases involving inflammation processes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                           placenta; inflammation reduction; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schindler DG, Huang KS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pure fragment of human lipocortin - useful for reducing inflammation or for treating arthritis, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23; DB 11; Le
Pred. No. 2.1e+05;
0; Mismatches 2;
                                                                                                                                                                                                                    phospholipase A2 inhibitor; tryptic fragment T32
                                                                                                                                              Tryptic fragment T32 of human N-lipocortin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garwin JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 25; 51pp; English
R07966 standard; protein; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R09414 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.18;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             86US-0929199.
85US-0772892.
85US-0765877.
85US-0712376.
                                                                                                                                                                                                                                                                                                                                                                                                                86US-0929199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85US-0690146
                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pepinsky RB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-AUG-1990 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
                                                                                                                                                                                           Human N-lipocortin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-274549/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R09414;
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Bedi GS, Evans RT,
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                                                                                                                                                                                                                                                                                                                         :||||
| ngadl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Holmstrom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palva ET,
                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                      R88476;
                                                                                                                                                                                                                                                                                                                                                              RESULT 21
R88476
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                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gingivalis adhesion inhibitor comprising fimbrillin residues 240-245.
                                                                                                                                                                                                                                                              The alpha-subunit (a-SU), contg. al least one of the polypeptides given in R09404-417, can bind to ICAM-1 (or other natural ligands) on the surface of cells, and can associate with the beta-SU to form a heterodimer (also able to bind to ICAM-1). a-SU, and its derivs., are useful in suppressing inflammation, metastasis and growth of a-SU expressing tumour cells and is used in the treatment of viral infections.
                            Lymphocyte function associated antigen; inflammation; metastasis.
                                                                                                                                                                                                   Pure alpha subunit of lymphocyte function associated antigen and encoding DNA sequences, useful eg for suppressing inflammation or metastasis
                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fimbrillin gene; inhibition; adhesion; saliva; coated surface; prevention; periodontitis; teeth; gums; dentifrices; mouthwash;
                                                                                                                                                                                                                                                                                                                                                                                          Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Le
2.1e+05;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYNY ) UNIV NEW YORK STATE RES FOUND,
        LFA-1 alpha subunit polypeptide (k)
                                                                                                                                                                                                                                                                                                                                        The pref. dose is 1 pg - 10 mg/kg
                                                                                                                                                                                                                                            Claim 6; Page 19; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W02264 standard; peptide; 6 AA.
                                                                                        89EP-0115160
                                                                                                            88US-0235227
89US-0321017
                                                                                                                                          (DANA-) DANA FARBER CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92US-0994277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porphyromonas gingivalis.
                                                                                                                                                              Larson R;
                                                                                                                                                                                 WPI; 1990-108985/15.
                                                                                                                                                              Springer TA,
                                                                                       17-AUG-1989;
                                                                                                                      09-MAR-1989;
                                                                                                            23-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                          1111
2 ylsg 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                               1 YLSG 4
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                                                EP362526-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5536497-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-JUL-1996
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W02264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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Gaps
                                                                                                                                                                                                       The present peptide was prepd. by chemical synthesis, on the basis of an amino acid sequence deduced from the DNA sequence of the cloned P. gingivalis fimbrillin gene described in J. Bacteriol, 170, 1658, 1988. The peptide inhibits the adhesion of P. gingivalis to saliva coated surfaces, and is therefore useful for preventing periodontitis by application to teeth and gums, esp. in dentifrices, mouthwashes or topical formulations, or by admin. as a P. vaccine. In an assay to determine the effect of the peptide on P. gingivalis binding to saliva coated hydroxapatite beads, the approx. 30 %.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New transgenic plants with increase trehalose contents - prepd. by transforming plants with a trehalose-6-phosphate synthase gene fused to a non-constitutive promoter
                                                                     Peptide inhibitor of Porphyromonas gingivalis adhesion to saliva coated surface - useful for preventing periodontitis by application to the teeth and gums esp. in dentifrices, mouth:washes or topical formulations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tryptic peptide; trehalose-6-phosphate synthase; M. smegmatis; probe
trehalose; transgenic plant; heparin-activated; preservation; food;
antigenic determinant; yeast; TSP1; fruit; berry; puree; jelly; jam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequences given in R88473-80 are internal tryptic peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 21; DB 17; Length b; Pred. No. 2.1e+05; 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Internal tryptic peptide from Tre6P synthase (peak 29) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mantyla E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mandal A,
Sojar HT;
                                                                                                                                                                      Claim 1; Columns 17-18; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
Genco RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R88476 standard; peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      K, Londesborough J,
Tunnela O, Welin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95WO-FI00377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 80.0
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium smegmatis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ALKO-) ALKO GROUP LTD.
                                  WPI; 1996-341445/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-077499/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AA;
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9 AA;

Seguence

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                                             Plant with increase trehalose content. Tre6p in M. Smegmatis is heparin-activated and was isolated and purified. These peptides were derived from a protein which was purified with a mol. wt. of 55 kD which shared antigenic determinants with the yeast Tre6p synthase protein. Using these peptides probes may be designed for the isolation of the Tre6p gene (TSP1) for the production of the Transgenic plants. The trehalose may be isolated from the transgenic plants and used in bulk preparation including the preservation of the flavour and structure of food stuffs during drying. Fruits and berries form the transformed plants may be processed into purees, jellies and jams which have a fresher and richer flavour due to the increased
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation - by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
derived from trehalose-6-phosphate (Tre6P) synthase from M. smegmatis. Tre6P is the key enzyme in the synthesis of trehalose via Tre6P. The aim of the invention is to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R-specific amidohydrolase; hydrolysis; racemate; nltrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                      Up 1.18+05;
                                                                                                                                                                                                                                                                                                                                            Score 21; DB 17; Length 6; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Naughton A, Robins K, Shaw N, Tinschert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K. oxytoca R-specific amidohydrolase peptide T5.
                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 10.2; Page 29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W40267 standard; Protein; 9 AA
                                                                                                                                                                                                                                                                                                                                          46.7%;
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96CH-0001723.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klebsiella oxytoca.
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                         trehalose content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LONZ ) LONZA AG.
                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zimmermann T;
                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGA 5
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| ylega 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brieden W,
                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W40267;
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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA-B or C) and induce a cytotoxic T cepponse against the antigen from which the peptide is derived.

The A-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to a HLA molecule, rather than the intact foreign antigen itself, and are particularly important in tumour rejection and in flighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.

They can be administered as vaccines to elicit an immune response in cancindiduals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic relations. They contacting a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
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                                                                                                                                                                                                                                                                                                                                 Immunogenic peptide having a human leukocyte antigen binding motif #2429
                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                          ;
    Length 9;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grey HM,
  Score 21; DB 19; L. Pred. No. 2.1e+05; 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 124; 150pp; English.
                                                                                                                                                                                                              Y47818 standard; Peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sidney J,
  46.78;
62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US05039
                                                                                                                                                                                                                                                                                           (first entry)
Query Match 46.7
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIM-) EPIMMUNE INC.
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                                                                            8
                                                                            1 YLSGADLN
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| ytvgamln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9945954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1998;
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                                                                                                                                                                                                                                                                                           01-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                          RESULT 23
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9 AA;

Sequence

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         forms of enzyme inhibitors, e.g. proteases, Kinases and phosphatases. (Ab) are used for affinity purification of recombinant peptides and in the identification of naturally occurring protease inhibitors. Enzyme-inhibiting peptides identified can be used to treat a serpin deficiency or a disorder of serine proteases.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
latent; substrate subtraction phage display peptide library;
identification; kinase; phosphatase; serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substrate subtraction phage display peptide libraries - used to distinguish between active and latent forms of enzyme, e.g. serine
                                        ó;
   Length 9;
                                        Indels
 Score 21; DB 20; L
Pred. No. 2.1e+05;
; Mismatches 2;
                                                                                                                                                                                                                                                                                                                    Enzyme inhibitor peptide SEQ ID NO:80.
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                                                                                                                                                                                                      W56879 standard; peptide; 6 AA.
 46.78;
57.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US09760
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                                                                                                                                                                                                                                                                              28-JUL-1998 (first entry)
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                                      4; Conservative
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Query Match
Best Local Similarity
Matches 4; Conserv
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                                                                       1 YLSGADL 7
                                                                                                            1 ylsegdm 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                  RESULT 24
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arthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features: (b) identifying at least one chosen feature whose relative abundance of each chosen feature in the sample with the abundance of each chosen feature in the sample with the abundance of that chosen feature in plasma from one or more persons without RA, where the relative abundance of the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy compounds that promote or inhibit their activity, which are then used as processent expression reference protein isoform peptides and 225066 to 225068 represent expression reference protein isoform peptides and 125066 to the exemplification of the present invention.
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                   Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
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                                                                                                                                                                                                                                                                                                                    Rheumatoid arthritis diagnostic protein isoform peptide #113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosis of human rheumatoid arthritis by two-dimensional
Score 20; DB 19; Length b; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 20; 157pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Townsend RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ile, Leu
                                                                                                                                                                                                          Y41962 standard; Peptide; 7 AA.
                  44.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-GB00763.
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                                                                                                                                                                                                                                                                                  (first entry)
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parekh RB, Patel TP,
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-571871/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 electrophoresis
                                                                                    8
                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W09947925-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAR-1998;
                                                                                                                                                                                                                                                                                  09-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1999
                                                                                    4 GADLN
                                                                                                                    2 gvdmn
                                                                                                                                                                                                                                               x41962;
                                                                                                                                                                         25
                                                                                                                                                                           RESULT
                                                                                                                                                                                              X41962
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Enzyme inhibitor peptide SEQ ID NO:184.
                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1995-167251/22
                                                                                            Query Match
Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 4; Conserv
                                                      7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YLSGADLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :|: |||:
| hltradls 8
                                                                                                                                                                                                                                                                                                                                                                                                                                JP07089991-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-SEP-1993;
                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUL-1998
                                                                                                                                                                             2 sgad 5
                                                                                                                                                                                                                                                                                                        12-DEC-1995
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                                                                                                                                                    SGAD
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibody
                                                                                                                                                                                                                                                                             R73336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W56983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                        27
                                                                                                                                                                                                                        RESULT
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W56983
                                                                                                                                                                                                                                        R7333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BX BX SX B
  SSSXS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arthritis (RA) using two-dimensional electrophoresis to generate a ruthritis (RA) using two-dimensional electrophoresis to generate a two-dimensional array of features. The method can be used for screening, diagnosis and prognosis of RA in a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synovial fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance correlates with the presence or absence of RA, and (c) comparing the abundance of each chosen feature in the sample with the abundance of that chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature in serum or plasma from one or more persons without RA, where the relative abundance of the chosen feature in classification of the chosen feature or features in the sample indicates the presence or absence of RA in the subject. The method can also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy proteocls. Y41844 to Y42100 represent RPI peptides, Y42101 to Y42103
                                                                                 ö
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                   Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection; rheumatoid arthritis diagnostic feature. BRPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                                 ;
                                                                                                                                                                                                                                                                                        Rheumatoid arthritis diagnostic protein isoform peptide #179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosis of human rheumatoid arthritis by two-dimensional
                                                   44.4%; Score 20; DB 20; Length 7; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Key Location/Qualifiers Misc-difference 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 21; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Ile, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend
                                                                                                                                                                                                      Y42028 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98GB-0005477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-GB00763
                                                                                                                                                                                                                                                             09-DEC-1999 (first entry)
                                                                 Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patel TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-571871/48.
            7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               electrophoresis
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W09947925-A2
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                                                                                                                          |||||
2 sgad 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAR-1999;
                                                                                                         3 SGAD 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-SEP-1999.
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            Sequence
                                                      Query Match
                                                                                                                                                                                                                                  Y42028;
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                                                                                                                                                                                                                Gaps
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represent expression reference protein isoform peptides and 225066 225068 represent degenerate probes for RPIs, which are all used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptides with affinity to human TSH (thyroid stimulating hormone) receptor antibody are used for detection of the antibody. (See also R73201-592).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide(s) having affinity for the human TSH receptor ody - used in detection of the TSH antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thyroid stimulating hormone receptor; TSH; human; Homo sapiens; antibody; affinity; detection.
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                                                                                                                                                               Length 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 8;
                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB 16; Length 8;
Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                                                                                                                                             DB 20; Le
2.1e+05;
hes 0;
                                                                                                                                                             11arity 100.0%; Pred. No. 2.1
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MITP ) MITSUBISHI PETROCHEMICAL CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human TSH receptor (residues 271-278).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 24; 54pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                         R73336 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W56983 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.4%;
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(CYTE-) CYTEL CORP.
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Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                      04-MAR-1994;
                                                                                                                                                                             05-MAR-1993;
                                                                                                                                                                                                      29-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1994;
                                                                                                     WO9420127-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 dln1 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 DLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                 The present sequence represents an enzyme inhibitor peptide used in the method of the invention to distinguish between t-PA and u-PA. The present invention describes a substract subtraction ilbrary for the identification of peptide substrates selective between a first enzyme (E1) and a second enzyme (E2), comprising a collection different substrates selective between a first enzyme (E1) and a second enzyme (E2); (2) a compound comprising the amino acid sequence of a peptide substrates selective between a first enzyme (E1) and a second enzyme (E2); (2) a compound comprising the amino acid sequence of a peptide identified by M1; (3) a polypeptide for use as an enzyme inhibitor comprising one of 237 amino acid sequences (see W56801 to W56947, and W56949 to W57038); (4) a recombinant DNA vetor comprising DNA (1) encoding a protease inhibitor including the sequence identified by the missing one of 237 amino acid sequence identified by the encoding a protease inhibitor including the sequence identified by the missing perveen and latent forms of protease inhibitors, that uses (Ab). The control of a dispossite assay for distinguishing between citive and latent forms of proteases inhibitors, that uses (Ab). The control of an encoding a proteases inhibitors, e.g. proteases, kinases and phosphatases. The identification of naturally occurring protease inhibitors. Enzymethe inhibiting peptides identified can be used to treat a serpin deficiency or a disorder of serime proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
             serine protease; active; peptide library;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                            Substrate subtraction phage display peptide libraries - used to distinguish between active and latent forms of enzyme, e.g. serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19; Length 8;
2.1e+05;
ches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Peptide fragment (1.0164) of HIV binds HLA-A2.1.
           Enzyme inhibitor; t-PA; u-PA; chymotrypsin;
latent; substrate subtraction phage display
identification; kinase; phosphatase; serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 20; DB ]
Pred. No. 2.1e-1; Mismatches
                                                                                                                                                                                                                                                                                                            Claim 25; Page 102; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.4%;
                                                                                                                                      97WO-US09760
                                                                                                                                                              96US-0019495
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                                                                                                                                                                                     (SCRI ) SCRIPPS RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                      WPI; 1998-062746/06
                                                                                                                                                                                                              Madison EL;
                                                                                    WO9747314-A1
                                                                                                                                    10-JUN-1997;
                                                                                                                                                              10-JUN-1996;
                                                             Homo sapiens
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                                                                                                             18-DEC-1997,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 gydmn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                             Ke S,
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qq
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R59104-264 are immunogenic 9mer peptides that contain a HLA-A2.1 binding motif. These peptides bind HLA-A2.1 and have a binding affinity of at least 1% as compared to a reference peptide (R71293). R59233 has an IC50 of 0 and the sequence occurs at position 614 in the HIV POL protein. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg. prostate cancer or lymphoma, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hepatitis B virus polymerase; cytotoxic T cell response; prophylactic; vaccine; chronic; acute HBV infection; carrier.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EF HIVI; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; 10mer; anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nseq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic peptide(s) having an HLA-A2.1 binding motif - of for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.4%; Score 20; DB 15; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sidney J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 5; Page 105; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R70067 standard; peptide; 9 AA.
                                                                                                                                                                                                                Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93US-0027146.
93US-0073205.
93US-0159184.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grey HM, Kast WM, Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US02353
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                                                                                                                                             human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1994-302678/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases
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Gaps

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Length 9; 1; Indels

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The sequence encoding the jojoba embryo long chain fatty acyl-CoA reductase may be used in recombinant constructs which in turn can be used to transform E. coli. Such constructs are useful for the expression of the jojoba embryo long chain fatty acyl CoA reductase in host cells. The enzyme catalyses the formation of a fatty alcohol from a fatty acyl substrate. Analysis of the enzyme by SDS PAGE gave two prominent bands having apparent molecular masses of approximately 52 and 54 kb. As the apparent size of the reductase enzyme in the native state is approximately 49 kb as determined by size exclusion chromatography, these bands probably represented two related forms of the enzyme instead of two different subunits of the enzyme. This sequence is a peptide fragment from the 54 kb protein.
expression of the jojoba embryo long chain fatty acyl CoA reductase in host cells. The enzyme catalyses the formation of a fatty alcohol from a fatty acyl substrate. Analysis of the enzyme by SDS PAGE gave two prominent bands having apparent molecular masses of approximately 52 and 54 kb. As the apparent size of the reductase enzyme in the native state is approximately 49 kb as determined by size exclusion chromatography, these bands probably represented two related forms of the enzyme instead of two different subunits of the enzyme. This sequence is a peptide fragment from the 56 kb protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant constructs for transforming plants of E. colicontg. nucleic acid encoding jojoba embryo long chain fatty acyl-CoA reductase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jojoba; fatty acyl CoA reductase; fatty acyl; fatty alcohol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jojoba fatty acyl-CoA reductase 54kd protein fragment.
                                                                                                                                                                                                                                                                                                      Score 20; DB 16;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 4; Column 26; 30pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R67613 standard; Protein; 9 AA.
                                                                                                                                                                                                                                                                                                         44.48;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0659975.
91US-0767251.
91US-0796256.
92US-0920430.
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                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metz JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Simmondsia chinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-021884/03
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                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 3; Conserv
                                                                                                                                                                                                                                   9 AA;
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gldinv 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-1995
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20-NOV-1991
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Best Local S
Matches 3
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                                                                                                                                                                                                                                                                       Peptides R70066-7 are control peptides in an assay for stimulation of cytocoxic T cells (CTLs) by epitopes from the hepatitis B virus (HBV) polymerase (HBpol) (see R700044-59). The HBpol peptides can be used, prophylactically as vaccines, together with, or conjugated to, HBV helper epitopes (R70066-4). The peptides can be used, particularly ex vivo, to stimulate CTL cells,which cells can be reintroduced into patients who have chronic or acute HBV infections or are carriers, especially in treatments to prevent conversion from acute to chronic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                       New peptides inducing cytotoxic T lymphocytes to hepatitis B virus - are regions of HB polymerase protein, for treating acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant constructs for transforming plants of E. co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jojoba fatty acyl-CoA reductase 56kd protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.4%; Score 20; DB 16; I 100.0%; Pred. No. 2.1e+05; ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Column 26; 30pp; English.
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                                                                                                                                                                                                                                   Example 1; Page 35; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R67605 standard; Protein; 9 AA.
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91US-0767251.
91US-0796256.
92US-0920430.
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  (SCRI ) SCRIPPS RES INST
                                                                                                                                                                                     and chronic infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Simmondsia chinensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-021884/03.
                                                                                         WPI; 1995-082004/11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contg. nucleic acid
scyl-CoA reductase.
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Best Local Similarity
Matches 4; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jojoba; fatty
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-FEB-1991;
27-SEP-1991;
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                                                Chisari FV;
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R67605
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                                                                                                                                                                                              W54515;
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Matches
Matches
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Sequences shown in W70077 to W70086 represent methionyl-tRNA (Met-tRNA)
Synthetase fragments from different bacterial species. These are used
for designing degenerate primers (W43887 to V43890) used for isolating
Wet-tRNA sythetase gene fragment by PCR from M. tuberculosis and M.
Met-tRNA sythetase under control of transcriptional signals that can be
to used to transform sultable host cells. The nucleict acids and host cells
Wet-tRNA) synthetases, especially of methionyl tRNA synthetase. The enzymes are
to used for the recombinant production of mycobacterial amino acyl tRNA
Synthetases, especially of methionyl tRNA synthetase. The enzymes are
used by the organism in protein synthesis, and as such, the recombinant
consyme can be used to identify candidate drugs for use as antibiotics
towards mycobacteria, especially M. tuberculosis, which is responsible
for tuberculosis. Antisense constructs of the nucled acids can also be
used in antisense inhibition of the synthetase gene. The recombinant
consyme allows quick assays in screening of antibiotics. Present testing
protocols involve exposing whole mycobacteria to candidate drugs and
seeing their effect. This is time consuming as the bacteria are generally
convert with nathemenic attains
                                                                   ö
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis, mycobacterial, methionyl-tRNA synthetase, enzyme; antiblotic, tuberculosis; Thermus thermophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant genes encoding mycobacterial amino acyl tRNA synthetases - useful for recombinant production of the enzyme for use in screening of antibiotics against Mycobacterium tuberculosis
                                                                 0;
                               Length 9;
                                                               Indels
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                                                                                                                                                                                                                                                                                                                                 Thermus thermophilus methionyl-tRNA synthetase fragment.
                          Score 20; DB 16; Le
Pred. No. 2.1e+05;
2; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Columns 33-34; 32pp; English.
                                                                                                                                                                                                                     W70077 standard; peptide; 9 AA.
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                            44.48;
50.08;
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work with pathogenic strains
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96US-0584226
                                                                                                                                                                                                                                                                                            28-OCT-1998 (first entry)
                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CUBI-) CUBIST PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                         Thermus thermophilus
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                          Query Match
Best Local Similarity
Matches 3; Conserv
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2 qldinv 7
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                                                                                                 4 GADLNL
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Length 9;

Score 20; DB 19; Pred. No. 2.1e+05;

44.48; 50.08;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                              Carbohydrate-specific; cytolytic T cell; therapeutic; tumour; major histocompatibility complex; vaccine; protective immune response; pathogenic bacteria; virus; CTL response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The polypeptides are used as vaccines to generate therapeutic or protective immune responses, particularly against tumours but also against pathogenic bacteria and viruses (e.g. mycobacteria that cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for stimulating carbohydrate-specific cytotoxic T
lymphocytes - comprises synthetic peptide with attached carbohydrate
hapten, designed to bind to class I molecule, used in vaccines
against cancer or infectious disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LJOL-) LA JOLLA INST ALLERGY & IMMUNOLOGY.
                                                                                                                                                                                                    Synthetic polypeptide HBV Pol 42-50.
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W54515 standard; peptide; 9 AA.
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ID Y70832 standard; peptide; 9 AA.
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                                                                                                                                    01-SEP-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
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Mouse; truncated BAX protein; tBAX; BAX alpha; BCL-2 family; head trauma; metron; anti-apoptotic; cerebroprotective; neuroprotective; neuroactive; apoptosis; treatment; neurodegenerative disease; peripheral nerve injury; spinal cord injury; stroke; pro-apoptotic; PCD; programmed cell death; BH3 domain; BCL-2 homology domain; BAK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The patent discloses specific truncated BAX (tBAX) proteins which inhibit neuronal apoptosis induced by trophic factor deprivation. The anti-apoptotic taxx proteins include tBAX70. tBAX78 and their mutants. These proteins contain the N-terminal region and at least a portion of the BH3 domain of BAX alpha and lack the BH1. BH2 and C-terminal transmembrane domains. The tBAX protein lacking only the transmembrane domain has been shown to have anti-apoptotic activity. The tBAX proteins are used to treat diseases associated with neuronal apoptosis, e.g. neurodegenerative diseases, peripheral nerve injury, spinal cord injury, head trauma and stroke. tBAX proteins truncating at amino acid 68 of the BH3 domain of BAX alpha also have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-apoptotic activity because Asp at position 68 is shown to be important for BAX activity and is conserved in all BCL-2 family members. The present sequence is a BH3 domain of mouse BAK protein, a pro-apoptotic protein belonging to BCL-2 family that is involved in regulation of neuronal programmed cell death. The present sequence contains the conserved Asp residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt Truncated} BAX polypeptides useful for preventing apoptosis of neurons for the treatment of nervous system disorders ^{\text{-}}
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                                                                                                                                                                                                   BH3 domain of mouse BAK protein.
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                                                                                                                       31-JUL-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-339513/29.
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                                      Y70832;
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Gaps ;

Best Local Similarity Matches 4; Conserv

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Search completed: December 16, 2000, 03:07:18 Job time: 8059 sec

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Ogyati pyrococcus
Ogyati aeropyrum p
Ogyadi hemo sapien
P78988 hebeloma ci
Ogytó drosophila
OSASIA pyrococcus
O64783 avian adeno
Q9we61 turnip mosa
                         024163 drosophila
09ved3 drosophila
09ved3 helicobacte
09v4d7 homo sapien
020421 caenorhabdi
00165 branchiosto
055201 synechocyst
09s1v4 pisum sativ
                                                                                                                                                                                                                                                                                                        Q44404 agrobacteri
O65678 arabidopsis
Q98182 oryza sativ
Q33154 suksdorfia
Q31903 bolandra or
Q31922 boykinia ro
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                                                                                                                                                    Q9wy57 thermotoga
O57709 pyrococcus
                                                                                                                                                                    pyrococcus
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 14, Last senotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
GLYCINE CLEAVAGE SYSTEM P PROTEIN.
DRIB09.
Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus group; Deinococcales; Deinococcus.
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Dunn M.G., Ellar D.J.;

Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; Y10168; CAA71249.1; -.

SEQUENCE 385 AA; 43949 MW; 6013163292D0329E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
SERINE/THREONINE KINASE.
PRI.
Bacillus thuringiensis.
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
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Pred. No. 18;
0; Mismatches
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Q9ST82
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09Y2D7
P78988
09VT60
058324
064783
                                           09VED3
048237
09Y4D7
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001675
055201
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Matches 7; Conservative
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278 YLSGPNLN 285
1 YLSGANLN 8
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Q9RTF5;
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Q35903 strongyloce
Q35773 synechocyst
Q9xvm8 caenorhabdi
Q9/480 drosophila
Q9/480 drosophila
Q9/480 drosophila
Q9/480 homo sapien
Q14628 homo sapien
Q14628 homo sapien
Q14628 homo sapien
Q14629 caenorhabdi
Q9/20 pectobacter
Q8/150 chlamydia t
P7/416 synechocyst
Q22575 hordeum spo
Q38766 avena sativ
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Q9rtf5 deinococcus
Q21962 caenorhabdi
Q9vh09 drosophila
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                         297973 seqs, 93374136 residues
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Maximum Match 100%
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Q9RTF5
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Gapop 10.0 , Gapext 0.5
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sp_human:*
sp_human:*
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sp_orgenele.*
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Match Length DB
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Maximum DB seq
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702 YLDGANMN 709
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Cracton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Parsons J., Percy C., Memurray A., Mortimore B., O'Callaghan M.,
Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 Mo of contiguous nucleotide sequence from chromosome III of C.
                                                                White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffatt K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchun K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
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0
                                                                                                                                                                                                                            "Genome Sequence of the Radioresistant Bacterium Deinococcus radiodurans R1.";
                                                                                                                                                                                                                                                                                                                                                                                                                   2; Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                           949 AA; 102122 MW; FDCBA42D4E0888D5 CRC64;
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108865 MW; F445CA0B46C7AA02 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SIMILAR TO GLYCINE DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB
Pred. No. 78;
1; Mismatches
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                                                                                                                                                                                                                                                                                             EMBL; AE002021; AAF11360.1; -. TIGR; DR1809; -.
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                                                                                                                                                                                                                                                                                                                                                                                                            77.8%;
75.0%;
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Submitted (JUL-1995) th
EMBL; U23510; AAC46780
SEQUENCE 979 AA; 10
SEQUENCE FROM N.A.
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                                           MEDLINE; 20036896.
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Q21962
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MEDLINE: ZU1960UD.

RA Addams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Galle R.F.,

R. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.C., Rogrers Y.-H.C., Blazel F.G., Change M., Péleiffer B.D.,

RA Man K.H., Doyle C., Barer E.G., Helt G., Welson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews. Pfannkoch C. Baldwin D.,

Ballow R.M., Bassu A., Berman B.P., Bhandari D., Bolshakov S.,

RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Gersy J.M., Cavley S., Dahlke C., Davenport L.B., Doyles P.,

RA Gersy J.M., Cavley S., Dahlke C., Boraca C., Ferraca C., Perraca C., Perraca C.,

RA Gersy J., Brownes M., Dong Z., Gelbart W.M., Glasser K.,

RA Durbin K.J., Evangelista C.C., Ferraca C., Perraca J.R., Retchum K.A.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D., Helman T.J., Hernandez J.R., Mocherson D.,

RA Mount S.M., Wattel B., McIncosh T.C., McLeod M.P., McPherson D.,

RA Mount S.M., Wattel B., McIncosh T.C., Moriecd M.P., Purly D., Lai Z.,

Raine B.E., Spradling A.C., Stapleton M., Stupsk M.P., Shin H.,

Raine E., Spradling A.C., Stapleton M., Stupsk M., Wang X.,

Raine E., Spradling A.C., Stapleton M., Stupsk M., Wang X.,

RA Beinert K., Remington K.A., Rubin S., Wang X., Wang X.-Y., Stapleton M., Stupsk M., Wang X.-Y., Wang X.-Y.,
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                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                    Last sequence update)
Last annotation update)
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Pred. No. 81;
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                                                                       Created)
                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly)
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75.0%;
                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 20196006.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
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                                                                                                                                                                 CG3999 PROTEIN.
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Gaps

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1; Indels

77.8%; Score 35; DB 5; Length 979;

Pred. No. 81; 1; Mismatches

75.0%;

Query Match Best Local Similarity Matches 6; Conserva

Conservative

Last sequence update)
Last annotation update)

Created)

259 AA.

PRT;

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S. Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N., Sugiura M., Tabata S.;
Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map posttions 64% to 92% of the genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.6%; Score 34; DB 2; Length 259; 100.0%; Pred. No. 30; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00805; Pentapeptide; 2.
Hypothetical protein.
SEQUENCE 259 AA; 27402 MW; B6D54CA59C6FCDE7 CRC64;
                                                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                 (strain PCC 6803)
                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Cre
01-NOV-1996 (TrEMBLrel. 01, Las
01-UNN-2000 (TrEMBLrel. 14, Las
HYPOTHETICAL 27.4 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D64002; BAA10422.1;
INTERPRO; IPR001440; -.
INTERPRO; IPR001646; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-PCC6803;
MEDLINE; 96127529.
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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31 YLSNSNINL 39
                                                                                                                                                                                                                                                                                 Synechocystis sp.
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                                                                                                                                            055773;
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MEDLINE; 91175684.
Thomas W.K., Maa J., Wilson A.C.;
"Shifting constraints on tRNA genes during mitochondrial DNA evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Li J., Tong S., Wands J.R.;
"Identification and Expression of Glycine Decarboxylase (p120) as a Duck Hepatitis B Virus Pre-S Envelope-binding Protein.";
J. Blol. Chem. 274:27658-27665(1999).
EMBL; AF137264; AAD56281.1;
SEQUENCE 1024 AA; 113473 MW; 657EFC89374DFEC3 CRC64;
                                                                                                                                                                                                                              Anas platyrhynchos (Domestic duck).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIP=PEKIN DUCK; TISSUE=LIVER;
MEDLINE; 96323119.
Li J.S., Tong S.P., Wands J.R.;
"Characterization of a 120 kilodalton pre-S-binding protein as candidate duck hepatitis B virus receptor.";
J. VICOL. 70:6029-6035(1996).
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Pred. No. 85;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 AA; 14405 MW; 903318CDAD6E4C0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
NADH DEHYDROGENASE SUBUNIT 5 (ND5) (FRAGMENT).
Strongylocentrotus pallidus.
                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
GLYCINE DECARBOXILASE P PROTEIN.
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PEKIN DUCK; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in animals.";
New Biol. 1:93-100(1989).
EMBL; M27524; CAB25461.1;
Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0.
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Best Local Similarity 66.7
Matches 6; Conservative
                                                                                         PRELIMINARY;
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SEQUENCE
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Q35903;
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                                                RESULT
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Last sequence update) Last annotation update)

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Q9VF80;
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MEDLINE; 98295987.

A Cols.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Erosch R., Parkhill J., Garnier T., Churcher C., Harris D., A Cols.T., Drown D., Chillingworth T., Connor R., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., A Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Antier S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., A Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murther S., Seeger K., Skelton S., Squares S., Squares T., Shitch S., Seeger K., Mitchead S., Barrell B.G.;

R. Taylor K., Whitchead S., Barrell B.G.;

R. Deciphering the biology of Mycobacterium tuberculosis from the RT complete genome sequence.";

R. Nature 393:537-544(1998).

E. Matur. 2970S0; CAB09749.1;

B. HSSP. P08659; LCCI.
                                                                        MEDLINE; 94150718.

Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Wilson R., Ainscough R., Connell M., Copsey T., Cooper J., Coulson A., Craxton M., Dar S., Du Z., Durbin R., Favello A., Fulton L., Gardher A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latrellie P., Lightning J., Lloyd C., Momurray A., Mortimore B., O'Callaghan M., Smaldon N., Smith A., Sonnhammer E., Staden R., Sladen R., Sustand J., Theory Miey J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
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         2.2 Mb of contiguous nucleotide sequence from chromosome III of
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                                                                                                                                                                                                                                                                                                                Score 34; DB 5; Length 272;
Pred. No. 31;
1; Mismatches 2; Indels
                                    Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 272 AA; 31908 MW; B00BDE57AFD40584 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
PROBABLE FATTY-ACID COA LIGASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             554 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00501; AMP-binding; 1.
                                                                                                                                                                                                                                                                                                                 75.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TUBERCULIST; Rv0166; -.
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                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                              SEQUENCE FROM N.A.
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SEQUENCE
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Length 554;

DB 2; 69;

Score 34; Pred. No.

75.6%; 75.0%;

Query Match Best Local Similarity

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RA MEDLINE; 20198006.

RA Sutton G.G., Wortman J.R., Zhang Q., Chen L.X., Becroff R. C., Scheners S.C., Changer M., Henderson S.N., Bratton G.G., Wortman J.R., Zhang Q., Chen L.X., Britton G.G., Wortman J.R., Zhang Q., Chen L.X., RA Brandon R.C., Baxter E.G., Helt G., Change M., Pichiffer B.D., RA Brandon R.C., Baxter E.G., Helt G., Nelson C., Baldwin D., Ballew R.M., Basu A., An H.-J., Andrews-Pfannkoch C., Baldwin D., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Buttis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I., Burtis K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Buttis K.C., Evangelista C.C., Ferraz C., Ferraz C., Ferraz C., Steleart W.M., Glasser K., Gabrielin A.B., Garg N.S., Gelbart W.M., Glasser K., Harris M., Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibeqwam C., Milshin A. Karpen G.H., Re Z., Kennison J.A., Ketchum K.A., Murphy B., Murphy C., Morita S., Kolp D., Liai Z., Liang Y., Lia X., Murphy B., Murphy C., Morita S., Kolp D., Lai Z., Liang Y., Liai Z., Liang Y., Liai Z., Liang Y., Liai Z., Liang Y., Murphy S., Murphy C., Morita S., Moshrei B., Murphy B., Murphy C., Morita S., Morpherson D., Melson D.R., Nelson K.A., Woodarg T., Worley G., Morita S., Moshrei B., Murphy B., Murphy C., Morita S., Morphy S., Murphy S.,
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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SEQUENCE 702 AA; 78620 MW; 0A3222A1886CFEE2 CRC64;
                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update).
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Pred. No. 90;
0; Mismatches
                                                                                                                                                                                                                                                        702 AA.
                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
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EMBL; AE003708; AAF55180.1; --
FLYBASE; FBgn0038325; CG6194.
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                                                                                                                                                                                                                                                    PRELIMINARY;
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                 217 YTSGANIN 224
1 YLSGANLN 8
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032915 032915

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RESULT 032915

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Jenkins J.K., Drong R.F., Shuck M.E., Blenkowski M.J., Slightom J.L., Arend W.P., Smith M.F. Jr., Intraceclular IL-1 receptor antagonist promoter: cell type-specific and inducible regulatory regions."; J. Immunol. 158:748-755(1997).
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                                   Gaps
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDINE, 9355865.
MEDINE, 9355865.
Introna M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
Introna M., Mantovani A., Colotta F.;
"Cloning and characterization of a new isoform of the interleukin 1
"receptor antagonist.";
J. Exp. Med. 182:623-628(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Slightom J.L.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; X84448; CAA59087.1; -.
EMBL; U65590; AAB92269.1; -.
HSSP; P18510; IIRP.
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INTERPRO; IPR000975; -.
PFAM; PF00340; interleukin-1; 1.
PRINTS; PR00254; INTERLEUKINI.
PROSITE; PS00253; INTERLEUKIN. 1; 1.
PROSITE; PS00253; INTERLEUKIN. 1; 1.
                                                                                                                                                                                                                                                                                                                                ol-NoV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
ILTRACELLULAR IL-1 RECEPTOR ANTAGONIST TYPE II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                            180 AA
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     ed. No. 25;
Mismatches
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     Pred. No.
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  66.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.3
Best Local Similarity 66.7
Matches 6; Conservative
  Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                            PRELIMINARY;
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62 YLQGPNVNL 70
                                                                                                                       || | | |:||
25 YLQGPNVNL 33
                                                                                      1 YLSGANLNL
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044592
10 0444
AC 0444
DJ 01-
DJ 01-
DJ 01-
DJ 02-
CN EV8
CO EUK
CO EUK
CO RHA
RN ELS
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Q14628
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SEQUENCE FROM N.A.
MEDLINE; 98183404.
Welssbach L., Tran K., Colquhoun S.A., Champliaud M.F., Towle C.A.;
Welssbach L., Tran f., Colquhoun S.A., Champliaud M.F., Towle C.A.;
"Detection of an interleukin-1 intracellular receptor antagonist mRNA
"Detection of an interleukin-1 intracellular receptor antagonist mRNA
"Detection of an interleukin-1 intracellular receptor antagonist mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eiglmeier K., Honore N., Woods S.A., Caudron B., Cole S.T.; "Use of an ordered cosmid library to deduce the genomic organization
                                                                                                                                                                                                                                                                                                                                         Mycobacterium leprae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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01-JUN-2000 (TrEMBLEEL. 14, Last annotation update)
INTERLEUKIN-1 INTRACELLULAR RECEPTOR ANTAGONIST VARIANT (FRAGMENT)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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75.0%; Pred. No. 1.3e+02;
Live 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Mycobacterium leprae.";
Mol. Microbiol. 7:197-206(1993).
EMBL, ALO08609; CAR145464.1; -
SEQUENCE 952 AA; 101282 MW; ADC68B6265C3D8FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skelton J., Churcher C.M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLYCINE DEHYDROGENASE (DECARBOXYLATING).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variant.";
Biochem. Biophys. Res. Commun. 244:91-95(1998)
EMBL. R6043143; AAC39672.1; -.
IEMBL. PR000975; -.
PFAM; PF00340; interleukin-1; 1.
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                                                                                                                                         952 AA.
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                                                                                                                                         PRT;
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PROSITE; PS00253; INTERLEUKIN_1; 1.
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                                                                                                                                         PRELIMINARY;
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Best Local Similarity
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143 AA;
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674 YVDGANLN 681
114 SGANLNL 120
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RESULT 12

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Query Match

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                                                   Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lighthing J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Rooper A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
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STRAIN-SC2133;
MEDLINE; 99392458.
MAILS R., KOLV V., Laasik E., Mae A.;
MISOLation of an extracellular protease gene of Erwinia carotovora subsp. carotovora a frain SC23193 by transposon mutagenesis and the rool of protease in phytopathogenicity.";
Microbiology 145:1959-1966(1999).
MISTRPRO; IPRO0130;
INTERPRO; IPRO01343;
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Clarke K., Wohldmann P., Harrison M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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COMPRISING 60% CARBOHYDRATE. SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 7 IG-LIKE DOMAINS. BELONGS TO THE CARCINOEMBRYONIC ANTIGEN
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WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD66E.HTM".
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(POTENTIAL)

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The complete genome sequence of Escherichia coli K-12.";

Science 277:145-1474(1997).

1 Science 277:145-1474(1997).

1 FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE. THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THE REMAINING METHILAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COFACTOR OF THE H PROTEIN.

1 CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN - S-AMINOMETHYL-

1 LIPOAMIDE COFACTOR OF THE H PROTEIN.

1 COFACTOR: PYRIDOXAL PHOSPHATE.

1 COFACTOR: PYRIDOXAL PHOSPHATE.

1 SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:

2 INDUCTION: BY GLYCINE.

2 INDUCTION: BY GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
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                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-KIZ. 7 MG1655;
MMEDIANS, 97426617.
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Mayley J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., May B., Shao Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamura-Ikeda K., Ohmura Y., Fujiwara K., Motokawa Y.; "Cloning and nucleotide sequence of the gcv operon encoding the Escherichia coli glycine-cleavage system."; Eur. J. Blochem. 216:539-548(1993).
                                                                                                                  ;
                                                                                                                                                                                                                                                                                                          01-OCT-1993 (Rel. 27, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence Carlot (Rel. 37, Last sequence Carlot (Rel. 37, Last sequence Carlot (Rel. 37, Last sequence DELYCLNE DERYBROGENSE (BCRABOXYLATING) (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN).
                                                                            Score 45; DB 1; Length 702; Pred. No. 0.14;
                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE, 94237484.
Stauffer L.T., Fogarty S.J., Stauffer G.V.;
"Characterization of the Escherichia coli gcv operon.";
     MISSING (IN REF. 4).
6299AE26CDDBDB5C CRC64;
                                                                                                                ;
0
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
STRAIN-K12 / W3110;
MEDLINE; 93387305.
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76795 MW;
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                                                                                                              9; Conservative
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                  702 AA;
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Best Local Similarity
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P33195;
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   CONFLICT
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MITOCHONDRION (POTENTIAL).
GLYCINE DEHVENCENASE [DECARBOXYLATING].
PYRIDOXAL PHOSPHATE.
MW; 4446D7C66E0DC4BD CRC64;

MITOCHONDRION

Length 1004;

Score 35; DB 1;

77.8%; 75.0%;

111852

738 7. 1004 AA;

1004

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Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
  D90240; BAA14287.1;
              PIR; A27483; A27483.
PIR; A39521; A39521
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Matches 6; Conserv
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SEQUENCE
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                                                       TRANSIT
  EMBL;
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GCSP_HUMAN
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  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kume A., Koyata H., Sakakibara T., Ishiguro Y., Kure S., Hiraga K.; "The glycine cleavage system. Molecular cloning of the chicken and man glycine decarboxylase cDNAs and some characteristics involved in the deduced protein structures."; Biol. Chem. 266:3323-3329(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: PYRIDOXAL PHOSPHATE.
-i- SUBGUIT: HOMODIMER. THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS: P, T, L, AND H.
-i- SUBGELLULAR LOCATION: MITOCHONDRIAL.
-i- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                             01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCINE DEHYDROGENASE [DECARROXYLAING], MITOCHONDRIAL PRECURSOR
(EC. 1.4.4.2.) (GLYCINE DECARROXYLASE) (GLYCINE CLEAVAGE SYSTEM P-
                                                                                                                                                                                ö
                                                                                                                                                    1; Length 956,
                                                                                                                                                                              1; Indels
                                                                                                                                                  Score 35; DB 1
Pred. No. 21;
1; Mismatches
                                                                                                                                                                                                                                                                                                        1004 AA
                      EMBL; AE000373; AAC75941.1; -.
PIR; S36834; S36834.
ECOGENE; EG11810; GCVP.
Oxidoreductase; Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIHYDROLIPOYLPROTEIN + CO(2)
                                                                                                         956 AA; 104245 MW;
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EMBL; X73958; CAA52146.1; -. EMBL; U28377; AAA69071.1; -.
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75.08;
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Best Local Similarity 75.v.
6; Conservative
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P15505;
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Kure S., Takayanagi M., Narisawa K., Tada K., Leisti J.;

Kure S., Takayanagi M., Narisawa K., Tada K., Leisti J.;

"Identification of a common mutation in Finnish patients with
nonketotic hyperglycinemia.";
J. Clin. Invest. 90:160-164(1992).
-!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIHYDROLIPOYLPROTEIN + CO(2).

COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: HOMODIMEN. THE GIVETINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PYRIDINS: P, T, L, AND H.
SUBCELLULAR LOCATION: MITOCHONDRIAL.
DISEASE: DEFECTS IN GCSP ARE THE CAUSE OF TYPE I NONKETOTIC HYPERGLYCLINEMIA (NKH1). NKH IS AN ANTOSOMAL RECESSIVE DISEASE CHARACTERIZED BY ACCUMULATION OF A LARGE AMOUNT OF GLYCINE IN BODY FLUID AND BY SEVERE NEUROLOGICAL SYMPTOMES.
SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLYCINE. THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COFACTOR OF THE H PROTEIN.

CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN - S-AMINOMETHYL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kume A., Koyata H., Sakakibara T., Ishiguro Y., Kure S., Hiraga K.; "The glycine cleavage system. Molecular cloning of the chicken and human glycine decarboxylase cDNAs and some characteristics involved in the deduced protein structures."; J. Biol. Chem. 266:3323-3329(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kure S., Narisawa K., Tada K.; "Structural and mutant mRNA "Structural and expression analyses of normal and mutant mRNA encoding glycine decarboxylase: three-base deletion in mRNA causes nonketotic hyperglycinemia.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostoml;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLYCINE DEHYDROGENASE (DECARBOXILATING), MITCCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXILASE) (GLYCINE CLEAVAGE SYSTEM P-
                         ö
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 174:1176-1182(1991)
                                                                                                                                                                                                           PRT; 1020 AA
Pred. No. 22;
1; Mismatches
                       6; Conservative
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT NKH1 ILE-564.
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 91131643.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 91144593.
                                                                                       11 |||:|
709 YLDGANMN 716
                                                              1 YLSGANLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                           GCSP_HUMAN
P23378;
                                                                                                                                                                                                                                                                                                                                                         PROTEIN).
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                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                 MITOCHONDRION (POTENTIAL).
GLYCINE DEHYDROGENASE [DECARBOXYLATING].
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
S -> I (IN NRH1).
/FIId=VAR_004979.
A -> R (IN REF. 2).
H -> Y (IN REF. 2).
V -> M (IN REF. 2).
W -> M (IN REF. 2).
W -> M (IN REF. 2).
W -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sinclair D.A., Dawes I.W.; "Genetics of the synthesis of serine from glycine and the utilization of glycine as sole nitrogen source by Saccharomyces cerevisiae."; Genetics 140:1213-1222(1995).
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                      Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
GLYCINE DEHYDROGENASE (DECARBOXYLATING), MITOCHONDRIAL PRECURSOR (EC. 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-
                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 1; Length 1020; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIHYDROLIPOYLEPROFEIN + CO(2).
COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SUBCELLULAR LOCATION: MITOCHONDRIAL (BY SIMILARITY).
SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1034 AA.
                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCV2 OR GSD2 OR YMR189W OR YM9646.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetaceae; Saccharomyces.
                                                                                                         EMBL; M63635; AAA36478.1; -.
EMBL; M64590; AAA36463.1; -.
EMBL; D90239; BAA14286.1; -.
                                                                                                                                                                                                                                                                                                                                                                       77.8%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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1020
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                                                                                                                                                                                                                                                                                     396
                                                                                                                                                                                                                                                                                                                916
                                                                                                                                               PIR; B39521; B39521.
PIR; JN0124; JN0124.
MIM; 238300; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288C / AB972;
                                                                                                                                                                                                                                                                                    396 39
608 60
976 97
1020 AA;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                       Disease mutation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96120340.
                                                                                                                                                                                                                                                                                                                                                                                                                                          11 |||:|
725 YLDGANMN 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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754
564
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P49095;
                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                  TRANSIT
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                                                                                                                                                                                                                            MITOCHONDRION (POTENTIAL).

LICINE DEHYDROCENASE (DECARBOXXIATING).

PYRIDOXAL PHOSPHATE (BY SIMILARITY).

WW: F4D52642B0BDA041 CRC64:
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 95350630.

Fleischmann R.D., Addams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Addams M.D., White O., Clayton R.A., Merrick J.M., McKenney R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Soott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                         Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koonin E.V., Rudd K.E.;
Submitted (SEP-1995) to the SWISS-PROT data bank.
-!- FUNCTION: DEAMINATES L-THREONINE, BUT ALSO L-SERINE TO A LESSER
EXTENT (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: L-THREONINE + H(2)0 = 2-OXOBUTANOATE + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHILE VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME (BY SIMILARITY).
-!- PATHWAY: FIRST STEP OF ISOLEUCINE BIOSYNTHESIS.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SIMILARITY: TO THREONINE DEHYDRATASE CATABOLIC AND SERINE DEHYDRATASE.
                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
THREONINE DEHYDRATASE BIOSYNTHETIC (EC 4.2.1.16) (THREONINE
                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 1034; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd."; Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 AA
                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                       1034 AA; 114451 MW;
                                                                                                                                                 EMBL; U20641; AAB18933.1; -. EMBL; Z47815; CAA87810.1; -. SGD; S0004801; GCV2.
                                                                                                                                                                                                                                                                                                                                             77.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                  1034
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                           744 YLDGANMN 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILVA OR HI0738.1
                                                                                                                                                                                                                                                                                                                                                                                                                    1 YLSGANLN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THD1_HAEIN
P46493;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEAMINASE)
                                                                                                                                                                                                                                                                BINDING
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                                                                                                                                                                                                                                                  CHAIN
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30-MAY-2000 (Rel. 39, Last annotation update)
PROBABLE GLYCINE DEHYDROGENASE [DECARBOXYLATING] (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEADANGE SYSTEM P-PROTEIN).
GCVP OR GCVB OR RV1832 OR MTCYIA11.11C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE GLYCINE. THE PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COFACTOR OF THE H PROTEIN (BY SIMILARITY).

--- CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-DIHYDROLIPOYLPROTEIN + CO(2).

--- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

--- SUBUNIT: THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS:
P, T, L, AND H (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 98295987.

Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgimeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quall M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares T., Sulston J.E., Taylor K., Whitehead S., Barrell B.G., Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                    56662 MW; DF42CA8B6FDE4CD7 CRC64;
                                                                                                                                                                                                                                        PFAM: PF00291; S.T.dehydratase; 1.
PFAM: PF00585; Thr.dehydrat_C; 2.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         941 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%; Score 34; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                          EMBL; U32757; AAC22398.1; -. TIGR; HI0738.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                  INTERPRO; IPR000634; -.
                                                                                                                                                                                                     INTERPRO; IPR001721; -. INTERPRO; IPR001926; -.
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
'-hns 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                    513 AA;
                                                                                                                                                                                                                                                                                                                              Allosteric enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 LSGANLN 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 LSGANLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCSP_MYCTU
Q50601;
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L., Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N., Harris P.K.W. Yem A.W., Maszak G.A., Chosay J.G., Sieu L.C., Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrikson R.L., Truesdell S.E., Shelly J.A., Essalu T.E., Taylor B.M., Tracey D.E.; "Purification, cloning, expression and biological characterization of an interleukin-1 receptor antagonist protein.";
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
Brandhuber B.J., Thompson R.C.;
"Interleukin 1 receptor antagonist is a member of the interleukin 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheer D., Solari R.; "Cloning and chromosome mapping of the human interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T., Hannum C.H., Thompson R.C.; "Primary structure and functional expression from complementary DNA of a human interleukin-1 receptor antagonist.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
1-NOV-1990 (Rel. 16, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
INTERLEUKIN-1 RECEPTOR ANTAGONIST PROTEIN PRECURSOR (IL-1RA) (ICIL-
                                                                                                                                  ALA-RICH.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
BFFDE54EDA56B914 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92338323.
Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
Sheer D., Solari R.;
                                                                                                                                                                                                                     Score 34; DB 1; Length 941;
Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene family: evolution of a cytokine control mechanism.";
Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                Oxidoreductase, Pyridoxal phosphate.
DOMAIN 437 446 ALA-RIC
                                                                                                                                                     692 P
99510 MW;
                                                                                                                                                                                                                  75.6%;
75.0%;
                                                                                 EMBL; Z78020; CAB01470.1;
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                                                                                                                                                                                                                                 Local Similarity 75.0
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                   TUBERCULIST; RV1832; -.
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                                                                                                                                                                   941 AA;
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663 YVDGANLN 670
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ILIRN OR ILIRA.
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SEQUENCE FROM
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P18510;
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MEDLINE; 97146044

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Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L., Arend W.P., Smith M.F. Jr.; "Intracellular IL-1 receptor antagonist promoter: cell type-specific and inducible regulatory regions."; J. Immunol. 158:748-755(1997).
                                                                                                                                                                                                                                                                                                                                                           Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F., Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P., Tcopha cloning of an intracellular form of the human interleukin 1 receptor antagonist associated with epithelium."; Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 95172072.
Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E., Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
"Refined crystal structure of the interleukin-1 receptor antagonist. Presence of a disulfide link and a cis-proline.";
Eur. J. Biochem. 227:838-847(1995).
                                                                                                     Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J., Helmdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.; "Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92297633. Stockman B.J., Scahill T.A., Roy M., Ulrich E.L., Strakalaitis N.A., Strokman B.J., Yem A.W., Deibel M.R. Jr.; The Brunner D.P. Yem A.W., Deibel M.R. Jr.; The Secondary structure and topology of interleukin-1 receptor antagonist protein determined by heteronuclear three-dimensional NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE; 97215904.

Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A., Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;

A new cytchine-receptor binding mode revealed by the crystal structure of the IL-1 receptor with an antagonist.";

Nature 386:194-200(1997).

-: FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94230368.
Vigers G.P.A., Caffes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
Brandhuber B.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH ILIR.
                                                                                                                                                                                                                             Bienkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
Heinrikson R.L., Chosay J.G., Tracey D.E.;
"Purification and characterization of interleukin 1 receptor level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stockman B.J., Scahill T.A., Strakalaitis N.A., Brunner D.P.,
Yem A.W., Deibel M.R. Jr.;
"Solution structure of human interleukin-1 receptor antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-ray structure of interleukin-1 receptor antagonist at 2.0-A
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (INTRACELLULAR FORM).
                                                                                                                                                                                                                                                                                         antagonist proteins from THP-1 cells.";
J. Biol. Chem. 265:14505-14511(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EBS Lett. 349:79-83(1994).
                                                                                                                                                                      Nature 343:336-340(1990).
                                                                                                   90136920.
                                                                                                                                                                                                                   MEDLINE; 90354444.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last aequence update)
GLYCINE DEHYDROGENASE (BECARBOXYLATING) B, MITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE B) (GLYCINE CLEAVAGE SYSTEM P-
SUBCELLULAR LOCATION: SECRETED OR INTRACELLULAR (THE VARIANT
                                    ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
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PROSITE; PS00253; INTERLEUKIN_1; 1.
Glycoprotein; Signal; Alternative splicing; 3D-structure.
                                                                                 OF IL-1RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                           PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
SIMILARITY: BELONGS TO THE IL-1 FAMILY.
DATABASE: NAME-R&D SYSTEMS' CYTOKINE SOURCE DOOK;
WWW-"HTTP://WWW.RNDSYSTEMS.COM/CYT_CAT/ILIRA.HTML".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTRACELLULAR ISOFORM).
D1690776A7394057 CRC64;
                                                                           TISSUE SPECIFICITY: THE INTRACELLULAR FORM
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9.6;
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PDB; 11LR; 07-FEB-95.
PDB; 11LT; 01-APR-95.
PDB; 11RA; 17-JUN-95.
AARHUS/GHEMT-2DPAGE; 7104; IEF.
AARHUS/GHEMT-2DPAGE; 7105; IEF.
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EMBL; M63099; AAB41943.1; --
EMBL; X52015; CAA36562.1; --
EMBL; X53296, CAA37386.1; --
EMBL; U65590; AAB92268.1; --
EMBL; U65590; AAB92268.1; --
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66.7%;
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109
21
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S08160; S08160;
S08159; S08159.
A40956; A40956.
A39386; A39386.
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21RT; 15-OCT-94
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P49362;
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CARBOHYD
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PIR;
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PIR;
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PDB;
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1034 AA;
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                     Nan Q., Bauwe H.;
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049852;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                     -i- SUBUNIT: HOMODIMER (BY SIMILARITY). THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS: P, T, L, AND H.
-i- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-i- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYCINE DEHYDROGENASE [DECARBOXYLATING]
                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Asteroideae; Helenieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Asteroideae; Helenieae;
                                                                                                                         "Structure and expression analysis of the gdcsPA and gdcsPB genes encoding two P-isoproteins of the glycine-cleavage system from
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PYRIDOXAL PHOSPHATE (BY SIMILARITY). W; 713D6490B48C2932 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
61VCINE DEHYDROGENARE [DECARROXYLATING], MITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-
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59;
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                                                                                                                Bauwe H., Chu C.-C., Kopriva S., Nan Q.;
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Pred. No. 5
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62.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                         63
1034
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1034 AA;
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Matches 5; Conserv
                     Flaveria pringlei.
                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                Flaveria pringlei.
                                                                                                      MEDLINE; 96096729.
                                                                                                                                                                                                                                                                                                                                                                                                               Multigene family.
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                                                                                             LEAF
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049850;
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SEQUENCE
                                                               laveria.
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The GDCSP gene encoding P-protein of the glycine cleavage system in the C3-C4 intermediate plant Flaveria anomala.";

(In) Plant Gene Register PGR98-004.

-!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE. THE PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THROUGH ITS PRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPOAMIDE COFACTOR OF THE H PROTEIN.

-!- CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN - S-AMINOMETHYL-DIHYDROLIPOYLPROTEIN + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: HOMODIMER (BY SIMILARITY). THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS: P, T, L, AND H.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-!- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COSSU R., Bauwe H.;

"Two genes of the GDCSP gene family from the C4 plant Flaveria
"Two genes of the GDCSP gene family from the C4 plant Flaveria
"Two genes of the GDCSPA encoding P-protein and GDCSPB, a pseudogene.";

(In) Plant Gene Register PCRSB-002.

-!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION OF GLYCINE
THROUGH ITS PYRIDOXAL PHOSPHATE COFACTOR: CO(2) IS RELEASED AND
THE REMAINING METHYLAMIE MOIETY IS THE THEN TRANSFERRED TO THE
LIPOAMIDE COPACTOR OF THE H PROTEIN.

-!- CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-
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GLYCINE DEHYDROCENASE [DECARBOXYLATING].
PYRIDOXAL, PHOSPHATE (BY SIMILARITY).
MW; C2F424C76EF104BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; 299762; CAB16911.1; -.
Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Flaveria trinervia.
Bukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae;
euasterids II; Asterales; Asteraceae; Asteroideae; Helenieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GIVCINE DEHYDROGERARE [DECARBOXIALTHOG], TITOCHONDRIAL PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXILASE) (GLYCINE CLEAVAGE SYSTEM P-
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Pred. No. 59;
2; Mismatches 1; Indels
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62.5%;
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Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide;
                send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN A).
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P49361:
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
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DIHYDROLIPOYLPROTEIN + CO(2).
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-! SUBUNIT: HOWDIMER (BY SIMILITY). THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROFIENS: P, T, L, AND H.
-!- SUBCELLULAR LOCATION: MITOCHONDRIAL.
-! SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Solanum tuberosum (Potato).
Bukaryota; Virlditplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                      MITOCHONDRION (POTENTIAL).

GLYCINE DEHYDROCENASE [DECARBOXXLATING].

PYRIDOXAL PHOSPHATE (BY SIMILARITY).

MW: 14A71076C05A5062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
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15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
GLYCINE DEHYDROGENASE [DECARBOXYLAZING], MITOCHONDRIAL PRECURSOR (EC. 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN).
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STRAIN=CV. DESIREE; TISSUE=LEAF;
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62.5%;
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Best Local Similarity 62...
5; Conservative
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049954;
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TRANSIT 1 64 MITOCHONDRION (POTENTIAL)
CHAIN 65 1035 GLYCINE DEHYDROGENASE (DECARBOXYLATING).
SEQUENCE 771 771 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 1035 AA; 112914 MW; 76C8418ED1856AFB CRC64;
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Magnoliophyta, eudicotyledons, core eudicots, Asteridae,
euasterids II; Asterales, Asteraceae, Asteroideae, Helenieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-FBB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCINE DEHYDROGENASE (DECARBOXILATING) A, MITOCHONDRIAL PRECURSOR
(EC. 1.4.4.2) (GLYCINE DECARBOXYLASE A) (GLYCINE CLEAVAGE SYSTEM P-
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                                                                                                                                                                                                                                                             1; Indels
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Bauwe H., Kopriva S.;
"The gdcsPA gene from Flaveria pringlei (Asteraceae).";
Plant Physiol. 107:655-655(1995).
                                                                                                                                                                                                         Score 33; DB 1;
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                                                                                                                                                                                                                                                        2; Mismatches
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62.5%;
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EMBL; 299770; CAB16918.1;
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(Rel. 33,
(Rel. 38,
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Best Local Similarity
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SEQUENCE FROM N.A.
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MEDLINE; 94218395
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MITOCHONDRION (POTENTIAL).

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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. ALASKA.
Shah K.S., Kim Y., Ollver D.J.;
Shah K.S., Kim Y., Ollver D.J.;
Submitted (AUG-1990) to the EmBL/GenBank/DDBJ databases.
-!- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION -|- FUNCTION: THE GLYCINE CLEAVAGE SYSTEM CATALYSES THE DEGRADATION -|- FUNCTION: THE P PROTEIN BINDS THE ALPHA-AMINO GROUP OF GLYCINE THROUGH TTS PYRIDOXAL PHOSPHATE COFACTOR; CO(2) IS RELEASED AND THE REMAINING METHYLAMINE MOIETY IS THE THEN TRANSFERRED TO THE LIPORAMIDE COFACTOR OF THE H PROTEIN.
-!- CATALYTIC ACTIVITY: GLYCINE + LIPOYLPROTEIN = S-AMINOMETHYL-
             MITOCHONDRION (POTENTIAL).
GLYCINE DEHYDROGENASE [DECARBOXYLATING]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oxidoreductase; Mitochondrion; Pyridoxal phosphate; Transit peptide.
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Pisum sativum (Garden pea).

Pisum sativum (Garden pea).

Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Fabales; Fabaceae; Papilionoideae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIHYDROLIPOYLPROTEIN + CO(2).
--- COFACTOR: PYRIDOXAL PHOSPHATE.
--- SUBUNTT: HOWODIMER. THE GLYCINE CLEAVAGE SYSTEM IS COMPOSED OF FOUR PROTEINS: P T, L, AND H.
--- SUBCELLULAR LOCATION: MITOCHONDRIAL.
--- SIMILARITY: TO OTHER GLYCINE CLEAVAGE SYSTEM P-PROTEIN.
                                      A.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
E -> D (IN REF. 2).
T -> I (IN REF. 2).
WW: ED248FA227F9E0F3 CRC64;
                                                                                                                                                                                                                                                                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
62CYCINE DEHYDROGENNASE [DECARBOXXLATING], MITOCHONDRIAL PRECURSOR (EC 1.4.4.2.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM PPOTEIN).
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                                                                                                                               DB 1; Length 1037;
59;
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Cloning and characterization of the P subunit of glycine
decarboxylase from pea (Pisum sativum).";
J. Biol. Chem. 267:5355-5360(1992).
                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                               PRT; 1057 AA.
                                                                                                                                           Pred. No. 59;
2; Mismatches
                                                                                                                                Score 33;
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495 495
1037 AA; 113031 N
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                                                                                                                               73.38;
62.58;
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Best Local Similarity 62.5
Matches 5; Conservative
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1037
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Multigene :
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P26969;
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Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Rudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Masuchi Y., Shizuya H., Kikuchi H.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.",
DNA Res. 5:55-76(1998).
                       [DECARBOXYLATING].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                 GLYCINE DEHYDRÒGENASE (DECARBOXYLATII) PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                   2F2EA58E9A2AC447 CRC64;
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P -> A (IN REF. 2).
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60;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                        Mismatches
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Search completed: December 16, 2000, 03:05:18 Job time: 8038 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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182106 seqs, 63460219 residues Searched:

Total number of hits satisfying chosen parameters:

182106

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:* pir2:* pir3:* pir4:* PIR_65:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | car | monooxyqenase-rela | qlycine cleavage s | | | | dehy | | glycine dehydrogen | u | hypothetical prote | | | hypothetical prote | acid | | | | interleukin-1 rece | interleukin-1 rece | hypothetical prote | probable monooxyge | hypothetical prote | glycine dehydrogen | aminomethyltransfe | aminomethyltransfe | probable glycine d | aminomethyltransfe | P protein - Flaver |
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| SUMMARIES | ID | 63 | C81704 | E75352 | D81821 | S36834 | T16734 | A39521 | JN0124 | B39521 | S50917 | 876576 | T22562 | B81919 | E81182 | A70904 | A70722 | T44754 | S08109 | A30368 | A39386 | T28747 | E71551 | S76257 | T46636 | S63536 | T07826 | T05309 | S63535 | S40216 |
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| | Score | 45 | 39 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 35 | 34 | 34 | 34 | 34 | 34 | 34 | 34 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 | 33 |
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| probable glycine d | stripe a/b protein | major ring-forming | hypothetical prote | | _ | _ | hypothetical prote | nucleoside triphos | glycine dehydrogen | glycine dehydrogen | probable qlycine d | probable glycine d | probable qlycine d | deh |
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| T02615 | S69205 | S41525 | 164001 | T22220 | E71215 | G64404 | S74425 | S48859 | H72403 | B69959 | B71216 | D75030 | D72518 | DWBYT |
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| 333 | 33 | 33 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 | 32 |
| 30 | 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

RESULT

| | A36319 |
|---|--|
| | carcinoembryonic antigen precursor - human |
| | N; Alternate names: CEA; meconium antigen 100 |
| | C; Species: Homo sapiens (man) |
| | C; Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 31-Jan-2000 |
| | C; Accession: A36319; A27773; A31037; A25845; S08106; S31737; A44476; I54224; I59 |
| _ | R;Schrewe, H.; Thompson, J.; Bona, M.; Hefta, L.J.F.; Maruya, A.; Hassauer, M.; |
| _ | Mol. Cell. Biol. 10, 2738-2748, 1990 |
| _ | A; Title: Cloning of the complete gene for carcinoembryonic antigen: analysis of |
| _ | A; Reference number: A36319; MUID:90258861 |
| | A; Accession: A36319 |
| | A; Molecule type: DNA |
| | A; Residues: 1-702 <sch></sch> |
| | A;Cross-references: GB:M17303; NID:q178676; PIDN:AAB59513.1; PID:q178677 |
| | A; Note: the authors show the codons TTA for residue 641-Phe and CAG for residue |
| | R; Beauchemin, N.; Benchimol, S.; Cournoyer, D.; Fuks, A.; Stanners, C.P. |
| | Mol. Cell. Biol. 7, 3221-3230, 1987 |
| | A.Title: Isolation and characterization of full-length functional characterization |

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A:Title: Isolation and characterization of full-length functional cDNA clones for hum A:Reference number: A27773; MUID:88038876
A:Accession: A27773; MUID:88038876
A:Accession: A27773
A:Abolecule type: mRNA
A:Residues: 1-702 <BEA>
A:Coss-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
B:Barnett, T.: Goebel, S.J.; Nothdurft, M.A.; Elting, J.J.
Genomics 3, 59-66, 1988
A:Title: Carcinoembryonic antigen family: characterization of cDNAs coding for NCA an A:Reference number: A31037; MUID:89122014

A Accession: A31037
A Molecule type: mRNA
A Molecule type: mRNA
A Molecule type: mRNA
A Molecule type: mRNA
A Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
A Cross-references: GB:M29540; NID:g180222; PIDN:AAA51967.1; PID:g180223
A Molecule: the authors translated the codon GTG for residue 130 as Leu
B Colkawa, S. Makazato, H.; Kosaki, G.
B iochem. Blophys. Res. Commun. 142, 511-518, 1987
A MITCHEL PILMARY Structure of human carcinoembryonic antigen (CEA) deduced from CDNA
A Molecular number: A25845; MUID:87128144

A; Molecule type: mRNA A; Residues: 5-702 COIK> A; Cross-references: GB:M15042; NID:g180198; PIDN:AAA51963.1; PID:g180199 R;Oikawa, S. Submitted to the EMBL Data Library, September 1989 A; Reference number: \$08106 A; Accession: \$08106 A; Molecule type: mRNA A; Residues: 5-319, 321-702 <012>

A;Cross-references: EMBL:X16455; NID:q29854; PIDN:CAA34474.1; PID:g825638
R;Barnett, T.
submitted to the EMBL Data Library, September 1991
A;Description: Genomic DNA sequence upstream of the translational start of the carcin A;Reference number: S31737

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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe Nucleic Acids Res. 28, 1397—1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A;Reference number: A81500; MJID:20150255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-506 <TET>
A;Cross-references: GB:AE002309; GB:AE002160; NID:g7190464; PIDN:AAF39281.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91ycine cleavage system P protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: E75352
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R., M.; Shen, M.; Vanathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
A;Tilte: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896
                                                                                                                                                           monooxygenase-related protein TC0425 [imported] - Chlamydia muridarum (strain Nigg)
                                                                                                                                                                                        C;Species: Chlamydia muridarum, Chlamydia trachomatis Mopn
C;Date: 31-Mar 2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
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A;Molecule type: DNA
A;Residues: 1-949 <WHI>
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A;Gene: TC0425
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A Status; per laminary not compared with conceptual translation
A Maletule type: DM
A William Construction of the genomic organization of human carcinoembryonic antigen
A Reference number: 154224, MUID:91139119
A Reference number: 154224, MUID:91139119
A Reference number: 154224, MUID:91139119
A Residues 1-77 KRES
A RESIDUE 1-77 KRES
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                                                                                                           A)Cross-references: EMBL:X62151
R;Khan, W.N.; Fraengsmyr, L.; Teglund, S.; Israelsson, A.; Bremer, K.; Hammarstroem, S. Genomics 14, 384-390, 1992
A;Title: Identification of three new genes and estimation of the size of the carcinoembra R;Reference number: A44476; MUID:93052339
A;Accession: A44476
A;Status: preliminary; not compared with conceptual translation
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                         A; Status: preliminary
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glycine dehydrogenase (EC 1.4.2) NMA1934 [imported] - Neisseria meningitidis (group C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 05-May-2000

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C;Accession: D81821 R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre

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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-979 <FRA-
A;Cross-references: EMBL:023510; NID:9746453; PID:9746454; PIDN:AAC46780.1; CESP:R12C
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) precursor - chicken NyAlternate names: glycine decarboxylase; P-protein C; Species: Gallus gallus (chicken) 17-bul-1992 #text_change 05-bec-1998 C; Accession: A39521; C39521; A27483 R; Rime, A.; Koyate, H.; Sakathara, T.; Ishiguro, Y.; Kure, S.; Hiraga, K. J. Biol. Chem. 266, 3323-3329, 1991 A; Title: The glycine cleavage system. Molecular cloning of the chicken and human glych Preference number: A39521; MUID:91131643
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A; Residues: 1-13 <KUD240
A; Residues: 1-13 <KUD240
A; Note: part of this sequence was confirmed by protein sequencing
B; Fujiwara, K.; Okamura-Ikeda, K.; Motokawa, Y.
Biochem Biophys. Res. Commun. 149, 621-627, 1987
A; Title: Amino acid sequence of the phosphopyridoxyl peptide from P-protein of the ch
A; Reference number: A27483; MUID:88106483
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A;Gene: CESP:R12C12.1
A;Introns: 52/3; 149/3; 325/2; 393/1; 470/3; 546/3; 619/3; 749/2; 827/1; 883/1
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A; Residues: 703-756 (FUJ>
C; Keywords: mito2-hondrion; oxidoreductase; phosphoprotein; pyridoxal phosphate
F;737/Binding site: pyridoxal phosphate (Lys) (covalent) *status experimental
                                                        hypothetical protein R12C12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16734
R;Favello, T.
submitted to the EMBL Data Library, July 1995
A;Beference number: 218568
A;Reference number: 218568
A;Recession: T16734
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Pred. No. 38;
1; Mismatches 1; Indels
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Pred. No. 37;
1; Mismatches
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75.0%;
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75.0%;
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Matches 6; Conservative
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Best Local Similarity 75.0
Matches 6; Conservative
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A;Residues: 1.1003 <KUM>
A;Cross-references: GB:D90266
A;Accession: C39521
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702 YLDGANMN 709
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C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Accession: 53684; 141232; G65074
C.Accession: 53684; 141232; G65074
C.Accession: 216, 539-548, 1993
A.Filtie: Cloning and nucleotide sequence of the gcv operon encoding the Escherichia coli
A.Reference number: 536832; MUID: 93387305
A.Residues: 1-97 < 0KAB.
A.Residues: 1-97 < 0KBB.
A.Residues: 1-97 < 0KBB.
A.Residues: 1-97 < 0KBB.
A.Residues: 1-98 < 0K
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A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-957 <RES>
A;Residues: 1-957 <RES>
A;Cross-references: GB:L20872; NID:g304890; PIDN:AAA23867.1; PID:g304892
A;Cross-references: GB:L20872; NID:g304890; PIDN:AAA23867.1; PID:g304892
B;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A; Rose, D.J.; Mau, B.; Shao, Y.
A;Fithe: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617
A;Accession: G65074
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUD:2022556
A;Accession: D81821
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-950 cPAR>
A;Residues: 1-950 cPAR>
A;Cross-references: GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB85154.1; PID:g738056
C;Genetics
A;Genetics
A;Genetics
C;Keywords: oxidoreductase
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C;Keywords: oxidoreductase; phosphoprotein; pyridoxal phosphate
F;708/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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Pred. No. 36;
1; Mismatches
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Pred. No. 36;
1; Mismatches
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75.08;
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75.0%;
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A; Residues: 1-957 <BLAT>
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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669 YMDGANLN 676
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glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) - human N;Alternate names: glycine decarboxylase; P-protein

RESULT JN0124

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RESULT

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A;Residues: 1-1034 <PEA>
A;Residues: BMBL:47815; NID:9642280; PIDN:CAA87810.1; PID:9642281; MIPS:YMR1
A;Cross-references: BMBL:47815; NID:9642280; PIDN:CAA87810.1; PID:9642281; MIPS:YMR1
R;Sinclair, D.A.; Dawes, I.W.
submitted to the EMBL Data Library, February 1995
A;Description: Cloning and expression of glycine decarboxylase from Saccharomyces cer
A;Reference number: $59809
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C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-oct-1999
C;Accession: S76576
B;KandsO, T., Satuo, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the gene for the P-subunit of glycine decar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-77, 'V', 79-121, 'VS', 124-247,' L', 249-381,' T', 383-517,' H', 519-1034 <SIW>
C; Genetics:
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22562
R;Burton, J.
                                                                                                                                                                                                                                                                                                                 A.Molecule type: DNA
A.Residues: 1-1034 <SIN>
A.Rotecule type: DNA
A.Residues: 1-1034 <SIN>
A.Cross-references: EMBL/120641; NID:g676869; PIDN:AAB18933.1; PID:g676871
B.Sinclair, D.A.; Hong, S.P.; Dawes, I.W.
Mol. Microbiol. 19, 611-623, 1996
A.Title: Specific induction by glycine of the gene for the P-subunit of gly A.Reference number: S70896; MuID:96228709
A.Recession: S70896
A.Status: nucleic acid sequence not shown
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C;Keywords: phosphoprotein; pyridoxal phosphate; transferase
F;773/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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A;Accession: S76576
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DM
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14;
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Pred. No. 39;
1; Mismatches
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75.0%;
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Best Local Similarity
Matches 6; Conserv
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A: Residues: 1-259 <KAN>
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C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C; Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C; Accession: B39521
R; Kume, A.; Koyata, H.; Sakakibara, T.; Ishiguro, Y.; Kure, S.; Hiraga, K.
J. Biol. Chem. 266, 3323-3329, 1991
A; Title: The glycine Cleavage system. Molecular cloning of the chicken and human glycine
A; Reference number: A39521; MUID: 91131643
A; Accession: B39521
A; Molecule type: mRNA
A; Residues: 1-1020 <a href="https://www.nash.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.nchanses.n
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Nov-1999
C;Accession: JN0124
R;Kure, S; Narisawa, K.; Tada, K.
Biochem. Biophys. Res. Commun. 174, 1176-1182, 1991
A;Title: Structural and expression analyses of normal and mutant mRNA encoding glycine d. A;Reference number: JN0124 MUD:91144593
A;Accession: JN0124
A;Nolceule type: mRNA
A;Residues: 1-1020 <kUR>
A;Cross-references: GB:M63635; NID:9190286; PIDN:AAA36478.1; PID:9190287
A;Cross-references: GB:M63635; NID:9190286; PIDN:AAA36478.1; PID:9190287
A;Cross-references: GB:128611; OMIM:238300
A;Genetics: GB:128611; OMIM:238300
A;Map position: 9p22-9p22
C;Keywords: mitochondrion; oxidoreductase; phosphoprotein; pyridoxal phosphate
F;761-768/Region: 9lycine-rich
F;754/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
s55097
aminomethyltransferase (EC 2.1.2.10) - yeast (Saccharomyces cerevisiae)
N;Alternate names: glycin cleavage system protein P; protein YM9646.01; protein YMR189c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S50917; S59810; S70896
R;Pearson, D; Bowman, S.
R;Pearson, D; Bowman, S.
R;Reference number: S50917
A;Reference number: S50917
A;Accession: S50917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                glycine dehydrogenase (decarboxylating) (EC 1.4.4.2) precursor - human N.Alternate names: glycine decarboxylase; P-protein C.Species: Homo sapiens (man) C.Species: Homo sapiens (man) C.Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
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Pred. No. 39;
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75.0%;
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Best Local Similarity
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Matches 6; Conserv
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725 YLDGANMN 732
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Search completed: December 16, 2000, 01:51:13 Job time: 7634 sec
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87.5%;
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Best Local Similarity 75.0
المحتادة وفي Conservative
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Matches 7; Conservative
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217 YTSGANIN 224
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21 LDGANLNL 28
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C. Species: Neisseria meningitidis
C. Species: Neisseria meningitidis
C. Species: Neisseria meningitidis
C. Accession: B81919
B. Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
B. Parkhill, J.; Adels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000
A.Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A. Reference number: A81775; MUID:20222556
A. Scatus: preliminary
A. Molecule type: DNA
A. Residues: 1-473 < PAR>
A. Cross-references: GB:AL162754; GB:AL157959; NID:97379424; PIDN:CAB84036.1; PID:9737947
A. Gone: NMA0753
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A.Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Vå A.Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A.Reference number: A81000; MUID:20175755
A.Accession: E81182
A.Accession: E81182
A.Accession: E91182
A.Refeluer: J.473 <TET>
A.Resioues: 1-473 <TET>
A.Resperimental source: serogroup B, strain MMD58
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                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molccule type: DNA
A;Residues: 1-272 <WILD.
A;Cross-references: EMBL:281088; PIDN:CAB03123.1; GSPDB:GN00023; CESP:F53F1.6
A;Experimental source: clone F53F1
A;Genetics:
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Pred. No. 15;
1; Mismatches 2; Indels
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Pred. No. 27;
0; Mismatches 1; Indels
submitted to the EMBL Data Library, October 1996
A;Reference number: 219583
A;Accession: T22562
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66.7%;
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87.58;
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
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probable acid--CoA ligase (EC 6.2.1.-) - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: A70904
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Accession: A70904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:Z97050; GB:AL123456; NID:g3256008; PIDN:CAB09749.1; PID:g22135 A;Experimental source: strain H37Rv C;Genetics:
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Pred. No. 32;
   Length 473;
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Carcinoembryonic a Carcinoembryonic a CEA protein. Homo

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Perfect score:

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T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Method of selecting T cell peptide epitope(s) – by measuring the stability of HLA class I-peptide complexes on intact B cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
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  96EP-0203670.
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Homo sapiens
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26-APR-1996;
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  W39723;
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W39723
 CEA synthetic pept
CEA derived HLA-A2
Immunogenic peptid
Carcinoembryonic a
Immunogenic peptid
Protein sequence o
Sequence of carcin
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BGP (1-314)/CEA (4
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                                                                          Search time 108.84 Seconds (without alignments)
2.827 Million cell updates/sec
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    268485 seqs, 34193795 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM protein - protein search, using sw model
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W77134
W770045
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Y46555
W86133
P93499
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Gapop 10.0 , Gapext 0.5
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Result . و 4 7 7 10 11 11 11 12

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immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukocyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral limmune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A2.1.
                                                                                                                   Peptides W39430-W39734 are used in a novel method for the selection of immunogenic T-cell peptide epitopes present in polypeptide antigens. The
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Pred. No. 2.1e+05;
Mismatches 0;
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Example 3; Page 85; 109pp; English.
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Best Local Similarity 100.
Matches 9; Conservative
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\overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\times}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\overset{\mathsf{A}}{\circ}\ov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epitope.

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Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (CEA). The peptides can bind to a human leukocyte antigen (HLA), HLA-A2.1 and are used to exemplify the method of leukocyte antigen (HLA), HLA-A2.1 and are used to exemplify the method of invention of producing antigen-specific cytotoxic T cells (CILS) in viro. The method comprises contacting immunogenic peptides from an olecules with antigen presenting cells (APCS) pretreated with no presence of at least 2 incubating the APCS with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antigen-specific CTLS. A method for specifically killing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLS from a patient, contacting the cytotoxic T cells with APCS pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLS which are contacted with a carrier to form a composition can then be administered to the patient. The activated CTLS can be used for treating cancers, immune disorders, viral infections, contactions, contactions, contactions.
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                            human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA fungal infection; tuberculosis; melanoma; carcinoembryonic antigen
                                                                                                                                                                                                                                                                                                                                                       Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
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                  Length 9;
                                                                                                                                                                                                                                                                                                                       CEA derived HLA-A2.1 binding peptide 2 (residues 605-613).
                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsai V;
                                                      ;
                Score 45; DB 19;
Pred. No. 2.1e+05;
100.0%; Scor.
100.0%; Pred. No. 4.
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                                                                                                                                                                                                              W70045 standard; peptide; 9 AA.
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                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIM-) EPIMMUNE INC.
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               Query Match
Best Local Similarity
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                                                                                    1 YLSGANLNL
                                                                                                           Homo sapiens.
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tuberculosis.
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                                                  Matches
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Length 9;

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y45390 to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cespoose against the antigen from which the peptide is derived. Crownally induced by an antigen from which the peptide fragment bound or normally induced by an antigen from of a peptide fragment bound are particularly important in the form of a peptide fragment bound are particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) crossate cancer, hepatitis B and C, AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in they can be administered as vaccines to elicit an immune response in conversion and infection or the control or cont
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                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic peptide having a human leukocyte antigen binding motif #2266
                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLs ax vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful therapeutically and for immunisation as above.
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                                                         Length 9;
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                                                     Ouery Match
100.0%; Score 45; DB 19;
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 9; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 118; 150pp; English.
                                                                                                                                                                                                                                                                   Y47655 standard; Peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine; immunisation.
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                                                                                                                                                   1 ylsganlnl 9
                                                                                                                                 1 YLSGANLNL 9
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9 AA;
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   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (ID) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize bork (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or
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                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinoembryonic antigen; CEA; human; agonist; antagonist; immune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                             Indels
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100.0%; Score 45; DB 20; 100.0%; Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen peptide agonist CAP-1.
                                                          Mismatches
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                                                                Conservative
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Synthetic.
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Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunoglobulin; therapeutic; streptokinase; vaccine; 708.
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                                                                                                                                                       Protein sequence of vaccine 2 708 Vl.
    W86133
ID W86133 standard; Protein; 107 AA.
                                                                                                              03-MAR-1999 (first entry)
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                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                  WO9852976-A1
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31-JUL-1997;
28-NOV-1997;
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Tesponse against the artigen from which the peptide is derived.

Cytoctoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound in a HLA molecule, rather than the intext foreign antigen itself, and are particularly important in tumour rejection and in flighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) infections. The peptides are therefore useful therapeutically one cancer, heartis B and C, alloit an immune response in Individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytocoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
                                                                                                                                                              Immunogenic peptide having a human leukocyte antigen binding motif #1166.
                                                                                                                                                                                                     Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA; immune response; T cell activation; major histocompatibility complex; cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer; prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma; vaccine; immunisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 76; 150pp; English.
                                       Y46555 standard; Peptide; 10 AA.
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                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                  Y46555;
RESULT
                     746555
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98GB-0007751. 97GB-0010480. 97GB-0016197.

97GB-0025270 97US-0067235

(BIOV-) BIOVATION LTD

98WO-GB01473

21-MAY-1998;

L4-APR-1998;

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The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of products can be used for diagnosis and therapy. The present sequence represents the protein sequence of vaccine 2 708 VI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of carcinoembryonic antigen domain III.
Example 4; Fig 19; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YLSGANLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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100.0%; Score 45; DB 20; Length 10; 100.0%; Pred. No. 0.0043; live 0; Mismatches 0; Indels

Query Match 100.
Best Local Similarity 100.
Matches 9; Conservative

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RESULT

1 YLSGANLNL 9

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The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer; amplify; polymerse chain reaction; PCR; human; billary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen; CEA; chimaeric protein; PRIA3 epitope; anti-PRIA3 antibody; colorectal carcinoma; monoclonal antibody.
                                                                                                                                                                           New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 45; DB 16; Length 468; 100.0%; Pred. No. 0.31; ive 0; Mismatches 0; Indels (
                                                                                      Stewart LMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BGP (1-314)/CEA (490-C-terminal) chimaeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "CEA (490-C-terminal)"
                                                                                    Snary D,
                                                 (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
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                                                                                    Durbin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-GB01816.
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                93GB-0017423
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                                                                                                                                                                                                                                               Claim 16; ; 67pp; English.
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Matches 9; Conservative
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                                                                                    Bodmer WF,
                                                                                                                                      WPI; 1995-106813/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       468 AA;
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396 ylsganlnl 404
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                                                                                      Bates PA,
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                                                                                                        found S;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Carcinoembryonic antigen fragments - used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEA fragments can be used in assays to determine the presence and amt. CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128 kD antigen.
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billary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimaeric protein; PRIA3 epitope; anti-PRIA3 antibody;
colorectal carcinoma; monoclonal antibody.
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                  domain A; domain B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "CEA (490-643)"
                Carcinoembryonic antigen; domain III;
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/note= "BGP (1-314)"
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                                                 Location/Qualifiers
                                                     1..89
/note="domain A"
90..178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; page 4; 15pp; English.
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                                                                                                                       /note="domain B"
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N-PSDB; N92449.
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Best Local Similarity
Matches 9; Conserv
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94WO-GB01816.
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468..511
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                                          Bodmer WF,
                                                                                 WPI; 1995-106813/14
                                                                                                                          diagnosis and trea and purifications.
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                                                         Young
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                                                                                                                                                                                      The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies in the constraint of membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they expecifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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bilitary glycoprotein; BGP; membrane-bound; carcinoembryonic antigen;
CEA; chimaeric protein; PRLA3 epitope; anti-PRLA3 antibody;
colorectal carcinoma; monoclonal antibody.
                                                                                                       New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
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                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 45; DB 16; Length 493; 100.0%; Pred. No. 0.33;
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                                      Stewart LMD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                      Durbin H, Snary D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
          (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                                                                                                Claim 15; ; 67pp; English.
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/note= "B(
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hes 9; Conservative
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315.46
                                      Bodmer WF,
                                                                              WPI; 1995-106813/14.
                                                                                                                                      and purifications.
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                                                                                                                                                                                                                                                                                                                                                                                                      493 AA;
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                                    PA,
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Protein
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portions of human biliary giveoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies in no longer membrane bound did not react with anti-PRIA3 antibodies in not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They used in the study, isolation and purification of molecules to which they pecifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in R77435-38 are chimaeric proteins comprising
                                                                                                                                                                                                                                                                                                     New molecules which bind carcinoembryonic antigen – used for the diagnosis and treatment of colorectal carcinoma and for isolation
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                                                                                              Stewart LMD;
                                                                                          Snary D,
(IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                                                          Durbin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R77438 standard; Protein; 511 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; ; 67pp; English.
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R60619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine R60619 can be used in a reagent composition for detecting neoplastic diseases in biological samples, or in an immunoassay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood.
                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carcinoembryonic antigen; immunogen; breast cancer; lung cancer; colon cancer; therapy; immunotherapy; vaccine; baculovirus; vector; Spodoptera frugiperda; insect; pA9080 ACNPV-CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- ....
18.663
/label- Mat_protein
/note= "amino acids 1-3 of the mature protein
are derived from the baculovirus vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A recombinant, soluble, immunogenic carcinoembryonic antigen (rCEA) (R98519) is encoded by vector pA9080 AcNPV-CEA (see also T36495) in which a modified human CEA gene is joined to a baculovirus signal sequence under control of a polyhedrin promoter. The baculovirus signal peptide directs translation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic carcinoembryonic antigen produced using insect cell
baculovirus expression system – useful in cancer therapy
                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                     Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chimeric Autographa californica nuclear polyhedrosis virus;
Chimeric Homo sapiens.
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/note= "AcNPV 61k protein signal peptide"
                                                                                                                                                                                                                                                     Score 4.,
Pred. No. 0.44;
                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                   100.0%; Score 45; 100.0%; Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic carcinoembryonic antigen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                R98519 standard; Protein; 663 AA
Claim 2; Page 15; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Volvovitz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94US-0246981.
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-020581/02.
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                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                             The sequences given in R77435-38 are chimaeric proteins comprising portions of human biliary glycoprotein (BGP) and the human membrane-bound carcinoembryonic antigen (CEA). These chimaeric proteins were used to identify the PRIA3 epitope. The PRIA3 epitope was found to be an epitope of CEA within the B3-GPI region. Chimaeras in which the CEA is no longer membrane bound did not react with anti-PRIA3 antibodies indicating that the PRIA3 epitope is not present in non-membrane bound hybrid proteins. Antibodies which recognise the PRIA3 epitope are used in the detection of well and poorly differentiated colorectal carcinomas. The isolation of the specific PRIA3 epitope allows the development of monoclonal antibodies specific for colorectal carcinoma. They can be used in the study, isolation and purification of molecules to which they specifically bind and the imaging and treatment of cells exhibiting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                 New molecules which bind carcinoembryonic antigen - used for the diagnosis and treatment of colorectal carcinoma and for isolation
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                                                       Stewart LMD;
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                                                       Durbin H, Snary D,
               (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.
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                                                     Bodmer WF,
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396 ylsganini 404
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                                                                         Young S;
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R60619

ò q Search completed: December 16, 2000, 00:51:13 Job time: 18773 sec

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rCEA into the insect cell glycosylation pathway. rCEA can be produced at high levels in Sf900+ insect cells grown in serum-free media, and isolated to a purity of over 95%. It is used as an immunogen in humans to protect against cancer, partic. breast, lung or colon cancer.
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                                                                                                         Query Match 100.0%; Score 45; DB 17; Length 663; Best Local Similarity 100.0%; Pred. No. 0.46; Matches 9; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The human carcinoembryonic antigen (CEA) protein sequence is presented. Antibodies raised against human CEA are used to detect tumor tissue (colon carcinoma). See also N81611.
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                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen; antibody; tumor diagnosis.
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/label=signal peptide
31..668
/label=mature human CEA
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                                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen.
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N-PSDB; N81611.
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                                                                           Sequence
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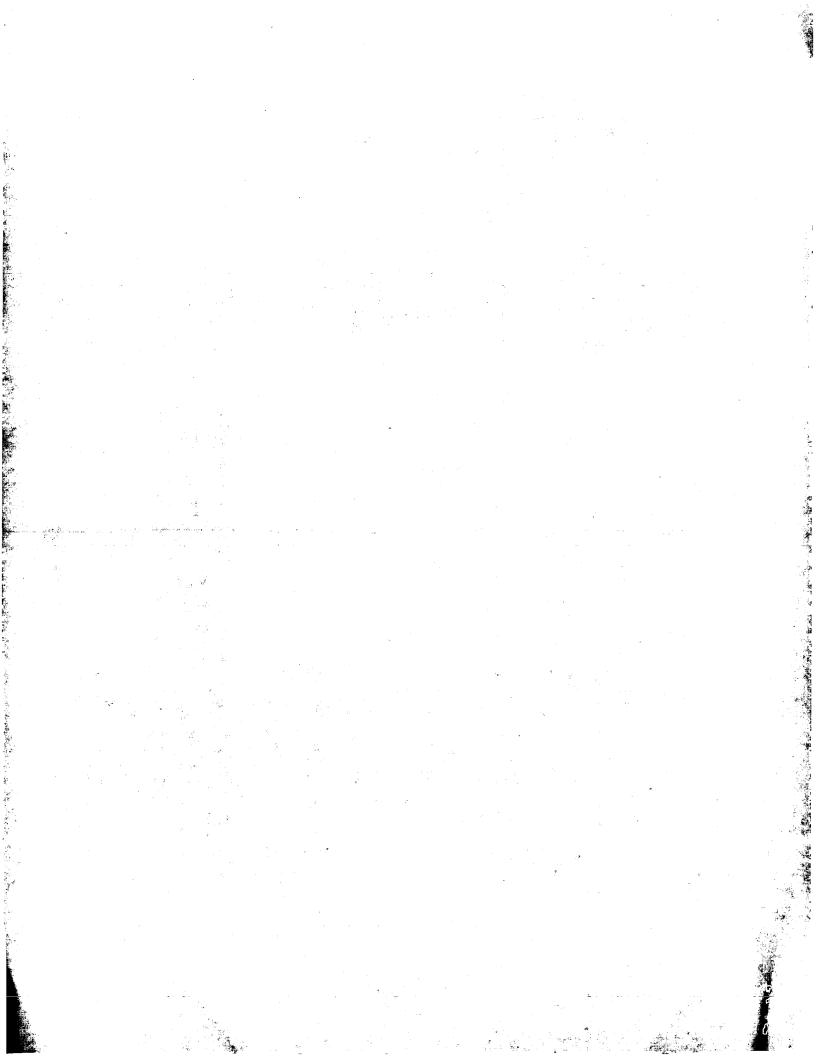
Gaps

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Query Match
Best Local Similarity 100.0%; Score 45; DB 9; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 9; Conservative 0; Mismatches 0; Indels

Qy Db -

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Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
Enterococcus.
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Suzuki A., Mori M., Sagakami Y., Isogai A., Fujino M., Kitada Craig R.A., Clewell D.B.;
Tisolation and structure of bacterial sex pheromone, CPDI.";
Science 226:849-850(1984).
-i- FUNCIION: CPDI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF
BACTERIOCIN PLASMID PPDI.
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01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
SEX.PHEROMONE CPD1.
                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                    FAR4_HOMAM
GLUR_HUMAN
HTE_TENMO
LCK3_LEUMA
LCK5_LEUMA
LCK5_LEUMA
VBCH_PANBO
UF06_MOUSE
VGLG_HSV2B
AL10_CARMA
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DSIP_RABIT
FAR5_ASCSU
FAR6_CALVO
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MOSH_CLYJA
OXYA_SCYCA
SAMP_MUSCA
TKL1_LOCMI
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UPA6_HUMAN
FAR4_HIRME
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FARP_ARTTR
CHOX_ALCSP
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AL15_CARMA
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75.0%;
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Best Local Similarity
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CPD1_ENTFA P13269;
SEQUENCE.
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Copyright (c) 1993 - 2000 Compugen Ltd
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FAR3_HIRME
PRCT_PERAM
TMOF_SARBU
FAR2_ASCSU
GFRP_MOUSE
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UNO6_PINPS
AKH_MELML
AL12_CARMA
AL17_CARMA
ALL1_CYDPO
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THYF_PIG
IGAO_DACDE
OXYA_SQUAC
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TPIS_CANFA
UXA4_CHLTR
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LCK8_LEUMA
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Gapop 10.0 , Gapext 0.5
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
Matches 2; Conserv
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21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
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9 AA;
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01-NOV-1995
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P42994;
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2 YIS 4
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2 YIS 4
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SEQUENCE
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P01255;
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ID OXXYT_RAJCL

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DT O1-NOV-
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OC BURSTY

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THYF_PIG
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"Characterization of neurohypophyseal hormones from a fresh water bony fish, the carpio (Cyprinus carpio). Comparison with hormones from sea water bony fishs.";

Comp. Biochem. Physiol. 14:245-254(1965).

-I. FUNCTION: ANTIDIURETIC HORMONE.

-I. SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.

INTERPRO: IPRO00981:

PRAM: PF00220; hormone4; 1.

PROSTE: PS00220; hormone4; 1.
                                                                                                                                                                                                                                      P41863;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CALLIFMRRAMIDE 8.
CALLIFOR vomitoria (Blue blowfly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptcrygota: Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Oestroidea; Calliphoridae; Calliphora.
     Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Cyprininae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-THORACIC GANGLION;
MEDLINE: 92196111.

Duve H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
Rehfeld J.F., Thorpe A.;
"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated calliFWRFamides) from the blowfly
Calliphora vomitoria.",
Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
-: SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
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     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES 8 AMIDATION.
SEQUENCE 8 AA; 957 MW; 72D40699CAA44DD8 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
                                                                                                                                                                                                                       8 AA.
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1; Mismatches
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Conservative
                                                                                                                                                                                                                         STANDARD;
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MOD_RES 8 8
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Best Local Similarity
Matches 3; Conserv
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TISSUE-PITUITARY;
                                                1 YLSG 4
3;
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ID FAR8_CALVO
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P42993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Acher R., Chauvet J., Chauvet M.-T., Crepy D., "Phylogeny of neurophyophyseal peptides: isolation of a new hormone, glumitocin (Ser 4-Gln 8-ocytocin) present in a cartilaginous fish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raja clavata (Thornback ray).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchli; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
Rajiformes; Rajides; Rajas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pleau J.-M., Dardenne M., Blouquit Y., Bach J.-F.;
"Structural study of circulating thymic factor: a peptide isolated
"Structural study of circulating thymic factor: a peptide isolated
J. Biol. Chem. 25:18045-8047(1977).
-!- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THYMIC FACTOR.
Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the ray (Raia clavata).";
Blochim. Biophys. Acta 107:393-396(1965).
-i - FUNCTION: ANTIDIURETIC HORMONE.
-i - SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
INTERPRO; IPRO00981; -.
                                                                                Score 13; DB 1; Length y;
Pred. No. 8.8e+04;
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AMIDATION.
17FF476EB455B04B CRC64;
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984 MW; 17E9C76EB455B04B CRC64;
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Pred. No. 8.8e+04; \
1; Mismatches 0;
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(Rel. 32, Last sequence update)
(Rel. 32, Last annotation update)
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                                                                                                                                                           1; Mismatches
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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Gaps

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FRR3_HIRME STANDARD; PRT; 4 AA.
P42562;
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
PMRFAMIDE-LIKE NEUROPEPTIDE YLRF-AMIDE.
HINDO medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annolida; Clitellata; Hirudinida; Hirudinea;
Arynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
BNDO-POLYGALACTURONASE (PG) (EC 3.2.1.15) (FRAGMENT).
Diaprepes abbreviatus (Sugarcane rootstalk borer weevil).
BUNATYOGE, METAZOA ARTHOROPASI TRACHERALS INSEAROPASI TRECERALS
PERTYGUE, MEDELEZ, ENGOPLEYGOTES, COLOGOPLERA; DIAPPABGS.
CUCUJIFOrmia; Curculionidae; Entiminae; Entimini: Diaprepes.
C. R. Acad. Sci., D, Sci. Nat. 274:313-316(1972).

INTERPO. IPRO00981.

PPAM: PF00220: hormone; hormone; hormone; hormone; hormone; midation.

DISULFID

MOD. RES

9 AMIDATION.

SEQUENCE 9 AA; 996 MW; 17:8376EB444404B CRC64;
                                                                                                                                                                                     Score 12; DB 1; Length 9;
Pred. No. 8.8e+04;
2; Mismatches 3; Indels
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                                                                                                                                                                                         26.7%;
28.6%;
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Best Local Similarity 28.0.
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Best Local Similarity
Local 2; Conservē
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2 YINNCPL 8
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4 YVIG 7
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P81179;
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"Identification of a peptide inhibitor of galactose oxidase from
"Identification of a peptide inhibitor of galactose oxidase from
Dactylium dendroides.";
Fed. Proc. 31:447-447(1972).
--- FUNCTION: BINDS ONE COPPER ION PER MOLECULE BUT DOES NOT BIND THE
GARACTOSE CXIDASE APOENZYME. IT MAY INACTIVATE THE ENZYME BY
BINDING TO ITS PROSTHETIC COPPER GROUP.
PIR; A01341; XEYDGD.
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 73031727.
Acher R., Chauvet J., Chauvet M.-T.;
"Phylogeny of the neurohypophysial hormones. Two new active peptides isolated from a cartilaginous fish, Squalus acanthias.";
Eur. J. Blochem. 29:12-19(1972).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE.
MEDLINE: 72128038.
MEDLINE: 7. Chauvet M.-T., Fontaine M.;
Tidentlication of 2 new neurohypophyseal hormones, valitocin (Val8-oxytocin) and aspartocin (Asn4-oxytocin) in a selachian fish, the spiny dog-fish (Squalus acanthias).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordatá; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchil; Squalea; Squaloidei; Squalidae; Squalus.
                                                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1989 (Rel. 30, Last annotation update)
GALACTOSE OXIDASE INHIBITOR.
Dactylium dendroides (Cladobotryum dendroides).
Eukaryota; Fungi; Ascomycota; Hypocreales; Hypomyces.
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                                   PYRROLIDONE CARBOXYLIC ACID. D500B87866C5B33D CRC64;
                                                                                                 28.9%; Score 13; DB 1; Length 9; 66.7%; Pred. No. 8.8e+04; Attive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 12; DB 1; Length 7; 50.0%; Pred. No. 8.8e+04; tive 1; Mismatches 1; Indels
ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED. PIR; A01523; YFPG.

MOD_RES
SEQUENCE 9 AA; 876 MW; D500B87866C5B33D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copper, Metalloenzyme inhibitor.
SEQUENCE 7 AA; 706 MW; 75BB01A456DB7DB0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
NOVERPARTOCIN (ASPARGTOCIN)
Squalus acanthias (Spiny dogfish).
                                                                                                                                                                                                                                                                                          7 AA.
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                                                                                                                                      Conservative
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                                                                                 Ouery Match
Best Local Similarity
Local 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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7 GSN 9
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P06294:
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P42999;
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Gaps

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649 MW; 71B7673B44600000 CRC64;

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5 AA;
   Neuropeptide.
SEQUENCE 5
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                                                                                                                                                                   TMOF_SARBU P41495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 NLN 8
                                                                                        1 YL 2
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                                                Query Match
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FAR2_ASCSU
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MEDLINE; 76074708.
Starratt A.N., Brown B.E.;
"Structure of the pentapeptide proctolin, a proposed neurotransmitter
                                                                                                                                             Gaps
        Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
-!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pericardial organs of the structure crab, Carcinus maenas.";
Peptides 7:67-72(1986).

-!- FUNCTION: STIMULATES CARDIAC OUTDUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
-!- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
PIR: A01644; HOROHA.
PIR: A01641; A60411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Shea M., Addms M.E.; "Pentapeptide (proctolin) associated with an identified neuron."; Science 213:567-569(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Identification of proctolin in the central nervous system of the horseshoe crab, Limulus polyphemus."; Peptides 11:205-211(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES-C.MAENAS;
MEDLINE; 86232789.
Stangier J., Dircksen H., Keller R.;
"Identification and immunocytochemical localization of proctolin
                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                            Periplaneta americana (American cockroach),
Limulus polyphemus (Atlantic horseshoe crab), and
Carcinus maenas (Common shore crab) (Green crab).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blattoidea; Blattidae; Periplaneta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES=L.POLYPHEMUS;
MEDLINE: 90287800.
Groome J.R., Tillinghast E.K., Townley M.A., Vetrovs A.,
Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
Shabanowitz J.;
                                                                                                                                           0; Indels
                                                                                                                      DB 1; Length 4;
8.8e+04;
                                                                            AMIDATION.
69D4073B30000000 CRC64;
                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
                                                                                                                                                                                                                                            5 AA.
                                                                                                                     24.4%; Score 11; DB 100.0%; Pred. No. 8.8 ive 0; Mismatches
                                                                                                                                                                                                                                             PRT;
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                                                                                     4 AA; 598 MW;
                                                              Neuropeptide; Amidation.
MOD_RES 4 4
SEQUENCE 4 AA; 598 MW;
                                                                                                                                          2; Conservative
                                                                                                                                                                                                                                            STANDARD;
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Matches 2; Conserv
92195954.
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P01373;
                                                      FAMILY
                                                                                                                                                                                                                                                                                                  PROCTOLIN.
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PRCT_PERAM
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MEDLINE; 93324431.
Cowden C., Stretton A.O.W.;
"AF2, an Ascaris neuropeptide: isolation, sequence, and bioactivity.";
Peptides 14:423-430(1993).
                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
TRYPSIN MODULATING COSTATIC FACTOR (TMOF).
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Endopteryota; Diptera; Brachyceryota;
Oestroidea; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de LOOF A.;

"Sequencing and characterization of trypsin modulating oostatic
"Sequencing and characterization of trypsin modulating oostatic
factor (TMOF) from the ovaries of the grey fleshfly, Neobellieria
(Sarcophaga) bullata.".

Regul. Pept. 50:61-72(1994).

-1- FUNCTION: HAS AN OOSTATIC ACTIVITY. INHIBITS TRYPSIN BIOSYNTHESIS
IN THE MIDGUT WHICH INDIRECTLY REDUCES THE VITELLOGENIN
CONCENTRATION IN THE HEMOLYMPH RESULTING IN INHIBITION OF OOCYTE
DEVELOPMENT.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DEVELOPMENTAL STAGE: SYNTHESIZED AND RELEASED FROM FOLLICULAR
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                                                          Indels
     Length 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 6;
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24.4%; Score 11; DB 1; Le
100.0%; Pred. No. 8.8e+04;
ive 0; Mismatches 0;
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Pred. No. 8.8e+04;
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01-JUL-1993 (Rel. 26, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                               6 AA.
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                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FMRFAMIDE-LIKE NEUROPEPTIDE AF2.
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66.7%;
                                                          Conservative
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                                                                                                                                                                                                                                                                                                               STANDARD;
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                          Best_Local Similarity
Matches 2; Conserv
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Gaps

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MEDLINE; 85051889.

MOTI M., Sagakami Y., Narita M., Isogai A., Fujino M., Kitada C.,
Craig R.A., Clewell D.B., Suzuki A.;

Isolation and structure of the bacterial sex pheromone, CADI, that
induces plasmid transfer in Streptococcus faecalis.";

FEBS Lett. 178:97-100(1984).

-i- FUNCTION: CADI IS INVOLVED IN THE CONJUGATIVE TRANSFER OF THE
HEMOLYSIN PLASMID PADI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEUCOKININ VIII (L-VIII).
LEUCORINAN VIII (L-VIII).
Leucophaea maderae (Madeira cockroach).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Plerygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blaberidae; Leucophaea.
                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                            Score 11; DB 1; Length 8; Pred. No. 8.8e+04; 1; Mismatches 0; Indels
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                                                                                                                                                                                                   8 AA; 819 MW; 047DD732C735B9C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 8.8e+04;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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01-NOV-1991 (Rel. 20, Last sequence update)
01-MRT-1992 (Rel. 21, Last annotation update)
PROBABLE MSRA LEADER PEPTIDE.
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                                                                                                                                                                                                                                              24.48;
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Neuropeptide; Amidation.
MOD_RES 8
SEQUENCE 8 AA; 902 MW;
                                                                                                                                                                                                                                                                          Conservative
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nes 2; Conserv
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                             Enterococcus.
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P23211;
                                                                                                                                                                                                                                                                                                                     |:|
6 LAG 8
                                                                                                                                                                                                                                                                                                                                                                                                      LCK8_LEUMA
P19990;
                                                                                                                                                                                     Pheromone.
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LPMS_STAEP
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LCK8_LEUMA
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                                                     Gaps
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-I- FUNCTION: MEDIATES TETRAHYDROBIOPTERIN INHIBITION OF GTP
CYCLOHYDROLASE I. THIS INHIBITION IS REVERSED BY L-PHENYLALANINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GTP CYCLOHYDROLASE I FEEDBACK REGULATORY PROTEIN (P35) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Sanchez J.-C., Rouge V., Frutiger S., Hughes G., Yan J.X.,
Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                               69D4073B5B11E350 CRC64;
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                                                                                                                                                                                                                                                         DB 1; Le
8.8e+04;
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.larity 100.0%; Pred. No. 8.8e+04;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
SEX PHEROMONE CADI.
                                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
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                                                                                                                                                                                                                                                         24.4%; Score 11; 100.0%; Pred. No.
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SWISS-2DPAGE; P99025; MOUSE.
                                                                                                                                                                                                   AMIDATION
                                                                                                                                                                                                                7 AA; 992 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             806 MW;
                                                                                                                                                                                    Neuropeptide; Amidation.
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                             SPECIES-P.REDIVIVUS;
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Best Local Similarity
2; Conservé
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Best Local Similarity
Matches 2; Conserv
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P99025;
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                                                                                                                                                                        FAMILY
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4 YL 5
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OXYTOCIN (OCYTOCIN).

Oryctolagus cuniculus (Rabbit), Hippopotamus amphibius (Hippopotamus),
Balaenoptera physalus (Finback whale) (Common rorqual),
Tachyglossus aculeatus aculeatus (Australian echidna), and
Hydrolagus colliei (Spotted ratfish) (Pacific ratfish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       "Purification and structure of mosact and its derivatives from the egg jelly of the sea urchin Clypeaster japonicus.";
Zool. Sci. 4:649-655(1987).
- FUNCTION: STIMULATES SPERM RESPIRATION AND MOTILITY.
PIR: JN0027; JN0027, JN0027.
SEQUENCE 9 AA; 924 MW; 93245729GDC5BAB5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 72215060.
Chauvet J., Chauvet M.-T., Acher R.;
"Evolution of neurohypophyseal hormones: isolation of active principles from rabbits and rats.";
Biochimie 53:1099-1104(1971).
                                                                                                                                                                                                                                                   Clypeaster japonicus (Sand dollar).
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Gnathostomata; Clypeasteroida;
                                                                                                                                                                                                                                                                                                                                                                    TISSUE=EGG JELLY;
Suzuki N., Kurita M., Yoshino K.I., Kajiura H., Nomura K.,
Yamaguchi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 11; DB 1; Length 9;
Pred. No. 8.8e+04;
1; Mismatches 1; Indels
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Acher R., Chauvet J., Chauvet M.-T.;
"Isolation of finback whale oxytocin and vasopressin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 71232719.
Ferguson D.R., Pickering B.T.;
"Arginine and lysine vasopressins in the hippopotamus
                                                                                                                                                                  01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-FEB-1991 (Rel. 17, Last annotation update)
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                                                                                                                                  9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24.48;
50.08;
                                                                                                                                                                                                                                                                                                                 Clypeasteridae; Clypeaster.
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                                                                                                                                STANDARD;
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6 FLIG 9
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4 DLN 6
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P19853;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE.
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OXYT_RABIT
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Matches
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                                                                                                                                                                               "Inducible erythromycin resistance in staphylococci is encoded by a member of the ATP-binding transport super-gene family."; Mol. Microbiol. 4:1207-1214(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- TISSUE SPECIFICITY: NEURONS LOCATED IN TWO VENTRAL CELL CLUSTERS IN THE SUBGESOPHAGEAL GANGLION.

PIR: A60065; AKLOIM.

AMIdation; Neuropeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 92179466. Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.; Isolation, identification and synthesis of locustamyoinhibiting peptide (LOM-MIP), a novel biologically active neuropeptide from Locusta migratoria."; Regul. Pept. 36:111-119(1991).
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01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 27, Last amortation update)
LOCUSTANYOINHIBITING PEPTIDE (LOW-MIP).
Locusta migratoria (Migratory locust).
Eukaryota; Metazoa; Arthropoda; Tranheata; Hexapoda; Insecta;
Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
Acridomorpha; Acridoidea; Acrididae; Locusta.
                                                                                                    STRAIN=968;
MEDLINE; 91041730.
Wootton J.C.; Bady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24.4%; Score 11; DB 1; Length 8; 40.0%; Pred. No. 8.8e+04; 1; Indels 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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387D7DD4472AB6C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leader peptide; Plasmid.
SEQUENCE 8 AA: 937 MW; FA37340685BDC1A6 CRC64;
                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
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9 AA; 1060 MW;
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Best Local Similarity 40.0
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
                                                                               SEQUENCE FROM N.A.
Plasmid pUL5050.
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Canis familiaris (Dog).
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Matches 2; Conserv
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Matches 2; Conserv
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                     9 AA;
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NON_TER
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GIHCN 6
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P38005;
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TPIS_CANFA
ID TPIS_CANFA
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                                                                                                                           Pickering B.T., Heller H.;
Oxytocin as a neurophyophysial hormone in the holocephalian elasmobranch fish, Hydrolagus collei.";
J. Endocrinol. 45:597-606(1969).
I. Endocrinol. AS:597-606(1969).
I. FUNCTION: OXYTOCIN CAUSES CONTRACTION OF THE SMOOTH MUSCLE OF THE UTENUS AND OF THE MAMMARY GLAND.
I. SIMILARITY: BELONGS TO THE VASOPRESSIN/OXYTOCIN FAMILY.
PIR; A91466. A91466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 75145197.

Tsolas O., Sun S.C.;

Tsolas O., Sun S.C.;

Tsolation of a peptide containing a histidinyl-cysteinyl sequence from the active center of transaldolase.";

Arch. Blochem. Blophys. 167:525-533(1975).

-!- FUNCTION: TRANSALDOLASE IS IMPORTANT FOR THE BALANCE OF METABOLITES IN THE PRIVOSE-PHOSPHATE PATHWAY.

-!- CATALVIIC ACTIVITY: SEDOHBETULOSE 7-PHOSPHATE + D-GIYCERALDEHYDE 3-PHOSPHATE = D-ERYTHROSE 4-PHOSPHATE + D-FRUCTOSE 6-PHOSPHATE.
-!- SAMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY.

PIR; A11497; A11497.

INTERPRO; IPR001585; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
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                                           MEDLINE; 73223515.
Acher R., Chauvet J., Chauvet M.-T.;
"Neurohypophysial hormones and evolution of tetrapods.";
Nature New Biol. 244:124-126(1973).
                                                                                                                                                                                                                                                                                                                                                                                                 Score 11; DB 1; Length 9; Pred. No. 8.8e+04; 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                       AMIDATION.
17F8376EB456D04B CRC64;
                                                                                                                                                                                                                                                                                                                                Hormone; Hypothalamus; Amidation; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
TRANSALDOLASE III (EC 2.2.1.2) (FRAGMENT).
Pichia jadinii (Yeast) (Candida utilis).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 AA.
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PROSITE; PS01054; TRANSALDOLASE_1; PARTIAL.
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PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
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28.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
Nature 201:191-192(1964)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                         1XX1; 15-0CT-90
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                                                                                                                                                                                                                                                                                               IPR000981;
                                  SPECIES-A. ACULEATUS;
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B90667; B90667.
                                                                                                                                                                                                                                         A93147; A93147
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Best Local Similarity
Matches 2; Conserv
                                                                                                                SPECIES=H.COLLIEI;
                                                                                                                        MEDLINE; 70088110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SINILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
HSC-2DPAGE; P54714, DOG.
INTERRAN; IPRO00652; --
PROSITE; PS00171; TIM; PARTIAL.
ISOMERASE; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=L2/434/BU;
Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
Comanducci M., Christianen G., Birkelund S., Vtretou E., Ratti G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dog heart proteins.";
Electrophoresis 18:2795-2802(1997).
-:- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE - DIHYDROXY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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01-0cT-1994 (Rel. 30, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.2%; Score 10; DB 1; Length 5; 66.7%; Pred. No. 8.8e+04; ive 0; Mismatches 1; Indels
                                                                                                                                 2; Indels
                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM) (FRAGMENT).
                                                                           Score 11; DB 1; Length
Pred. No. 8.8e+04;
1; Mismatches 2; Inde
325A31A44EB1E058 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64444862C9A00000 CRC64
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 AA.
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                                                                           24.48;
1033 MW;
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50.0%;
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(Rel. 39, I
(Rel. 39, L
                                                                         Query Match
Best Local Similarity
"Thes 2; Conserve
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Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                  CARCINUSTATIN 3.
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30-MAY-2000 (
30-MAY-2000 (
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P81806;
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P81807;
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                                                                                                                                               3 YAFG
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ALL4_CARMA
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                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
        Submitted (SEP-1994) to the SWISS-PROT data bank.
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 4.5, ITS MW IS: 28 KDA.
5 5
                                                                                                                                                                                                                                                      Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carcinus maenas (Common shore crab) (Green crab).
Usukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Plecoyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                     0; Indels
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                                                                                DB 1; Length 5;
8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.2%; Score 10; DB 1; Length 6; 100.0%; Pred. No. 8.8e+04;
                                      6 AA; 621 MW; 72C9C6876DD81000 CRC64;
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TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-DEC-1998 (Rel. 37, Last annotation update)
CONTRACTION-INHIBITING PEPTIDE II (MIP II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 AA.
                                                                                                                                                                                               6 AA.
                                                                              12.2%; Score 10; DB 10.0%; Pred. No. 8.8 Conservative 0; Mismatches
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ive 0; Mismatches
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                                                                                                                                                                                              STANDARD;
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                                                                      Query Match
Best Local Similarity
Local 2; Conserve
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Hormone; Amidation.
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Best Local Similarity
Matches 2; Conservi
                                                                                                                                                                                                                                                                                                                   MEDLINE; 88240357.
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Pallini V.;
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P81805;
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CIP2_MYTED
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Eur. J. Biochem. 250:727-734(1997).
-1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-1- SIMILARITY: BELONGS TO THE ALLANOSTATIN FAMILY.
Neuropeptide; Amidation; Multigene family.
MOD_RES 7 7 AMIDATION (POTENTIAL).
SEQUENCE 7 AA; 770 MW; 672879CDCB5DB70 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazóa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
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Pred. No. 8.8e+04;
                                                                                                                                                                                                                         22.2%; Score 10; DB 1; Length 7; 50.0%; Pred. No. 8.8e+04; 1ve 0; Mismatches 2; Indels
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SEQUENCE 7 AA; 796 MW; 672879CDCB476B70 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
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Last annotation update)
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UN06_PINPS
P81675;
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P25423;
                                               FAMILY
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SEQUENCE
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UN06_PINPS
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Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROFFAANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide: Muligene family.
SEQUENCE 7 AA, 782 WW. 672879CDCB476AC
                                                                                                                                                                                                                                                                                                                                                                          "Isolation and identification of multiple neuropeptides of the
                                                                                                                                                                                                                                                                                                                                                                                     allatostatin superfamily in the shore crab Carcinus maenas.";
Eur. J. BLOCHEM. 250.727-734 (1997).
-i- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-i- SIMILARITY: BELLONGS TO THE ALLATOSTATIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                     Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                Carcinus maenas (Common shore crab) (Green crab).

Bukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Bumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Procambarus clarkii (Red swamp crayfish).
Bukaryota: Metazoa: Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
Astacoidea; Cambaridae; Procambarus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 93248032.
Mercier A.J., Orchard I., Tebrugge V., Skerrett M.;
"Isolation of two FMRFamide-related peptides from crayfish
                                                                 Score 10; DB 1; Lengtn /, Pred; No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10, _______Pred: No. 8.8e+04;
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                                                                                                                                                                                                                                                                                                                               TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CARDIOEXCITATORY FMRFAMIDE HOMOLOG NF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 AA.
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pericardial organs.";
Peptides 14:137-143(1993).
                                                                          Query Match 22.2
Best Local Similarity 50.0
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                STANDARD;
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Best Local Similarity
These 2; Conserve
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                                                                                                                                                                                                                                                      CARCINUSTATIN 5.
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30-MAY-2000
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                                                                                                                                          3 YAFG 6
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P81808;
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FUNCTION: INCREASES THE RATE AND AMPLITUDE OF SPONTANEOUS
CONTRACTIONS OF SEMI-ISOLATED HEBRITS. INCREASES THE AMPLITUDE OF
EXCITATORY POSTSYRAPTIC POTENTIALS IN ABDOMINAL EXTENSOR MUSCLE.
SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last sequence update)
16-JUL-1999 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-NEEDLE;
MEDLINE: 99274088.
Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
Frigerio J.-M., Plomion C.;
"Separation and characterization of needle and xylem maritime pine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Electrophoresis 20:1098-1108(1999).
-!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-M.MELOLONTHA, AND G.STERCOROSUS; TISSUE-CORPORA CARDIACA; MEDLINE; 91248100.
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01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
01-FEB-1994 (Rel. 28, Last annotation update)
ADIPONINEIC HORMONE (AKH).
Melolontha melolontha (Cockchafer),
Geotrupes stercorosus (Dor beetle), and
Pachnoda marginata (Flower beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Scarabaeiformia; Scarabaeidae; Melolonthinae; Melolontha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 1; Length 7; Pred. No. 8.8e+04; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                7 7 AMIDATION.
7 AA; 966 MW; 69D40729C4540420 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 AA; 823 MW; 69D76724486B5740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coniferopsida; Coniferales; Pinaceae; Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN IS: 6.6, ITS MW IS: 25 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.28;
66.78;
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Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
'-has 2; Conserva
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8 AA.

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Cydia pomonella (Codling moth).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Plerygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98121193.
Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-LARVA;
MEDLINE; 98054539.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley layer M., East P.D., Thorpe A.;
"Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1997).
                                                                                                                                                                                        Carcinus maenas (Common shore crab) (Green crab).

Wataryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;

Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22.2%; Score 10; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neuropeptide; Amidation; Multigene family.
MOD_RES 8 AMIDATION (POTENTIAL).
SEQUENCE 8 AA; 858 MW; C82879D5AB46D865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY
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8 AA; 934 MW; C82879C45B51F775 CRC64;
                                                                                                                                                                                                                                                                                                   TISSUE=CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 10; DB 1; L. Pred. No. 8.8e+04;
                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.2%; Scor
100.0%; Pre
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                                                                                 STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                                                       CARCINUSTATIN 17
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                                                                                                                  30-MAY-2000
                                                                                                                                     30-MAY-2000
30-MAY-2000
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                                                                               AL17_CARMA
P81820;
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P82152;
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                                                                                                                                                                                                                                                                                                                                                        Thorpe A.
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                                                                                                                                                                                                                                                                                  SEQUENCE.
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ALL1_CYDPO
                                                            AL17_CARMA
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Gaede G.,
"A unique charged tyrosine-containing member of the adipokinetic hormone/red-pigment-concentrating hormone peptide family isolated and sequenced from two beetle species.";
Blochem. J. 275:671-677(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                 Gaede G., Lopata A., Kellner R., Rinehart K.L. Jr.;
"Primary structures of neuropeptides isolated from the corpora
cardiaca of various cetonid beetle species determined by
pulsed-liquid phase sequencing and tandem fast a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                      spectrometry.";
Biol. Chem. Hoppe-Seyler 373:133-142(1992),
-!- FUNCTION: THIS HORMONE. RELEASED FROM CELLS IN THE CORPORA
CARDIACA AFTER THE BEGINNING OF FLIGHT, CAGUES RELEASE OF
DIGLYCERIDES FROM THE FAT BODY AND THEN STIMULATES THE FLIGHT
MUSCLES TO USE THESE DIGLYCERIDES AS AN ENERGY SOURCE.
-!- SIMILARITY: BELONGS TO THE AKH / HRTH / RPCH FAMILY.
PIR; S15422; S15422.
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PIR; S21663; S21663.
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0
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Eur. J. Biochem. 250:727-734(1997).
-!- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
-!- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
Neuropeptide; Multigene family.
SEQUENCE 8 AA; 913 MW; 672879CDCB569AB7 CRC64;
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o
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Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuropeptide; Amidation; Flight.  1 \hspace{0.5cm} \texttt{PYRROLIDONE} \hspace{0.1cm} \texttt{CARBOXYLIC} \hspace{0.1cm} \texttt{ACID}. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.2%; Score 10; DB 1; Length 8; 100.0%; Pred. No. 8.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 1; Length 8; Pred. No. 8.8e+04; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 867AB775AB544736 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carcinus maenas (Common shore crab) (Green crab).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
                                                                                                                               SPECIES-P.MARGINATA; TISSUE-CORPORA CARDIACA; MEDLINE; 92265187.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMIDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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ilarity 50.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA; 1022 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.2
Best Local Similarity 100.
Matches 2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL12_CARMA
P81815;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOD_RES
SEQUENCE
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                                                                                                                SEQUENCE.
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                                                                                                                                                     Cydia pomonella (Codling moth).
Eukaryota, Metazoa, Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Tortricoldea; Tortricidae; Olethreutinae; Cydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                           TISSUE-LARVA;

BUDINE: 98054539.

MUDINE: 98054539.

Dave H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
Davey M., East P.D., Thorpe A.;
Lepidopteran peptides of the allatostatin superfamily.";
Peptides 18:1301-1309(1397).
-1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

MOD_RES 8 AMIDATION.

SEQUENCE 8 AA; 936 MW; 0B2879C45B573767 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Duve H., Johnson.

Thorpe A., The Shore Crab Carcinus maenas.";

Eur. J. Biochem. 250:727-734(1997).

-I.- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.

-I.- SIMICARITY: BELONGS TO THE ALLATOSTATIN FAMILY.

CHAIN 1 8 CARCINUSTATIN 6.

CHAIN 2 8 CARCINUSTATIN 1.

MOD_RES 8 AMIDATION.
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P81809; P81810; P81804;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
CARCINUSTATIN 7 (CONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1].
CARCINUSTATIN 7 LOONTAINS: CARCINUSTATIN 6; CARCINUSTATIN 1].
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
Eubrachyura; Portunoidea; Portunidae; Carcinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-CEREBRAL GANGLION, AND THORACIC GANGLION;
MEDLINE; 98121193.

Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.2%; Score 10; DB 1; Length 8; 50.0%; Pred. No. 8.8e+04; rative 0; Mismatches 2; Indels
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                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
CYDIASTATIN 6.
                                                  PRT;
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Best Local Similarity 50.0
Matches 2; Conservative
                                                 STANDARD;
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Best Local Similarity
Matches 2; Conserv
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P82157;
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            RESULT 34
ALL6_CYDPO
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Search completed: December 16, 2000, 04:23:31 Job time: 4566 sec

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04437 aeromonas t
04468 aeromonas v
043228 aeromonas v
0917h9 haemophilus
0917h9 haemophilus
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Q9rq57 buchnera ap
Q9rq54 homo sapien
Q9ucn4 homo sapien
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Q83332 murine hepa
Q85562 moloney mur
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moloney mur
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09866 spinacia ol
P7221 pseudomonas
09772 escherichia
09740 encecoccu
016428 homo sapien
094414 homo sapien
090mc7 homo sapien
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
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090004
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Q9YQ10
Q9RQ57
   Q15889
Q15901
Q95213
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Q9R7E8
Q9R635
Q16220
Q16220
Q9CCNS
Q28112
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Q47505
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Q9R7T2
Q9R4M3
Q16428
Q9Y4J4
Q9UMC7
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01-MAY-2000 (TFEMBLFEL. 13,
01-MAY-2000 (TFEMBLFEL. 13,
                                                                                                                                       Limnodynastes.
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    RESULT
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Ogu156 homo sapien
Ogps69 gallus gall
Ogy3kl prochloroco
O48686 lactococcus
Ogtrw2 oryctolagus
Ogtrw2 oryctolagus
Ogtrs0 me
P82082 limnodynast
P82083 limnodynast
Ogtrs0 lennodynast
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Q86871 cauliflower
                                                                                                      Search time 111.26 Seconds (without alignments)
7.553 Million cell updates/sec
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                      December 16, 2000, 03:05:26
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                                                                            OM protein - protein search, using sw model
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Q9UL56
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Q9XXXI
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sp_virus:*
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sp_organelle:*
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: sp_bacteria:*
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length: 9
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Maximum DB seq
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Prochlorococcus.
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                  TISSUE-TIBIAL GLAND:
Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
"Peptides from Australian frogs. The structure of the dynastins from the banjo frogs Limnodynastes interioras, Limnodynastes dumerilli and Limnodynastes terraereginae.";
                                                                                                                                                              Gaps
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Fukumaki Y., Higasa K.;
"Two novel mutations in Thai patients with hereditary
methemoglobinemia types I and II: a subtle amino acid change causes
                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MUTANT NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (FRAGMENT)
DIA1.
                                                                                                                                     37.8%; Score 17; DB 13; Length 8; 66.7%; Pred. No. 3e+05; Live 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%; Score 15; DB 3; Length 8; 100.0%; Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Wedler H., Wedler E., Scharfe M., Wambutt R.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z73169; CAA97518.2; -. NON_TER 1 18QUENCE 8 AA; 1019 MW; 4E21A9C449D5B73B CRC64;
                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                      Aust. J. Chem. 46:833-842(1993).
-1 MASS SPECTROMETRY: MW=729; METHOD=FAB.
Amphibian skin.
SEQUENCE 8 AA; 729 MW; 7C28772865B72728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA.
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                                                                                                                                                                                                                                                                             Created)
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           SEQUENCE, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                          01-JUL-1997 (TrEMBLrel. 04, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                           GIN11 PROTEIN (FRAGMENT).
                                                                                                                                                            Conservative
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Best Local Similarity
Matches 4; Conserv
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Matches 3; Conserv
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P87225;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LOW DENSITY LIPOPROFIN RECEPTOR-RELATED PROTEIN
Gallus gallus (Chicken)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92011685.
Stifani S., Barber D.L., Aebersold R., Steyrer E., Shen X., Nimpf J.,
Schneider W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            populations flow cytometrically Stream.";
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Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 15; DB 13; Length 8; Pred. No. 3e+05;
                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
instability of NADH-cytochrome b5 reductase.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AFF061830, AAF06818.1; -.
Oxidoreductase.
                                                                                                                                                                                                      Length 8;
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Last annotation update)
                                                                                                                 -> R.
76C5B73B5051F6D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor-related proteins.";
J. Biol. Chem. 266:19079-19087(1991).
SEQUENCE 8 AA; 846 MW; C007272DD865BAAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AA; 799 MW; 10376865B72866D3 CRC64;
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100.0%; Pred. No. 3e+05;
tive 0; Mismatches C
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Urbach E., Chisholm S W.;
"Genetic diversity in Prochlorococcus polysorted from the Sargasso Sea and Gulf St.
Limnol. Oceanog. 43:1615-1630(1998).
EMBL, AF070193; AAD23233.1; -.
SEQUENCE 8 AA; 799 WW; 10376865E7286
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80.0%;
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                                                                                                                                    888 MW;
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                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 4; Conserv
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CALCYCLIN-ASSOCIATED PROTEIN, CAPS0=CA2+/PHOSPHOLIPID-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      031415;
01-00V-1996 (TrEMBLrel. 01, Created)
01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota: Metazoa: Chordata; Crantata: Vertebrata: Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tokumitsu H., Miutani A., Minami H., Kobayashi R., Hidaka H.;
"A calcyclin-associated protein is a newly identified member of the calcyclin-binding proteins, annexin family.";
J. Biol. Chem. 267:8919-8924 (1992).
SEQUENCE 9 AA; 1010 MW; 64E419C44865B72B CRC64;
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Kanki T., Kuwasawa N., Sekiya Y., Ichikawa Y.;

"Responsive expression of a MHC class I epitope and genes following Marck's disease virus infection.";

Submitted (JAN-1992) to the EMBL/GenBank/DDBJ databases.
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01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
SODIUM CHANNEL, VOLTAGE-GATED, TYPE VIII, ALPHA POLYPEPTIDE
(TRUNCATED VOLTAGE-GATED SODIUM CHANNEL ALPHA SUBUNIT) (FRAGMENT).
                                                                                                                                                                                                                                 L-7 FRAGMENT.
Obyctologus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.1%; Score 14; DB 6; Length 9; 100.0%; Pred. No. 3e+05; ive 0; Mismatches 0; Indels
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2; Mismatches
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Matches 3; Conserv
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE.
MEDLINE; 92250478
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Ikebe M., Hornick T.;
"Determination of the phosphorylation sites of smooth muscle caldesmon by protein kinase C.";
Arch. Biochem. Biophys. 288:538-542(1991).
SEOUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 88105390.
van der Vossen J.M., der Lelie D., Venema G.;
"Isolation and characterization of Streptococcus cremoris Wg2-specific
                                                                                                    Gaps
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01-NOV-1996 (TrEMBLrel. 03, Last sequence update)
01-NOV-1996 (TrEMBLrel. 08, Last annotation update)
PROWOTER 23 DNA FRAGMENT (FRAGMENT).
Lactcocccus lactis (subsp. cremoris) (Streptococcus cremoris).
Bacteria: Firmicutes; Bacillus/Clostridium group; Streptococcus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
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Score 14; DB 2; Ler
Pred. No. 3e+05;
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Pred. No. 3e+05;
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Pred. No. 3e+05;
3; Mismatches
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Appl. Environ. Microbiol. 53:2452-2457(1987).
EMBL: M24763; AAA74720.1; -...
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ilarity 33.3%;
Conservative 3
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66.7%;
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SEQUENCE.
MEDLINE; 91378498.
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Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.; "Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae assessed by temperature gradient gel electrophoresis."; Electrophoresis 19:42-151(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosaurla; Aves; Neognathae; Passeriformes; Passeridae; Erythrura.
                                                                                                                                                                                                                                                                                                                                                                          MEDLINE, 90349591.
Cherif-Zahar B., Bloy C., Le Van Kim C., Blanchard D., Bailly P., Hermand P., Salmon C., Cartron J.-P., Colin Y., "Molecular cloning and protein structure of a human blood group Rh
                                                                                                                                                                                                                                             Matassi G., Cherif Zahar B., Mouro I., Cartron J.P.; "Characterization of the recombination hot spot involved in the genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                        Last sequence update)
Last annotation update)
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01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide.";
Proc. Natl. Acad. Sci. U.S.A. 87:6243-6247(1990)
EMBL; 297030; CAB09726.1; -.
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Pred. No. 3e+05;
                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                         Created)
                                                                                                                                                                                                                                                                                                              Am. J. Hum. Genet. 60:808-817(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erythrura gouldiae (Gouldian finch).
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50.0%;
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40.0%;
                                                                    01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, RHCE PROTEIN (FRAGMENT).
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Best Local Similarity
Local 2; Conserve
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MFDLINE; 98208049.
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01-MAY-2000 (
01-MAY-2000 (
                                                                                                                                                                                                                                 TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                phenotype.";
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4 HMNL 7
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                                                          STRAIN-RIII;
MEDLINES, 944-2476.
Plummer N.W., McBurney M.W., Meisler M.H.;
Plummer N.W., McBurney M.W., Meisler M.H.;
Alternative splicing of the sodium channel SCN8A predicts a truncated two-domain protein in fetal brain and non-neuronal cells.";
J. Biol. Chem. 272:24068-24015(1997).
EMBL: U97672; AAB80914.1;
MGD; MGI:103169; Scn8a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=ECOR11;
MEDITHE; 9640908

MEDITHE; 9640908

Boyd E.F., Hill C.W., Rich S.M., Hartl D.L.;

"Mosaic structure of plasmids from natural populations of Escherichia
                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Plasmid IncFII R1.
Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Pred. No. 3e+05;
2; Mismatches 0; Indels
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Last annotation update)
                                                                                                                                                                                                                       9 AA; 898 MW; 22D92865B735B737 CRC64;
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P77556;
P77556;
01-FEB-1997 (TrEMBLRE1. 02, C)
01-FEB-1997 (TREMBLRE1. 02, L)
01-FEB-1097 (TREMBLRE1. 09, L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics 143:1091-1100(1996).
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50.0%;
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8 AA; 834 MW;
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Best Local Similarity
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                                            SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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NON_TER 1
SEQUENCE 9 AA;
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US0659;
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RESULT 11

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Spittaels K., Verhaert P., Shaw C., Johnston R.N., Devreese B., Van Beeumen J., De Loof A.; "Insect neuropeptide F (NPF)-related peptides: isolation from Colorado
                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                            Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.; "Peptides from Australian frogs. The structure of the dynastins from Limnodynastes salmin1 and Fletcherin from Limnodynastes fletcheri."; Aust. J. Chem. 46:1235-1244(1993).

-I. MASS SPECTROMETRY: MW-786; METHOD=FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MYY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
LED-NPF-1-NEUROPEPTIDE F.RELATED PEPTIDE.
Leptinotarsa decemlineata (Colorado potato beetle).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
Cucujiformia; Chrysomelidae; Chrysomelinae; Leptinotarsa.
                                                                                                                                                                                                                                                                                                                                                                                                                                28.9%; Score 13; DB 13; Length 8; 40.0%; Pred. No. 3e+05; 1; Indels ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         potato beetle (Leptinotarsa decemiineata) brain.";
Insect Biochem. Mol. Biol. 26:375-382(1996).
SEQUENCE 9 AA; 1066 MW; 7E02340736C76864 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TR4-NS ORPHAN RECEPTOR (FRAGMENT).
                                                                       01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
DYNASTIN 5.
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                                                                                                                               Limnodynastes salmini (Salmin's-striped frog)
                   8 AA.
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                                                                                                                                                                                                                           SEQUENCE, AND MASS SPECTROMETRY.
                                                        01-MAY-2000 (TrEMBLrel. 13,
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Best Local Similarity 40.۰۰
اتام 2; Conservative
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Matches 3; Conserv
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4 SNLGI 8
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Q63480;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Passeriformes; Meliphagidae; Manorina.
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Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
Breptides from Australian frogs. The structure of the dynastins from Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
                                                                                                                                                                                                                                                                                                                                                                      Heslewood M.M., Elphinstone M.S., Tidemann S.C., Baverstock P.R.;
"Myoglobin intron variation in the Gouldian Finch Erythrura gouldiae
assessed by temperature gradient gel electrophoresis.";
Electrophoresis 19:42-13[11998].
EMBL: U40497; AAC60364.1;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                       01-NOV-1998 (TrEMBLrel. 08, Last annotation update) MYOGLOBIN (FRAGMENT).
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SEQUENCE 8 AA; 772 MW; 7B58772455A2C728 CRC64;
                                                                                                                                                                    01, Created)
01, Last sequence update)
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-!- MASS SPECTROMETRY: MW=772; METHOD=FAB.
                                                                                                                                                                                                                                              Manorina melanocephala (noisy miner).
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Best Local Similarity
Matches 2; Conserv
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Best Local Similarity
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MEDLINE; 98208049
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3 ISGVH 7
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P82082
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Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M., Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y., Caskey C.T.H.; Hur. Mol. Genet. 0:0-0(0). EMBL; L32070; AAA73879.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-PLACENTA;
Lee C.C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUB-BONE MARROW;
MEDILINE; 95002916.
Tighe J.E., Calabi F.;
"Alternative, out-of-frame runt/MTG8 transcripts are encoded by the derivative (8) chromosome in the t(8;21) of acute myeloid leukemia M2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RUNT/68NT/MTG8.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 50.0%; Score 12; DB 4; Length 8; Similarity 50.0%; Pred. No. 36+05; 2; Conservative 1; Mismatches 1: Indole
                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
RUNT/68NT/MTGB PROTEIN (FRAGMENT).
                                                                                                                               8 AA; 865 MW; 0474472325A761E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 AA; 860 MW; 37D72878676729CB CRC64;
                                                                                                                                                                                     Score 12; DB 4;
Pred. No. 3e+05;
                                                                                                                                                                                                                                                                                                                                                                            8 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                 26.78;
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EMBL; L32080; AAA73891.1; -.
NON_TER 1 1 1
NON_TER 8
SEQUENCE 8 AA; 860 MW; 37
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-AUG-1998 (TrEMBLrel. 07, CLONE XP7B11B) (FRAGMENT).
                                                                                                                                                                                                   Best Local Similarity 42.9
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood 84:2115-2121(1994).
                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                              1 LHPSKLN 7
                                                                                                                                                                                                                                                     2 LSGANLN 8
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2 FLPG 5
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NON_TER
SEQUENCE
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Best Local 3
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Q15901;
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Q15901
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Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                    MEDLINE; 96198747.
Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,
Detera-Wadleigh S.D.;
"Splice variants of rat TR4 orphan receptor: differential expression
of novel sequences in the 5'-untranslated region and C-terminal
                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=11/3-7;
MEDLINE; 95053898.
al-Kaff N., Covey S.N.;
"Variation in biological properties of cauliflower mosaic virus
                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 26.7%; Score 12; DB 12; Length 7; Best Local Similarity 33.3%; Pred. No. 3e+05; Matches 2; Conservative 2; Mismatches 2; Indels
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
VIRION STRUCTURAL PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
                                                                                                                                                                                                                          NON_TER 1 1 1
SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 AA; 744 MW; 672054444DC5B030 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENE III.
Cauliflower mosaic virus.
Viruses; Retroid viruses; Caulimovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                        domain.";
Endocrinology 137:1562-1571(1996).
EMBL; U59125; AAB02827.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones.";
J. Gen. Virol. 75:3137-3145(1994).
EMBL; S75948; CAB33416.1; -
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                                                                                                                                                                                                                                                                                              Query Match 26.7%;
Best Local Similarity 33.3%;
Matches 2; Conservative
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                                                                       SEQUENCE FROM N.A
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TISSUE=PLACENTA;
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2 IRGGDL 7
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1 ISANNI 6
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Q15889;
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Q86871
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Q15889
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Gaps

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RESULT Q95213

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Peterson E.M., Cheng X., Markoff B.A., Flelder T.J., de la Maza L.M.; "Functional and structural mapping of Chlamydia trachomatis species-specific major outer membrane protein epitopes by use of neutralizing more consulantibodies."; Infect. Immun. 59:4147-4153(1991). SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;
                                                                                                                                                                                                                                                                              MEDLINE: 95180691.
ROSENOW C., Roberts I.S., Jann K.;
Roslow C., Roberts I.S., Jann K.;
Tsolation from recombinant Escherichia coli and characterization of CMP-Kdo synthetase, involved in the expression of the capsular K5 polysaccharide (K-CKS)...;
EMBL, S76943; CAB33515.1;
EMBL, S76943; CAB33515.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
MAJOR OUTER MEMBRANE PROTEIN VARIABLE DOMAIN IV, MOMP VD IV.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
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                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
9 AA; 899 MW; 3EBBB72042C33DD8 CRC64;
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66.7%; Pred. No. 3e+05;
iive 1; Mismatches
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Pred. No. 3e+05;
                                                                                               9 AA.
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                                                                                                                             Created)
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 50.0
Matches 3; Conservative
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                                                                                                PRELIMINARY;
                                                                                                                                                                          KPSD PROTEIN (FRAGMENT).
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Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 92040090.
                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 GANLNL 9
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2 GAKVIL 7
    11 ::
2 GAQVS 6
                                                                                                                                                                                                                        Plasmid pCR3
                                                                                                                                                                                                                                                     Escherichia.
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7 ISG 9
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid
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Q14715
ID Q14715
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Q9R7E8
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                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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Bailly J.L., Borman A.M., Peigue-Lafeuille H., Kean K.M.;
Builly J.L., Borman A.M., Peigue-Lafeuille H., Kean K.M.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X90724; CAA62259.1; -.
NON_TER
SEQUENCE 8 AA; 821 MW; EFC1B5A2D6DDD876 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 12; Length 8;
Pred. No. 3e+05;
2; Mismatches 1; Indels
                                                                             Score 12; DB 4; Length 8;
Pred. No. 3e+05;
1; Mismatches 1; Indels
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 07, Last annotation update)
5.UTR IN IRES SEQUENCES (ISOLATE TH222) (FRAGMENT).
Echovirus 25.
                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
GERMLINE DH (DF) GENE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5CA861B5AB58677B CRC64;
                                 30B764405B17244B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-F-I/RGM;
Mage R.G., Chen H.T., Alexander C.B., Chen F.F.;
Mol. Immunol. 0.0-0(0).
EMBL: U62585; AAB18735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 12; DB 7;
Pred. No. 3e+05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AA.
                                                                                                                                                                                                                                                     8 AA.
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                                                                             26.7%;
50.0%;
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50.0%;
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40.0%;
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8 8
8 AA; 845 MW;
EMBL; S74094; AAD14973.2;
NON_TER 1
SEQUENCE 8 AA; 929 MW;
                              8 AA; 929 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 26.7
Best Local Similarity 40.0
Matches 2; Conservative
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                             Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 2; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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2 NLEI 5
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Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
6-PHOSPHOFRUCIO-2-KINASE/FRUCTOSE-2, 6-BISPHOSPHATASE (FRAGMENT).
                                                                                                                                                                                                                                                                  Raboudi N., Julian J., Rohde L.H., Carson D.D.; "Identification of cell-surface heparin/heparan sulfate-binding proteins of a human uterine epithelial cell line (RL95)."; J. Biol. Chem. 267:11930-119391992). SEQUENCE 9 AA: 1008 MW: CBSED0544732C732 CRC54;
                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
CELL-SURFACE HEPARIN/HEPARANSULFATE-BINDING PROTEIN PEPTIDE
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Suarez C.E., Palmer G.H., Hines S.A., McElwain T.F.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, L77336, AAA96415.1; -.
SEQUENCE 9 AA; 931 MW; 6D5BD2C865B05044 CRC64;
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Pred. No. 3e+05;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-1999 (TrEMBLrel. 10, Last annotation update)
RHOPTRY ASSOCIATED PROFEIN 1.
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6D5BD2C865B05044 CRC64;
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Pred. No. 3e+05;
                                              9 AA.
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66.7%;
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nes 2; Conservative
                                              PRELIMINARY;
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Best Local Similarity
Matches 2; Conserv
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SEQUENCE FROM N.A.
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                                                            Q9UCN5;
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"A novel mutation of Leu122 to Phe at a highly conserved hydrophobic residue in the helix initiation motif of keratin 14 in epidermolysis
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MEDLINE; 94320083.
Nagalla S.R., Spindel E.R.;
"Functional analysis of the 5'-flanking region of the human gastrin-releasing peptide gene in small cell lung carcinoma cell lines.";
Cancer Res. 54:4461-4467(1994).
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                                                                                                                                                                                         MEDLINE; 92005680.

Coulombe P., Hutton M., Letai A., Hebert A., Paller A., Fuchs E.;

Point mutations in human keratin 14 genes of epidermolysis bullosa simplex patients: genetic and functional analyses.";
Cell 66:1301-1311(1994).
                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Catarrhini; Hominidae; Homo.
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Pred. No. 3e+05;
0; Mismatches 1; Indels
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NON_TER 9 9 9 SEQUENCE 9 AA; 1070 MW; 77FE37672B040864 CRC64;
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Pred. No. 3e+05;
1; Mismatches
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Hum. Mol. Genet. 3:1171-1172(1994).
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014715;
01-NOV-1996 (TrEMBLrel. 01, Ct
01-NOV-1996 (TrEMBLrel. 01, Le
01-JAN-1999 (TrEMBLrel. 09, Le
KERATIN 14 (FRAGMENT).
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates;
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37.58;
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ilarity 66.7%;
Conservative
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9 AA; 1138 MW;
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Best Local Similarity 37.5
Matches 3; Conservative
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                                                                                                         Homo sapiens, (Human)
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Best Local Similarity
Matches 2; Conserv
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NON_TER
SEQUENCE
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to produce the
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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J. Bacteriol. 177:7131-7140(1995).
EMBL: X57583; CAA40808.1;
                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PLASMID PMCCC7 MCCA, B, C, D, E, F GENES.
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007624;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL PROTEIN (FRAGMENT).
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Pred. No. 3e+05;
0; Mismatches
      Pred. No. 3e+05;
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16.7%;
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Best Local Similarity 66.7-
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Best Local Similarity
Matches 1; Conserv
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 Best Local Similarity
Matches 2; Conserv
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                                                                                                                                                                                                                                                                Escherichia coli.
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SEQUENCE
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MEDLINE: 87061199.
MEDLINE: 87061199.
"Three splicing patterns are used to excise the small intron common 'all minute virus of mice RNAs.";
J. virol. 60:1170-1174(1986).
ENBL; M12032; AAA69570.1;
ENBL; V02275; AAA67112.1;
EMBL; V01115; CAAZ4311.1;
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MDDLINE; 86115415.
Astell C. R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, "DNA sequence of the lymphotropic variant of minute virus of mice, MVM(L), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=LYMPHOTROPIC VARIANT;
MEDLINE; 86115415.
Astell C.R., Gardiner E.M., Tattersall P.;
"DNA sequence of the lymphotropic variant of minute virus of mice, MVM(1), and comparison with the DNA sequence of the fibrotropic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-MVM(P);
MEDLINE; 83143341.
Astell C.R., Thomson M., Merchlinsky M., Ward D.C.;
"The complete DNA sequence of minute virus of mice, an autonomous
                                          Vidal H., Crepin K.M., Rider M.H., Hue L., Rousseau G.G.;
"Cloning and expression of novel isoforms of 6-phosphofructo-2-
Kinase/fructose-2,6-bisphosphatase from bovine heart.";
FEBS Lett. 330:329-333(1993).
EMBL: X74564; CAA52652.1; -.
NON_TER 9 837 MW; 859CA5BDC7644865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               01-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-NOY-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 1.1 KDA PROTEIN.
Murine minute virus (Murine parvovirus).
Viruses; ssDNA viruses; Parvoviridae; Parvovirus.
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Pred. No. 3e+05;
1; Mismatches (
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Nucleic Acids Res. 11:999-1018(1983)
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                 Query Match 26.7%;
Best Local Similarity 66.7%;
Matches 2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prototype strain.";
J. virol. 570:656-669(1986)
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SEQUENCE 9 AA; 100
[1]
SEQUENCE FROM N.A.
MEDLINE; 93387464.
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1 MSG 3
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Search completed: December 16, 2000, 04:22:12 Job time: 4606 sec

1 YL 2 |-| 3 YL 4

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T-cell receptor glucan 1,3 beta-gl hypothetical prote

hypothetical prote Ig heavy chain CRD glutathione transf probable H+-transp microcin C7 - Esch

hypothetical

spinal cord peptid lipopeptide WS1279

copper resistance proctolin - Atlant spinal cord peptid

T-cell receptor be probable msrA lead 205k exoantigen -leucokinin VIII -

penalbumin - Adeli Ig heavy chain CRD T-cell receptor be

aspartate kinase (blood cell protein locustamyoinhibiti

hypothetical prote ribosomal protein 180K exoantigen -

platelet glycoprot

gramicidin S synth

oxytocin - hippopo oxytocin - spotted oxytocin - finback oxytocin - Austral oxytocin - rabbit calsequestrin, car dissimilatory sulf

T-cell receptor be T-cell receptor be hemoglobin alpha c

[Phe-6]-mosact - s c-rel protein - ch Ig heavy chain CRD

cell surface adhes transaldolase (EC neuropeptide Grb-A neuropeptide Grb-A

ribosomal protein

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Result No.

Searched:

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SS8797
Serine/threonine-specific protein kinase c-mos - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 23-Feb-1997
C;Accession: S58797
R;Nagao, Y
Biochim: Biophys. Acta 1245, 130-143, 1995
A;Title: Expression of c-mos protein in cultured rat spermatogenic cells and A;Reference number: S58797; MUID:95383384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 2; Length 7;
Pred. No. 1.8e+05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: c-mos
C;Keywords: phosphotransferase; protein kinase
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                                                                                                                                                                                                                                                                                             PT0542
LFSAME
JS0318
A61467
PT0621
PT0621
PT0621
PT0621
A81474
A931474
A931497
A93149
A9314
A9
                                                                           A60411
C23751
JU0355
JU0355
PT0280
S71867
PC2370
S45311
S42407
I140504
S13098
C56793
                              S43014
HOROHA
A41225
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Best Local Similarity 75.0%;
Matches 3; Conservative
                                A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <NAG>
C; Genetics:
sperm-activating p
cytochrome oxidase
Ig heavy chain CRD
T-cell receptor ga
T-cell receptor be
T-cell receptor be
T-cell receptor be
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variant surface gl
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neuropeptide Grb-A
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Ig mu chain V regi
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photosystem II pro
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cytotoxic T-lympho
galactose oxidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seminal plasma
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Compugen Ltd
                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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             GenCore version
Copyright (c) 1993 - 2000
                                                                                                             December 16, 2000, 02:01:07
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Maximum Match 100%
Listing first 75 summaries
                                                                              sw model
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Gapop 10.0 , Gapext 0.5
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E60588
PT0288
G41946
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A60957
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I51434
I49424
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PN0649
A34818
PQ0701
PL0184
A21440
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                                                                              - protein search, using
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2: pir2:*
3: pir3:*
4: pir4:*
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length: 9
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rat spermatogenic cells and evidence

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Ig heavy chain CRD3 region (clone 4-106) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: Pr0288
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 113, 395-407, 1991
A;Tile: Preferential utilization of specific immunoglobulin heavy chain diversity an A;Reference number: Pr0222; MUID:91108337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cell receptor gamma chain (2t.23) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O3-reb-1994 #sequence_revision 03-reb-1994 #text_change 07-May-1999
C;Date: 03-reb-1994 #sequence_revision 03-reb-1994 #text_change 07-May-1999
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A;Reference number: A41946; MUID:92049316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
PT0605
T-cell receptor beta chain V-D-J region (120-1L) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Jr-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
A; Cross-references: EMBL: Y09527; NID:e1011465; PID:e329906; PIDN: CAA70718.1
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A;Residues: 1-9 <WHE>
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                             Length 8;
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Mismatches 0;
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Pred. No. 1.8e+05;
0; Mismatches 1;
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Pred. No. 1.8e+05;
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                                                                                                                                                                                     Score 15;
Pred. No.
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                                                                                                                                                                                  33.3%; Scoilarity 100.0%; P. Conservative 0;
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75.0%;
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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C;Reywords: T-cell receptor
                           C;Genetics:
A;Genome: mitochondrion
A;Note: COI
C;Keywords: mitochondrion
                                                                                                                                                                                                                Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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                                                                                                                                                                                             calliffwRFamide 8 - bluebottle fly (Calliphora vomitoria)
C; Species: Calliphora vomitoria
C; Species: Calliphora vomitoria
C; Species: Calliphora vomitoria
C; Species: Scap-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C; Accession: H41978
R; Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorpe
Proc. Natl. Acad. Sci. U.S.A. and azicivity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A; Fifter Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (desi
A; Reference number: A41978; MUID:92196111
A; Reference number: Protein
A; Molecule type: protein
A; Residues: 1-8 - Duvy
C; Reywords: amidated carboxyl end; neuropeptide
F; 8/Modified site: amidated carboxyl end (Phe) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sperm-activating peptide a - sea urchin (Pseudoboletia maculata)

N.Alternate names: speract homolog

C.Species: Pseudoboletia maculata

C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun-2000

C.Accession: E60588

R.Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc

Comp. Biochem. Physiol. B 94, 733-751, 1989

A.Title: A halogenated amino acid-containing sperm activating peptide and its related pe

A.Reference number: A60527

A.Accession: E60588

A.Molecule type: protein

A.Residues: 1-8 <105>
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T13818
Cycochrome oxidase subunit I - Atlantic hagfish mitochondrion (fragment)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Species: mitochondrion Myxine glutinosa (Atlantic hagfish)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C;Accession: T13818
R;Delarbre, C.; Barriel, V.; Tillier, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 807-813, 1997
Mol. Biol. Evol. 14, 807-813, 1997
A;Tille: The main features of the craniate mitochondrial DNA between the NDI and the COI A;Reference number: Z17775; MUID:97398704
A;Reference number: Z17775; MUID:97398704
A;Status: preliminary; translated from GB/FMBL/DDBJ
A;Residues: 1-8 <DBL>
A;Residues: 1-8 <DEL>
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Pred. No. 1.8e+05;
0; Mismatches 2; Indels
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1.8e+05;
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Best Local Similarity 60.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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Kawasaki igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne A;Reference number: PN0041
A;Reference number: PN0043
A;Molecule type: protein
A;Residues: 1-8 <kAT>
A;Residues: 1-8 <kAT>
C;Comment: The molecular mass is 23,500 and the pI is 4.8. The amino-terminus is bloc C;Keywords: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C;Accession: A44873
R;Ikabe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A;Title: Determination of the phosphorylation sites of smooth muscle caldesmon by pro A;Reference number: A44873; MUID:91378498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neuropeptide Grb-AST B3 - two-spotted cricket
C;Species: Gryllus bimaculatus (two-spotted cricket)
C;Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 26-Jan-1996
C;Accession: C5744
R;Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.
B;Lorenz, M.W.; Kallner, R.; Hoffmann, K.H.
A;Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the A;Reference number: A57444; MUID:95403341
                                                                                                                                                                                    phosphatidylethanol amine-binding protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A; Residues: 1-9 < IKE>
A; Experimental source: skeletal myosin
A; Note: sequence extracted from NCBI backbone (NCBIP:63199)
C; Superfamily: caldesmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.1%; Score 14; DB 2; Lv 100.0%; Pred. No. 1.8e+05; ative 0; Mismatches 0;
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33.3%; Pred. No. 1.8e+05;
Live 3; Mismatches 1.
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A:Molecule type: protein
A:Residues: 1-9 <LOR>
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Best Local Similarity
Matches 3; Conserv
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Matches 2; Conserv
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A; Status: preliminary
                                                                                                                                                                                                                                                                                                    C; Accession: PN0043
R; Kato, H.
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1 GSSLKI 6
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5 LSG 7
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               SGA
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C;Accession: PT0605
R:Feeney, A.J.
J. Exp. Med. 115-124, 1991
A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601
A;Accession: PT0605
A;Accession: PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A;Reference number: PT0509; MUID:91277601
A;Status: PT0593
A;Status: translation not shown
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Affiltle: Junctitonal sequences of fetal T cell receptor beta chains have few N regions.
A: Reference number: PT0509; MUID:91277601
A: Accession: PT0654
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C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cell receptor beta chain V-D-J region (121-1BK) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0654
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1.8e+05;
thes 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-6 <FEE>
A;Experimental source: day 19 fetal thymus, strain BALB/c
C;Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.1%; Score 14; DB 2; Le
100.0%; Pred. No. 1.8e+05;
Live 0; Mismatches 0;
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
Matches 3; Conserv
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A; Residues: 1-7 <FEE>
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R; Feeney, A.J.
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SGA 6
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2 SGA 4
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A.Accession: A60983
A.Molecule type: protein
A.Residues: '2', 2'-4', 2'-6-8AC>
C.Comment: This peptide induces DNA synthesis in immature thymocytes, but not periphe in a variety of immunoassays.
C.Comment: See PTR:A60957 (sheep) for discussion of another possible N-terminal modif C.Superfamily: thymic factor
C.Superfamily: thymic factor
C.Superfamily: thymic factor
C.Reywords: pyrroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C;Species: Cyprinus carpio (common carp)
C;Date: O95-pep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C;Accession: A61364
R;Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Blochen. Physiol. A 14, 245-254, 1965
A;Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau do A;Reference number: A61364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N'Alternate names: FTS (facteur thymique serique)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 07-May-1999
C;Accession: A01523; A60983
R;Pleau, J.M.; Dardenne, M.; Blouquit, Y.; Bach, J.F.
A;File: Structural study of circulating thymic factor: a peptide isolated from pig
A;Reference number: A01523; MUID:78026571
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A.Molecule type: protein
A.Rosidues: 1-9 <ACH
C.Superfamily: oxytocin-neurophysin
C.Superfamily: oxytocin-neurophysin
C.Keywords: amidated carboxyl end; neuropeptide; posterior pituitary
F:9/Modified site: amidated carboxyl end (Gly) #status experimental
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A. Residues: 1-9 < PLE>
R. Bach, J. E., Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A. Title: Biochemical characterisation of a serum thymic factor.
A. Reference number: A60983; MUID:77123829
                                                                                                                                                      Score 13; DB 2; Length 7;
Pred. No. 1.8e+05;
2; Mismatches 0; Indels
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                A;Cross-references: GB:M55577; NID:g555438; PID:g211661
C;Genetics:
A;Gene: c-rel
                                                                                                                                                      28.9%;
50.0%;
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                                                                                                                             Query Match
Best Local Similarity 50...
3; Conservative
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Best Local Similarity 60...
2: Conservative
A; Residues: 1-7 <KAB>
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1 MAGA 4
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A61364
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                                                                                                                                                                                                                                                                                                                                C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 24-Feb-1995
C; Accession: J00914
R; Kankl, T: Kuwasawa, N.; Sekiya, Y.; Ichikawa, Y.
submitted to JIPID, May 1991
A; Abescription: Responsive expression of a MHC class I epitope and genes following Marek'
A; Reference number: J00914
A; Accession: J00914
A; Molecule type: mRNA
A; Residues: 1-9 cknNA
A; Residues: 1-9 cknNA
A; Experimental source: kidney, strain cornell N
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C:Species: Homo sapiens (man)
C:Date: 20.0ct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Date: 20.0ct-1994 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999
C:Accession: 843959
R:Wagner, S.D.; Williams, G.T.; Larson, T.; Neuberger, M.S.; Kitamura, D.; Rajewsky, K.; Mucleic Acids Res. 22, 1389-1393, 1994
A:Title: Antibodies generated from human immunoglobulin miniloci in transgenic mice. A;Reference number: 843956; MuID:94248036
A:Accession: 843959
A:Accession: 843959
A:Accession: 843959
A:Residues: 1-4 <MAG>
C:Keywords: immunoglobulin
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C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Sacesies: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Feb-1997
C;Accession: 150210
R;Kabrun, N.; Bumstead, N.; Hayman, M.J.; Enrietto, P.J.
MOI. Cell. Biol. 10, 4788-4794, 1990
A;Fitle: Characterization of a novel promoter insertion in the c-rel locus.
A;Reference number: 150210; MUID:90355995
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MHC class I histocompatibility antigen heavy chain - chicken (fragment)
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                31.1%; Score 14; DB 2; Length 9; llarity 100.0%; Pred. No. 1.8e+05; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 50.0%;
Matches 2; Conservative
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Best Local Similarity 50.0
Matches 2; Conservative
                Query Match
Best Local Similarity
Matches 3; Conserv
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1 YCAG 4
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5 LSG 7
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cytotoxic T-lymphocyte proteinase 3 (EC 3.4.21.-) - western wild mouse (fragment) C; Species: Mus spretus (western wild mouse)
C; Species: O2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: 149424
R; Ko, M.S.; Wang, X.; Horton, J.H.; Hagen, M.D.; Takahashi, N.; Maezaki, Y.; Nadeau, Mamm. Genome 5, 349-355, 1994
A; Title: Genetic mapping of 40 cDNA clones on the mouse genome by PCR.
A; Reference number: 148934; MUID:94319082
PEBS Lett. 382, 15-17, 1996
A;Title: Crystallization and preliminary X-ray diffraction analysis of boar seminal A;Tetle: Crystallization and preliminary X-ray diffraction analysis of boar seminal A;Accession: 562883 MUD:96196555
A;Molecule type: protein A;Residues: 15 <ROM>
C;Complex: heterodimer; seminal plasma protein I and seminal plasma protein II
C;Keywords: glycoprotein; heterodimer; semen
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C;Keywords: hydrolase; serine proteinase
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Pred. No. 1.8e+05;
1; Mismatches 1;
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A;Molecule type: DNA
A;Residues: 1-6 <RES>
                                                                                                                                                                                                                              26.7%;
50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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A; Residues: 1-9 < ERN>
C; Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunoassays.
C; Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca
C; Comment: This peptide was isolated in two forms, one form contained the pyrrolidone ca
C; Superfamily: thymic factor
C; Superfamily: thymic factor
C; Keywords: blocked amino end; pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental
F:1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           photosystem II protein psbM - Chlamydomonas reinhardtii (fragment)
C;Species: Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 30-Sep-1993
C;Accession: C41170
R;de Vitry, C; Diner, B.A.; Popot, J.L.
A; Biol. Chem. 266, 16614-16621, 1991
A;Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecula A;Reference number: A41170; MUID:91388452
A;Accession: C41170
A;Accession: C41170
A;Accession: preliminary
A;Accession: preliminary
A;Residues: 1-9 <DES>
                                                                                                                                                                                                                                                                                                                C; Accession: A60957
R; Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
Bisci. Rep. 10, 403-412, 1990
A; Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship A; Reference number: A60957; MUID: 91064427
A; Accession: A60957
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C;Species: Sus scrofa domestica (domestic pig)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S62883
R;Romero, A.; Varela, P.F.; Sanz, L.; Toepfer-Petersen, E.; Calvete, J.J.
                                                                                                                                                                                                                                              N.Contains: FTS (facteur thymique serique)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
                            Gaps
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Pred. No. 1.8e+05;
2; Mismatches 0; Indels
                            Indels
  Pred. No. 1.8e+05;
1; Mismatches 0;
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Matches 2; Conservative
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50.0%;
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Best Local Similarity 66.7
Matches 2; Conservative
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Best Local Similarity
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4 IAGA 7
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Gibedies: Oryza sativa (rice)
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Cibedies: Oryza sativa (rice)
Cibedies: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
Cifecesion: P00701
Theor. Appl. Genet. 86, 935-942, 1993
Airlite A rice protein library; a data-file of rice proteins separated by two-dimens Aircession: P00701
Airlite Protein adata-file of rice proteins separated by two-dimens Aircession: P00701
Airlite Protein adata-file of rice proteins separated by two-dimens Aircession: P00701
Airlite Protein ary
Aircession: P00701
Airlite A rice Protein
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C;Species: murine poliovirus, Theiler's encephalomyelitis virus
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C;Accession: PLO184
R;Zurbriggen, A.; Hogle, J.M.; Fujinami, R.S.
J. Exp. Med. 170, 2037-2049, 1989
A;Titler Alteration of amino acid 101 within capsid protein VP-1 changes the pathogen A;Reference number: PLO184
A;Reference number: PLO184
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C;Species: Trypanosoma brucei
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Mar-1998
C;Accession: A1440
R;Parsons, M.; Nelson, R.G.; Watkins, K.P.; Agabian, N.
Cell 38, 309-316, 1984
A;Title: Trypanosome mRNAs share a common 5' spliced leader sequence.
A;Reference number: A90853; MUID:84282716
A;Accession: A21440
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A,Residues: 1-8 <PAR>
A;Cross-references: GB:K02195; NID:g162150; PID:g162151
C;Keywords: glycoprotein
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50.0%;
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nes 2; Conservative
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A, Residues: 1-8 <ZUR>
C, Keywords: capsid protein
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Matches
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          galactose oxidase inhibitor - fungus (Cladobotryum dendroides)
(Species: Cladobotryum dendroides
(Species: Cladobotryum dendroides
(Spacies: Oladobotryum dendroides
(Spacies: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 31-Dec-1993
(SAccession: A01341
RAVIGAG, G.; Markus, Z.
RAVIGAG, G.; Markus, Z.
A.Reference number: A01341
A.Accession: A01341
A.Accession: A01341
A.Accession: A01341
A.Residues: 1-7 <AVI-
C.Comment: The mycelia of this imperfect fungus produce the metalloenzyme galactose oxid C.Superfamily: galactose oxidase inhibitor
C.Superfamily: galactose oxidase inhibitor
C.Superfamily: galactose oxidase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Bacillus sp. C. C. Cobace: 1994 #sequence_revision 19-May-1994 #text_change 07-May-1999 C; Accession: PN0649 #sequence_revision 19-May-1994 #text_change 07-May-1999 C; Accession: PN0649 #sequence_revision 19-May-1994 #text_change 07-May-1999 R; Kim, C.H.; Choi, H.I.; Lee, D.S. Bisci. Blockennol. Biochem: 57, 1632-1637, 1993 A; Title: Purification and biochemical properties of an alkaline pullulanase from alkalop A; Reference number: PN0649; MUID:94080025
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: PN0649
A;Molecule type: protein
A;Residues: 1-7 < KINA.
C;Comment: This enzyme is used togther with glucoamylase to improve the efficiency of ntent in high maltose syrups.
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
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C;Species: Cajanus cajan (pigeon pea)
C;Species: Cajanus cajan (pigeon pea)
C;Bate: 13-011-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C;Accession: A34818
R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biocchem. Biochys. Res. Commun. 166, 1446-1452, 1990
A;Reference number: A34818; MUD:90165956
A;Accession: A34818
A;Actus: preliminary
A;Molecule type: protein
A;Residues: 1-7 <AAAW>
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50.0%;
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Best Local Similarity 50.0
Matches 2; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 2; Conserv
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1 AGQN 4
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A.Wolecule type: protein
A.Rosidues: 1-5 <STA>
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A.Rosidues: 1-5 
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C;Species: Periplaneta americana (American cockroach)
C;Species: 29-ul-1301 #sequence_revision 29-ul-1301 #text_change 23-Aug-1996
C;Date: 29-ul-1301 #sequence_revision 29-ul-1301 #text_change 23-Aug-1996
C;Accession: A01644
R;Starratt, A.N.; Brown, B.E.
Life Sci. 17, 1253-1256, 1975
A;Title: Structure of the pentapeptide proctolin, a proposed neurotransmitter in inse A;Reference number: A30408; MUID:76074708
A;Accession: A01644
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S43014
hypothetical protein URF-2Y - Yersinia enterocolitica transposon TN3926
C;Species: Yersinia enterocolitica
C;Species: Versinia enterocolitica
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C;Accession: S43014
Sibbourn, S.E.V.; Turner, A.K.; Grinsted, J.
Submitted to the EMBL Data Library, March 1994
A;Reference number: S43011
A;Reference number: S43011
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A) Residues: 1-4 <OSB>
A) Cross-references: EMBL:X78059; NID:g460067; PIDN:CAA54980.1; PID:g581836
C) Genetics:
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Pred. No. 1.8e+05;
0; Mismatches 1; Indels.
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Pred. No. 1.8e+05;
1; Mismatches 0;
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     A;Molecule type: protein
A;Residues: 1-9 <PIT>
C;Keywords: glycosidase; hydrolase
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ilarity 66.7%;
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Best Local Similarity 100.
Matches 2; Conservative
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Best Local Similarity
Matches 2; Conserv
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Matches 2; Conserv
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7 ANI 9
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C;Species: Acremonium persicinum persici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G:Species: Naja naja oxiana (Asian cobra, Oxus cobra)
C:Species: Jr.Mar.1992 #sequence_revision 27-Mar.1992 #text_change 23-Jun-1993
C:Accession: A41117
R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
R:Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
A:Title: Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo A:Reference number: A41117; MUID:91296772
A:Reference number: A41117
A:Accession: A41117
A:A
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A:Title: Junctional sequences of fetal T cell receptor beta chains have few N regions. A:Reference number: PT0509; MUID:91277601
A:Reference number: PT0725
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-8 <FEE>
A:Experimental source: newborn thymus, strain BALB/C
C:Keywords: T-cell receptor
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C;Accession: PT0/25
R;Feeney, A.J.
                                                        Gaps
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Pred. No. 1.8e+05;
1; Mismatches 1; Indels
                                                        Indels
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Best Local Similarity 66.7%; Pred. No. 1.8e+05;
Matches 2; Conservative 1; Mismatches 0;
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Pred. No. 1.8e+05;
0; Mismatches 2;
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34

RESULT

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Copper resistance protein A - Pseudomonas syringae pv. tomato (fragment)

C;Species: Pseudomonas syringae pv. tomato
C;Species: Pseudomonas syringae pv. tomato
C;Species: Pseudomonas syringae pv. tomato
C;Species: Jo-Jun-1992 #sequence_revision 19-Jun-1992 #text_change 24-Jun-1993
C;Accession: A41225
R;Cha, J.S.; Cooksey, D.A.
R;Cha, J.S.; MulD:92020961
R;Cha, J.S.; Cooksey, D.A.
R;Cha, J.S.; MulD:92020961
R;Cha, J.S.; Cha, J.S.; MulD:92020961
R;Reference number: A41225
R;Cha, J.S.; MulD:92020961
R;Reference number: A41225
R;Ref
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C;Spécies: Limulus polyphemus (Atlantic horseshoe crab)
C;Spécies: Limulus polyphemus (Atlantic horseshoe crab)
C;Date: 03-Feb-1993 #sequence_revision 03-Feb-1993 #text_change 17-Mar-1999
C;Accession: A60411
R;Groome, J.R.; Tillinghast, E.K.; Townley, M.A.; Vetrovs, A.; Watson III, W.H.; Hunt, I Reptides 11, 205-211, 1990
A;Title: Identification of proctolin in the central nervous system of the horseshoe crab
A;Accession: A60411
A;Accession: A60411
A;Accession: Drotein
A;Accession: Drotein
A;Accession: Drotein
A;Residues: 1-5 <GRO
C;Comment: This neuropeptide stimulates cardiac output and hindgut motility in the horse
C;Keywords: neuropeptide
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Pred. No. 1.8e+05;
1; Mismatches 0; Indels
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66.78;
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Best Local Similarity 66.73
Matches 2; Conservative
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2 SGS 4
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Search completed: December 16, 2000, 03:35:12 Job time: 5645 sec

| K. oxytoca R-spect LFA-1 alpha subuni Internal tryptic p V beta 6 clone fou Peptide encoded by | B. thuringiensis e IL-6 antagonist pe Antigen fragment 1 Human cytohesin-1 Rheumatoid arthrit | B. thuringlensis d B. thuringlensis e E. coli DNA polyme Nonameric mimotope | Synthetic pMEL17 p Fragment of enzyme HLA binding plu-1 | HLA binding piu 1 HLA binding plu-1 Immunogenic peptid | Immunogenic pertid Phytase derived pe Monomeric peptide | Protease Noxin-1 P Enzyme inhibitor p Peptide fragment o Human MHC class II | Human leucocyte an Human leucocyte an B. stearothermophi | VatC peptide fragm Tyrosinase 2 deriv Factor Xa inhibiti | Pyrrolobenzodiazep Human bc12 proto-o Rheumatoid arthrit | Heat shock protein Amino acid sequenc Heat shock protein | VIF-derived HIV pr PVX-2 viral replic | 1ryptic Iragment 1 Peptide derived fr Peptide framment (| Antigen fragment 1 Antigen fragment 1 Antigen fragment 1 | Control peptide 92 Class II MHC antig | Synthetic pMEL17 p Chlamydia trachoma | Containgura trachoma Human cytohesin-1 Synthetic polybept | HLA binding plu-1 | pind | plu-l arthri | | | | |
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| W40267 R09414 R88476 Y23411 R29031 | R78208 R37221 R73808 W54298 Y41847 | R34629 R78218 W36092 R69993 | W38383 W19861 Y55448 Y55529 | Y55623 Y46533 Y47062 | Y47532 R46809 R46700 | R74536 W57004 R41929 R87430 | W49339 W49340 W70078 | W96297 Y56575 Y28182 | Y83831 Y21209 Y41846 | Y17023 Y54382 Y16852 | W94102 W82429 | R22425 R59233 | R73856 R73809 R87433 | R70067 R87006 | W38393 W15173 W15173 | W54299 W54515 | Y55366 Y55506 | Y55507 | Y41907 | Y42029 Y42038 Y31774 | ALIGNMENTS | | AA . |
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| 22222 | | | | | | | | | | | | | | | | | | | | | | - | 1 19723 19723; |
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| ນ ດ | oo: | Title: US-09-529-121-1 Perfect score: 45 Sequence: 1 YLSGANLNL 9 | Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 | Searched: 268485 seqs, 34193795 residues Total number of hits satisfying chosen parameters: 61695 | Minimum DB seq length: 0 Maximum DB seq length: 9 | Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries | Database : A_Geneseq_36:* 1: /SIDS6/gogdata/geneseq/geneseqp/AA1980.DAT:* | <pre>.: />1.00/yguquard/yeneseqf/geneseqf/AA1991.bAT:* 3: /S1DS6/gcgdata/geneseqf/geneseqg/AA1982.bAT:* 4: /S1DS6/gcgdata/geneseqf/geneseqp/AA1983.bAT:* 4: /S1DS6/gcgdata/geneseqf/geneseqp/AA1983.bAT:*</pre> | 7: /SIDS6/gcgdata/geneseg/genesegp/AA1984: DAT:* 7: /SIDS6/gcgdata/geneseg/genesegp/AA1985:DAT:* 7: /SIDS6/gcgdata/geneseg/genesegp/AA1986.DAT:* | 8: /SIDS6/gogdata/geneseqp/AA11947.DAT:* 9: /SIDS6/gogdata/geneseqp/AA1988.DAT:* 10: /SIDS6/gogdata/geneseqp/AA11989.DAT:* | 11: /SIDS6/gcgdata/geneseq/geneseqp/AA1990.DAT:* 12: /SIDS6/gcgdata/geneseq/geneseqp/AA1991.DAT:* 13: /SIDS6/gcgdata/geneseq/geneseqp/AA1903.DAT:* | 14: /SIDS6/gcgdata/geneseq/AA1993 DAT:* 15: /SIDS6/gcgdata/geneseq/geneseqp/AA1993 DAT:* | 16: /SIDS6/gcgdata/geneseq/geneseqp/AA1995.DAT:* 17: /SIDS6/gcgdata/geneseq/geneseqp/AA1996.DAT:* 18: /SIDS6/gcgdata/geneseq/geneseqp/AA1997.DAT:* | 19: /SIDS6/gcgdata/geneseq/geneseqp/AA1998.DAT:* 20: /SIDS6/gcgdata/geneseq/geneseqp/AA1999.DAT:* | /sinso/g | r than or equal to the score of the result ed by analysis of the total score distribut | SUMMARIES | | Score Match Length DB ID Description | 45 100.0 9 18 W39723 Human carcin 45 100.0 9 19 W77134 CEA synthetic | 45 100.0 9 19 W70045 CEA derived HLA-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A-A- | 43 95.5 9 20 42 93.3 9 21 40 88.9 9 9 20 | 8 84.4 9 17 W00680 Peptide comprision 8 84.4 9 20 Y09527 Carcinoembryonic 6 80.0 9 20 Y09529 · Carcinoembryonic 6 80.0 9 17 W00690 · NCA analogue of r |

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The peptide epitope W77119-W77138 were created for human tumour-specific cytocoxic T lymphocyte response. These peptides are are cysteinedepleted mutants of a native disease-specific CTL epitope. The cysteinedepleted CTL epitopes elicit a stronger or more specific CTL response than the native epitope. The epitopes can be used in a disease-specific immunogen to protect a mammal against disease in particular melanomas. The peptides may also be used to screen a sample for the presence of an antigen with the same epitope, or with a different cross-reactive
                                                                                                                                                                                                                                                                                               Disease specific immunogen – comprises disease specific cytotoxic \tau lymphocyte epitope used to elicit melanoma specific CTL response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human leukocyte antigen; HLA; tumour associated antigen; cancer; antigen presenting cell; APC; immunogenic peptide; immune disorder; viral infection; AIDS; hepatitis; bacterial infection; malaria; CEA; fungal infection; tuberculosis; melanoma; carcinoembryonic antigen.
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                                                                                                                                                                                                                     Slingluff CL;
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                                                                                                                                                                                                                       Kittlesen D,
                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27; 93pp; English.
                                                                                                                                                                            (UYVI-) UNIV VIRGINIA PATENT FOUND.
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides W39430-W39734 are used in a novel method for the selection of immunogenic T-cell peptide epitopes present in polypeptide antigens. The method involves the identification of peptide sequences capable of binding to an HLA (human leukcoyte antigen) class I molecule and measuring the binding of this epitope peptide to the HLA class I peptide. The stability of binding of the peptide and MHC (major histocompatability complex) class I molecule is measured on intact human B cells carrying the MHC molecule at their cell surfaces. The method can be used to select peptide epitopes for generating vaccines against a disease associated with the polypeptide, e.g. cancers or AIDS. The peptide epitopes are especially T-cell peptide epitopes with strong anti-tumour and anti-viral fammune responses. Peptide W39723 is derived from the human carcino-embryonic antigen (CEA) and has the ability to bind to the human MHC class I allele HLA-A2.1.
                                                                                          T cell epitope; immune response; human leukocyte antigen; HLA Class I; vaccine; immunogenic; major histocompatablilty complex; MHC; B cell; disease; anti-tumour; anti-viral.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Van Der Burg SH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                     Human carcina-embryonic antigen (CEA) peptide (pos. 571-579).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of selecting T cell peptide epitope(s) - by measuring ity of HLA class I-peptide complexes on intact B cells
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(SCIS-) SCI SEED CAPITAL INVESTMENTS BV.
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96EP-0201145
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Best Local Similarity 100.
Matches 9; Conservative
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Anying a human major histocompatibility complex (MHC) class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLAA subtypes HLA-AZ.1, AI, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound or HLA molecule, rather than the intact foreign antigen litself, and are particularly important in tummour rejection and in fighthing vital infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) are prostate cancer, hepatitis B and C AIDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLS x vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful can but immunisation as above.
                                             New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases
                                                                                                                                                                     1mmunogenic peptides
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100.0%; Pred. No. 2.1e+05;
ive 0; Mismatches 0;
                                                                                                                                                                Y45390 to Y48214 represent specifically claimed
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                                                                                                                   Claim 1; Page 118; 150pp; English
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Best Local Similarity luv.v.
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WPI; 1999-551214/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences shown in W70044 to W70052 represent peptides derived from carcinoembryonic antigen (REA). The peptides can bind to a human leukocyte antigen (HLA), HLA-2.1 and are used to exemplify the method of invention of producing antigen. Specific cytotoxic T cells (TLS) in viro. The method comprises contacting immunogenic peptides from an antigen that binds class I major histocompatibility complex (MHC) molecules with antigen presenting cells (APCS) pretreated with pretreatment growth factors, and incubating the APCS with purified CDB cells in the presence of at least 2 incubation growth factors, thereby producing antiger specific CTLs. A method for specifically Willing target cells in a human patient is also provided which comprises obtaining a fluid sample containing CTLs from a patient, contacting the cytotoxic T cells with APCS pretreated with pre-treatment growth factors, where the APCs comprise class I MHC molecules. The pretreated APCs are incubated with the cytotoxic growth factors, thereby producing activated CTLs which are contacted with a carrier to form a composition. The composition can then be administered to the patient. The activated CTLs can be used for treating cancers, immune disorders, viral infections, and be used for treating cancers, immune disorders, viral infections.
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                                        Production of antigen-specific cytotoxic T cells - by incubating immunogenic peptide(s) from antigen that binds class I major histocompatibility complex molecules with pre-treated antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Match 100.0%; Score 45; DB 19; Length 9; Local Similarity 100.0%; Pred. No. 2.1e+05; les 9; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                         Example 6; Page 75; 104pp; English.
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                                                                                                                 presenting cells
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                                                                                                                               The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or
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Peptide agonists and antagonists of carcinoembryonal antigen
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Pred. No. 2.1e+05;
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                                                               Claim 1; Page 53; 72pp; English.
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immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allele-specific binding motif; major histocompatibility complex; MHC; HLA; HLA-A2.1; cytotoxic T cell response; antigen; microbial infection; hepatitis; AIDS; malaria; condyloma acuminatum; cancer; prostate cancer; renal carcinoma; cervical carcinoma; lymphoma; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressing a specific Mic class I allele) with the present peptides. The peptides are used to treat and prevent microbial infection (e.g. in viral hepatitis B and C, human papilomavirus (HPV) infection, AIDS, cytomegalovirus (CMV), malaria, and condyloma acuminatum) and cancer (e.g. prostate cancer, renal carcinoma, cervical carcinoma, lymphoma). Patients in the acute phase of infection can be treated with the peptides in conjunction with other treatments. The antigenic peptides may be used to elicit cytotoxic T lymphocytes (CTLs) ex vivo and in vivo. The resulting CTLs can be used to treat chronic infections (viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA binding immunogenic peptides used to induce T cell activation
                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides Y54171-Y54236 represent immunogenic peptides comprising an
                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                Length 9;
                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                Score 43; DB 20;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                               YS4173
ID YS4173 standard; peptide; 9 AA.
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                                                                                                                                                                                            95.68;
88.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-APR-2000 (first entry)
                                                                                                                                                                                                                Best_Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-106018/09.
                                                                                                                                     9 AA;
                                                                                                                                                                                                                                                                       1 YLSGANLNL 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Y54173;
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Generation of human cytotoxic T-cells specific for CEA - useful in therapy, epitope mapping and drug screening
                                                                                                                                                                                            Peptide comprising residues 571-579 of Carcinoembryonic antigen.
                                                                                                                                                                                                                       Carcinoembryonic; antigen; human; cytotoxic T cell; pox virus; vector; epitope; determination; screening; tumour; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                     (THER-) THERION BIOLOGICS CORP. (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Page 57; 76pp; English.
                                                                                                          W00680 standard; peptide; 9 AA.
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1996-402364/40.
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| ylsgadln1
               1 YLSGANLNL
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                                                                                                                                                                                                                                                                                                                                                  13-FEB-1996;
                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                  01-MAY-1997
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                                                                                                                                       W00680;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but CEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (Ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
or bacterial) or tumours in patients that do not respond to conventional forms of therapy. The peptides may also be used to produce monoclonal antibodies, which are useful as potential diagnostic or therapeutic agents. The peptides may also be used as diagnostic reagents.
                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                         Carcinoembryonic antigen; CEA; human; agonist; antagonist; limmue response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                         Score 42; DB 21; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Carcinoembryonic antigen peptide agonist SEQ ID NO:2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 53; 72pp; English.
                                                                                                                                                                                                                                                              Y09526 standard; peptide; 9 AA.
                                                                                                          93.3%;
88.9%;
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                                                                                                                                       8; Conservative
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                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                     Matches
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Tsang KY;

96WO-US02156. 95US-0396385

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cells (CTC), comprises introducing a lst pox virus vector, having at least 1 insertion site containing a DNA segment encoding a CEA peptide (i.e. the present peptide) to a host to stimulate CTC production, and at least 1 periodic interval after that, contacting the host with an additional antigen. The CEA specific CTC can be compounds which enhance the ability of the antigen to create a creen for compounds which enhance the ability of the antigen to create a cTC response. A host with a CEA expressing tumour can be treated by introducing the CTC to the host, and at least 1 periodic interval after that introducing a CEA peptide, i.e. the present peptide. The present peptide is positive for binding to HLA-A2, and scored supropriate peptide results in the upresponding of an appropriate peptide results in the upresponding of an appropriate peptide results in the upresponding of surface HLA-A2 antibody (background 280 and 300).
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Producing carcinoembryonic antigen (CEA) specific human cytotoxic T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.4%; Score 38; DB 17; Length 9; 100.0%; Pred. No. 2.1e+05; ive 0; Mismatches 0; Indels
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Best Local Similarity
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Gaps

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DB 20; Length 9; 2.1e+05; thes 0; Indels

Score 40; DB 2 Pred. No. 2.1e+ 1; Mismatches

88.9%; 88.9%;

Conservative

Query Match Best Local Similarity Matches 8; Conserv

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1 ylsgacini
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              sapiens.
                                            WO9919478-A1
                                                                                                               10-OCT-1997;
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                       Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                     or antigonists (ID) of human carchinomic policy and carchine used in vaccines to kill or inhibit carchinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carchinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (ID) are used to inhibit CEA-specific. Ammune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but GEA-expressing cells). (Ia) are more active than native sequence (I) and generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
                                                                                                                                                                                                                                                                                                                                                                           The present invention describes peptides (A) that comprise agonists (Ia)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                         Carcinoembryonic antigen; CEA; human; agonist; antagonist; mimmune response; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carcinoembryonic antigen; CEA; human; agonist; antagonist; miner esponse; carcinoma; gastrointestinal; breast; pancreatic; bladder; ovarian; lung; prostatic; T cell proliferation; cancer; adoptive transfer therapy; autoimmune reaction; immunotherapy.
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                                                                                                                                                                                                                                                                                                                              Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
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                                                      Carcinoembryonic antigen peptide agonist SEQ ID NO:3.
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Pred. No. 2.1e+05;
2; Mismatches 0;
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77.88;
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                              20-JUL-1999 (first entry)
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Best Local Similarity 77.8
Matches 7; Conservative
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| ylsgadinl
                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                  Barzaga E,
                                                                                                                                            Synthetic.
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          Y09527;
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The present invention describes peptides (A) that comprise agonists (Ia) or antagonists (Ib) of human carcinoembryonal antigen (CEA). (Ia) are used in vaccines to kill or inhibit carcinoma cells that express CEA or its epitopes, particularly for treating gastrointestinal, breast, pancreatic, bladder, ovarian, lung or prostatic carcinoma. They can also be used to proliferate T cells, e.g. from vaccinated subjects, for use in adoptive transfer therapy. (Ib) are used to inhibit CEA-specific immune responses, e.g. in vaccinated subjects, to prevent an autoimmune reaction to cancer immunotherapy (i.e. to prevent attack on normal but generate a highly specific and systemic anti-CEA response. Cytotoxic T cells generated recognize both (ia) and native CEA epitopes. The present sequence represents a specifically claimed example of (Ia).
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                                                                                                                                                                                                                                                                 Peptide agonists and antagonists of carcinoembryonal antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 20; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 1; Indels
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                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 53; 72pp; English
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88.9%;
97us-0061589
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                                                                                                                                                                                                WPI; 1999-326544/27.
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Best Local Similarity
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Gaps
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                                                        Gaps
                                                                                                                                                                                                                                                                            Lymphocyte function associated antigen; inflammation; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pure alpha subunit of lymphocyte function associated antigen and encoding DNA sequences, useful eg for suppressing inflammation or metastasis
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                           Score 22; DB 19; Length 9;
Pred. No. 2.1e+05;
0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 11; I Pred. No. 2.1e+05; 0; Mismatches 0;
                                                                                                                                                                                                                                                 LFA-1 alpha subunit polypeptide (k).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of viral infections.
The pref. dose is 1 pg - 10 mg/kg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46.7%; Sco.
100.0%; Pre
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6; Page 19; 27pp; English.
                                                                                                                                                                      R09414 standard; Peptide; 6 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 AA
                            48.98;
                                       62.5%;
                                                                                                                                                                                                                                                                                                                                                        89EP-0115160
                                                                                                                                                                                                                                                                                                                                                                                88US-0235227
89US-0321017
                                                                                                                                                                                                                                                                                                                                                                                                                       (DANA-) DANA FARBER CANCER
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Springer TA, Larson R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
4; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1990-108985/15.
                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R88476 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AA;
                                                                              1 YLSGANLN 8
                                                                                                      æ
                                                                                                      1 ytvgamln
                                                                                                                                                                                                                                                                                                                                                      17-AUG-1989;
                                                                                                                                                                                                                          23-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                23-AUG-1988;
                                                                                                                                                                                                                                                                                                                              11-APR-1990
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                                                                                                                                                                                                                                                                                                    EP362526-A.
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2 ylsg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R88476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                                                                                               14
                                                      Matches
                                                                                                                                              RESULT
R09414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W40264-W40275 are peptide fragments of an R-specific amidohydrolase isolated from Klebsiella oxytoca strain PRS1. This enzyme allows the microorganism to utilise 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide as its sole nitrogen source. This amidohydrolase is used in a process for preparing (R)-1soforms of 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide which is cheaper than prior art optical resolution of the racemate using dimethoxy strychnine or (S)-(-)- alpha -methylbenzylamine.
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tri:fluoro-2-hydroxy-2-methyl-propionic acid enantiomer preparation - by stereoselective hydrolysis of corresponding racemic amide using microorganism or derived enzyme, used as drug intermediate
                                                    ŗ
                                                                                                                 The present peptide is negative for binding to HLA-A2, and scored 252 and 225 in T2 cell binding assays, where the binding of an appropriate peptide results in the upregulation of surface HLA-A2 on the T2 cells, which can be quantified via FACScan using an anti-HLA-A2 antibody (background 280 and 300).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R-specific amidohydrolase; hydrolysis; racemate; nitrogen source; 3,3,3-trifluoro-2-hydroxy-2-methyl propionamide; isoform.
                                                Generation of human cytotoxic T-cells specific for CEA - useful therapy, epitope mapping and drug screening
                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                   DB 17; Length 9;
                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tinschert
                                                                                                                                                                                                                                                                                                                                                                                                                                                            K. oxytoca R-specific amidohydrolase peptide T5.
                                                                                                                                                                                                                                   Score 29; DB 17;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shaw N,
                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10.2; Page 29; 68pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Robins K,
                                                                                         Example 2; Page 60; 76pp; English
                                                                                                                                                                                                                                                                                                                                                                               W40267 standard; Protein; 9 AA.
 Tsang
                                                                                                                                                                                                                                    64.48;
66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-EP03670.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97CH-0000500.
96CH-0001723.
                                                                                                                                                                                                                                                                                                                                                                                                                                 16-JUN-1998 (first entry)
                                                                                                                                                                                                                                                              6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Naughton A,
Schlom J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-101063/09.
                         WPI; 1996-402364/40
                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LONZ ) LONZA AG.
                                                                                                                                                                                                                                                                                     1 YLSGANLNL 9
                                                                                                                                                                                                                                                                                                              1 yrpgeninl 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AA;
                                                                                                                                                                                             9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zimmermann T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-MAR-1997;
10-JUL-1996;
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                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        W40267;
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Frective amounts of T cell receptor (TCR) peptides. The TCRs are present on the surface of T cells. The TCRs are chosen from V beta 6.2/3, V beta 6.7, V beta 7 or V beta 13.

The V beta TCR peptide-based vaccines are useful for prevention or treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears to be particularly associated with multiple sclerosis and can be used to determine an individual's susceptibility to multiple sclerosis.

Vaccinating, rather than passively administering heterologous antibodies, allows the host's own immune system to mobilize and suppress auto agressive T cells. Therefore, the suppression is persistent and may involve any and all immunological mechanisms in effecting that suppression. Such a multi-faceted response is more effective than monoclonal antibodies or extant-derived regulatory T cell clones.

Yanging represent peptides derived from TCR V beta 6 clones found in the cerebrospinal fluid (CFS) of MS patients, after vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                       The specification describes vaccines which comprise immunologically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                     Smith LR, Wilson DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 20;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide encoded by ant-active toxin gene probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      TO cell receptor peptide-derived vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                Example 11; Page 85; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                   Gold DP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'label= Arg or Lys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Trp or Tyr
                                                                                                                                                                                                                                          (KIMM-) KIMMEL CANCER CENT SIDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Ile or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R29031 standard; Protein; 8 AA.
                                                                                                                                                                                                                        (IMMU-) IMMUNE RESPONSE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.78;
                                                                                                                                                                               97WO-US23147.
                                                                                                                                     97WO-US23147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-APR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Conservative
                                                                                                                                                                                                                                                                                     Carlo DJ,
                                                                                                                                                                                                                                                                                                                           WPI; 1999-404801/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin protein; ant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with V beta 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSGANL 7
                                                W09927957-A1.
                                                                                                                                                                                                                                                                                     Brostoff SW,
          Homo sapiens
                                                                                                                                   03-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| ||
| lagtn| (
                                                                                         10-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R29031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 17
R29031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
        οy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequences given in R88473-80 are internal tryptic peptides derived from trehalose-6-phosphate (Tre6P) synthase from M. Smegmatis. Tre6P is the Keye mrzyme in the synthesis of trehalose via Tre6P. The aim of the invention is to produce a transgenic plant with increase trehalose content. Tre6P in M. smegmatis is chepatin-activated and was isolated and purified. These peptides were derived from a protein which was purified with a mol. wt. of 55 kD which shared antigenic determinants with the yeast Tre6P content. Using these peptides probes may be designed for the isolation of the Tre6P gene (TSPI) for the production of the transgenic plants. The trahalose may be isolated from the transgenic plants. The trahalose may be isolated from the transgenic plants and used in bulk preparation including the preservation of the content of stock and structure of food stuffs during drying. Fruits and berries form the transformed plants may be processed into purees, jellies and increased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                         Tryptic peptide; trehalose-6-phosphate synthase; M. smegmatis; probe; trehalose; transgenic plant; heparin-activated; preservation; food; antigenic determinant; yeast; TSP1; fruit; berry; puree; jelly; jam.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New transgenic plants with increase trehalose contents - prepd. by transforming plants with a trehalose-6-phosphate synthase gene fused to a non-constitutive promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6; multiple sclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  V beta 6 clone found in MS patients after vaccination with TCR.
Internal tryptic peptide from Tre6P synthase (peak 29) #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 17; Length 6; Pred. No. 2.1e+05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Mandal A, Mantyla E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Page 36; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Holmstrom K, Londesborough J,
Palva ET, Tunnela O, Welin B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y23411 standard; Peptide; 6 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46.7%;
80.0%;
                                                                                                                                                                                                                                                         95WO-FI00377.
                                                                                                                                                                                                                                                                                                   94FI-0003133.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                              Mycobacterium smegmatis
                                                                                                                                                                                                                                                                                                                                            (ALKO-) ALKO GROUP LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1996-077499/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trehalose content,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 AA;
                                                                                                                                                                      WO9600789-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YLSGA 5
                                                                                                                                                                                                                                                         29-JUN-1995;
                                                                                                                                                                                                                                                                                                   29-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                               11-JAN-1996
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                                                                                                       The nucleotide sequence which encodes R78208, a B. thuringlensis (B.t.) endotoxin derived peptide, specifies the degenerate probe Q94857. The probe can be used for the detection of endotoxin producing B.t. microbes. The probe aids in the search for useful microbes hosting toxin encoding genes, specifically from nematode species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IL-6; antagonist; cytokine; B cell differentiation; inflammation; tissue injury; B9.9 hybridoma cell line; Castleman's Disease; Lennart's T-cell lymphoma; Non-Hodgkin's lymphoma; allergy; Immune deficiency disease; cardiac myxoma; mesangial proliferative glomerulonephritis.
               Nucleotide sequence used as probes to identify Bacillus thuringiensis - are derived from the B.thuringiensis endotoxin genes, for identifying microbes which encode toxins
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide interleukin-6 antagonists - for treating and preventing auto-immune, immuno:inflammatory, neoplastic and infectious diseases etc.
                                                                                                                                                                                                                                                                         Score 21; DB 16; Length 8;
Pred. No. 2.1e+05;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scholz W;
                                                                            Claim 1; Columns 41-42; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Column 27; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagarajan G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R37221 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                         46.78;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0480868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IL-6 antagonist peptide #5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TANA ) TANABE SEIYAKU CO.
                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                           Lobl TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1993-166970/20
                                                                                                                                                                                                                          8 AA;
                                                                                                                                                                                                                                                                                                                                      1 YLSGAN 6
                                                                                                                                                                                                                                                                                                                                                                    8
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3 wingan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chiang S,
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                    a
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                                                                                                                                                                                                                                                                                                                                                     - for controlling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide (or point mutation variants as shown in the features) is encoded by nucleotide probes used in the rapid identification of Bacillus thuringlensis ant-active toxin genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endotoxin; probes; microbes; peptide; detection; nematode.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 13; Length 8; Pred. No. 2.1e+05; 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                          Uick HJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sick
                                                                                                                                                                                                                                                                                                                                                     Toxin proteins isolated from Bacillus thuringiensis – i
amts. e.g. fire, carpenter, argentine and pharaoh ants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schwab GE,
                                                                                                                                                                                                                                                                         Randall JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B. thuringiensis endotoxin derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schnepf HE,
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 56; 71pp; English.
                /label- Ala or Asn
                                                /label- Asn or Gln
                                                                                                                                                                                                                                                                          Payne JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R78208 standard; Peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92US-0968781.
89US-0427068.
91US-0737569.
                                                                                                                                                                        91US-0703977.
91US-0797645.
92EP-0304228.
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                                                                                                                                          92WO-US04316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Narva KE,
                                                                                                                                                                                                                                                                                                                       N-PSDB; Q31414, Q31415.
                                                                                                                                                                                                                                                                         Kennedy MK, Meier H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus thuringiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                                                           (MYCO ) MYCOGEN CORP.
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                                                                                                                                                                                                                                                                                                        WPI; 1992-415780/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 3; Conserv
Misc-difference 7
                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YLSGAN 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :::|||
3 wingan 8
                                                                                                                                                                        22-MAY-1991;
25-NOV-1991;
12-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaertner FH,
Thompson M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-OCT-1989;
                                                                                                                                            22-MAY-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1991;
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                                                                            WO9220802-A
                                                                                                            26-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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W54298 standard; Peptide; 9 AA.
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                                                                                                                                                                                                      W09745538-A1.
                                                                                           28-AUG-1998
                                                                                                                                                                                                                                                   30-MAY-1997;
                                                                                                                                                                                                                                                                        31-MAY-1996;
                                                                                                                                                                                                                             04-DEC-1997.
                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                  vaccines
                        RESULT
W54298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R73685-876 are potential peptide binders of HLA-A2.1 motif. Using motifs disclosed in the invention, these peptides were screened for further motifs. Only peptides with binding affinity of at least 1% (binding affinity is expressed as an IC50 value) as compared to the standard peptide (R71293) in assays. This peptide from LCWV (sic) Np antigen has a binding value of 0.0200. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg.
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                            antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2; MAGE-1; melanoma antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2.1; 9mer; loner; anchor; human leukocyte antigen; PLP; 8mer; ealgorithm prediction; MBP; CMV; cytomegalovirus; HSV; herpes simplex virus; influenza A; M1; LCMV.
                                                                                                                                                                                        Antigen fragment 124, from LCMV has binding affinity for HLA-2.1.
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Score 21; DB 14; Length 9; Pred. No. 2.1e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 9;
                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 15; Length 9;
Pred. No. 2.1e+05;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sidney J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 84; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate cancer or lymphoma, etc.
                                                                                                                      R73808 standard; peptide; 9 AA.
46.78; 62.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0027146.
93US-0073205.
93US-0159184.
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                                                                                                                                                                   (first entry)
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CYTE-) CYTEL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kast WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-302678/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity
Matches 4; Conserv
 Query Match
Best Local Similarity
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| laennln| 8
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                                            2 LSGANLNL 9
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04-JUN-1993;
29-NOV-1993;
                                                                                                                                                                   19-JUN-1995
                                                                                                                                                                                                                                                                                                                                                 WO9420127-A.
                                                                                                                                                                                                                                                                                                                                                                        15-SEP-1994
                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                              R73808;
                                                                                                  RESULT 20
                      Matches
                                                                                                               R73808
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This is a randomised AB loop encoded by clone 7 (see V26501) of a large peptide library (2 million clones) of synthetic Pleckstrin homology (PH) domains with randomised discontinuous surface epitopes. The progenitor AB sequence comprises amino acid residues (5.21 of a stabilised synthetic PH domain (see W54310) of human cytohesin 1. The peptide library was generated by randomisation of AB and CD loop regions using randomised oligonucleotide primers (see W5492-309) of the peptide library are provided. Randomisation did not compromise the structural integrity and folding stability of the progenitor domain. The invention provides vectors that are used for the production of PH domain-like peptide libraries, which can be screened to identify peptides that have desirable properties, continuous in research or therapy, or as vaccines. Novel synthetic protein structural templates for the generation, screening and continuous of functional molecular surfaces are provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vectors used to produce PH domain-like peptide libraries - which are screened for therapeutically useful peptide(s), e.g. to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                             Pleckstrin homology domain; PH domain; peptide library; functional molecular surface; protein structural template; vaccine; gene therapy; cytohesin 1; human.
                                                            Human cytohesin-1 PH domain randomised AB loop (clone 7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 21; DB 19; Length 9; Pred. No. 2.1e+05; 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steipe B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Fig 12; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y41847 standard; Peptide; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bruhn H, Funk M, Henkel T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-EP02840.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MEDI-) MEDIGENE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-230215/20.
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Best Local Similarity
Matches 4; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y41847
ID Y4
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2 LSGANLNL 9 : | | : | 2 isgynfsl 9

gg gs

Y41847;

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The sequences given in R35090-100 and R34628-32 are peptides which were used to design the probes given in Q40219-34. These probes can be used to identify Bacillus thuringiansis (Bt) DNA which encodes insecticidally active endotoxin. Probe (a) identifies genes encoding a toxin effective against any sort of insect. Sequences (b) and (e)-(l) are specific for toxins against lepidopters; sequences (c), (m) and (n) for toxins active against dipter and sequence (d), (o) and (p) for toxins active against coleoptera.
                                                                                              thuringiensis; Bt; insecticidal; active; endotoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene probe for identifying endotoxin sequences in Bacillus thuringiensis - are universal, type specific or gene specific, for rapid detection and characterisation of insecticidal activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 14; Length o; Pred. No. 2.1e+05;
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    B. thuringiensis dipteran toxin probe (m) design peptide.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 2; 5pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                    Sick AJ;
                                                                                                                   lepidoptera; diptera; coleoptera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R78218 standard; Peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.48;
60.08;
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91US-0737569.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Schwab GE,
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                                                                                                                                                                                                                                                                                                                                                                              (MYCO ) MYCOGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1993-143952/17.
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-FEB-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                    Gaertner FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 GANLN 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-OCT-1989;
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2 gtnmn
                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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R78218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Turbution and been developed for the diagnosts of numbers of the condition and such according to the diagnosts and prognosts of Rain a subject or for monitoring the effect diagnosis and prognosis of Rain a subject or for monitoring the effect of an anti-RA drug or therapy administered to a subject. The method comprises: (a) analysing a sample of serum or plasma and optionally synchal fluid by two-dimensional electrophoresis, to generate a two-dimensional array of features; (b) identifying at least one chosen feature whose relative abundance of each chosen feature in the sample of that chosen feature in the sample with the abundance of that chosen feature in the sample with the abundance of that chosen feature in chair one or more persons without RA, where the relative abundance of the chosen feature in the sample. The management of the chosen feature in the sample indicates the presence or absence of RA in the subject. The method on also be used in clinical studies for testing drugs for therapy of RA, for purification of RA-diagnostic feature (RADF) proteins can be used to identify compounds that promote or inhibit their activity, which are then used as RA drugs. Nucleic acid encoding RADFs can be used in gene therapy of proteocols. Y41844 to Y42100 represent RPI peptides, Y42101 to Y42103 represent expression reference protein isoform peptides and Z2566 to Z25068 represent of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A method has been developed for the diagnosis of human rheumatoid
                                                                                                                   Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                   rheumatoid arthritis diagnostic feature; ERPI; synovial fluid; rheumatoid arthritis diagnostic protein isoform; screening; expression reference protein isoform; prognosis.
                                                                           Rheumatoid arthritis diagnostic protein isoform 17 peptide #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosis of human rheumatoid arthritis by two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 7;
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Pred. No. 2.1e+05;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R34629 standard; Protein; 8 AA.
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                                                                                                                                                                                                                                                                                                                                        99WO-GB00763
                                                                                                                                                                                                                                                                                                                                                                              98GB-0005477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 20; Page 150; 157pp;
                                     (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patel TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
...hos 4; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-571871/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  electrophoresis
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| sgadls 7
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                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                           W09947925-A2
                                                                                                                                                                                                                                                                                                                                        15-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                              13-MAR-1998;
                                     09-DEC-1999
                                                                                                                                                                                                                                                                                                 23-SEP-1999
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Sequence

R34629

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RESULT 23 R34629

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Gaps

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4 GANLN 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-1987;
04-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1995
                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                              1 gfnln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                                                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                         R69993;
                                                                                                                                                                                                                                                                                                                                  RESULT 26
                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a tryptic peptide from the chi subur
of the E. coli DNA polymerase III holoenzyme (W36068). Probes derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                            thuringiensis (B.t.) endotoxin derived peptides, specify the probes 094868 respectively. The probes can be used for the detection of endotoxin producing B.t. microbes. The probes aid in the search for useful microbes hosting toxin encoding genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coli; DNA polymerase III holoenzyme; probe; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated theta, chi, psi, delta and delta' protein sub:units of E. coli polymerase III holo:enzyme - used to make man-made enzyme of or 6 sub:units, useful for long chain PCR
                                                                                                                                                                              Nucleotide sequence used as probes to identify Bacillus thuringiensis - are derived from the B.thuringiensis endotoxin genes, for identifying microbes which encode toxins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E. coli DNA polymerase III chi subunit tryptic peptide chi-4.
                                                                                                                                                                                                                                                                                           The nucleotide sequences which encode R78218 and R78219, B.
                                                                                          Sick AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schwab GE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 3; Column 57-58; 65pp; English.
                                                                                                                                                                                                                                                     Claim 1; Columns 49-50; 30pp; English.
                                                                                          Schnepf HE,
                                                                                                                                                                                                                                                                                                                                                                                   specifically from dipteran species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC.
89US-0427068
91US-0737569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W36092 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                          Narva KE,
                                                      (MYCO ) MYCOGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470038/43.
                                                                                                                                            WPI; 1995-245777/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Psi subunit; E. co.
hybridisation; PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                       8 AA;
                                                                                        FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'donnell ME;
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                  26-JUL-1991;
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 25-OCT-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUL-1994;
22-JAN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GANLN
                                                                                           Gaertner
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                            Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W36092;
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R69970-993 are nonameric mimotopes designed to show high diversity in hydrophobic moment and hydrophobic index, as well as charge distribution and size. The mimotopes are used in the method of the invention to obtain antibodies specifically and strongly reactive with a desired analyte. 16 of the peptides were tested for ability to bind the murine antibody Mab33-6, arbitrarily chosen, and known to bind to the peptides MB3 and MB4. 3 of the 16 peptides successfully bound Mab33-6. The mimotope is obtd. by reacting a panel of starting antibodies (Abs) representative of the resting B cell repertoire of a mimotope is obtd. by reacting analyte-reacting Abs) and then reacting each of a panel of candidate mimotopes representative of a random set of 3D contours with the analyte-reacting Abs. A subject is immunised with one or more mimotopes identified and the
from the tryptic peptides W36089-W36092 were used to isolate the chi subunit gene sequence from a lambda phage library.

The E. coli polymerase III subunits (thete, chi, psi, delta and delta (T98151-T98155 respectively)) are used to make man-made enzymes comprising 5 or 6 subunits and potentially for use in long chain pcR.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonameric mimotope 24 used to obtain highly specific antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing antibodies with high specificity and affinity for an analyte - by immunisation with selected mimotope, also analyte detection kits, useful for immunoassay of materials usually analysed by HPLC
                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mimotope; antibody; production; high specificity; detection; immunoassay; high performance liquid chromatography.
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                      Score 20; DB 18;
Pred. No. 2.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Arg-NH2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 5; Fig 6; 25pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R69993 standard; peptide; 9 AA.
                                                                                                                                                                                                                                                                                                                                   44.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87US-0108130
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93US-0072190.
                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                         8 AA;
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This sequence represents a V8 proteinase digestion product of an isolated pure enzyme which is capable of catalysing the conversion of bnA to CO-DNA. CO-DNA is a form of DNA in which a carbonyl group is attached to the 1' carbon of the sugar constituent of the DNA. The enzyme can be used to convert DNA to CO-DNA which reduces or eliminates the ability of a cell to divide. The enzyme can be used for inhibiting cell proliferation and for treating tumours.
                                                                                                                                     CO-DNA; cell division; cell proliferation; tumour; lysilendopeptidase; N-terminal fragment; V8 proteinase digestion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
                                                                                                      Fragment of enzyme capable of catalysing conversion of DNA to CO-DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New enzyme which converts DNA to CO-DNA - used to reduce or eliminate the ability of a cell to divide, for inhibiting cell proliferation and treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 20; DB 18; Length 9;
Pred. No. 2.1e+05;
3; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Tokimatsu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y55448 standard; peptide; 9 AA.
W19861 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                              96WO-1B01323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA binding plu-1 peptide.
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 42.9
                                                                                                                                                                                                                                                                                                                                                                                                                                   Kagawa H, Kagawa K,
                                                                                                                                                                                                                                                                                                                                                                                                 TOKIMATSU H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-319767/29
                                                                                                                                                                                         Gallus domesticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : |||:
3 idganvh 9
                                                                                                                                                                                                                                                                                                                                                               (KAGA/) KAGAWA
(KAGA/) KAGAWA
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                                                                                                                                                                                                                           WO9720919-A1
                                                                                                                                                                                                                                                                                              27-NOV-1996;
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                                                                  24-FEB-1998
                                                                                                                                                                                                                                                            12-JUN-1997
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                                  W19861;
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Matches
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                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present peptide was used in the preparation of a novel melanoma specific immunogen, comprising at least 1 melanoma specific cytotoxic T lymphocyte (CTL) epitope, where at least 1 of the epitopes is substantially homologous to a human leukocyte antigen-A1 (HLA-A1) and HLA-A3 restricted epitope of a melanoma antigen, either pMEL-17 or tyrosinase. The immunogen can be used in vaccines for protection against melanoma in mammals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Melanoma-specific immunogens of pMel-17 and tyrosinase – useful in vaccination for producing melanoma-specific cytotoxic {\tt T} lymphocytes
                                                                                                                                                                                                                                                                                                                                                                                                                 Melanoma; immunogen; cytotoxic T lymphocyte; CTL;
human leukocyte antigen-Al; HLA-Al; human leukocyte antigen-A3;
HLA-A3; epitope; pMEL-17; tyrosinase; vaccine; protection.
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Pred. No. 2.1e+05;
3; Mismatches 1; Indels
                                                                                  Length 9;
                                                                                                                     Indels
product Abs are recovered from the serum of the subject.
                                                                                  Ouery Match 44.4%; Score 20; DB 16; L
Best Local Similarity 100.0%; Pred. No. 2.1e+05;
Matches 4; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hunt DF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cox AL, Engelhard VH, Hendrikson RC, H
Shabanowitz J, Skipper J, Slingluff CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 9; Page 65; 106pp; English.
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                                                                                                                                                                                                                                                                            W38383 standard; peptide; 9 AA.
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50.08;
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96US-0013972
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Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic pMEL17 peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-479982/44.
                                  9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 AA;
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| ylaeadls 8
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| Sigan | 8
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19-MAR-1996;
                                                                                                                                                       3 SGAN 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
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WPI; 1999-591090/50.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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0
                                                                                                                                                                                                                                                                                                                      The invention relates to a human cancer-associated polypeptide plu-1. The plu-1 polypeptide can be recombinantly expressed by standard recombinant methodology. Detection of the plu-1 nucleic acid or the polypeptide is used for the following: (1) diagnosis (including imaging) and prognosis of, and determination of susceptibility to, cancer, specifically ovarian or breast cancer; and il) treating cancer (by inducing an immune response against cancer cells, e.g. as avecine, or by antisense inhibition). Antigens derived from the polypeptide are used to generate activated cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the patient for treatment of cancer. The polypeptide may also be used to identify inhibitors of plu-1 activity. Fragments of the polypeptide, and antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (conduce an anti-idiotype response or where
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conjugated to cytotoxic agents). The plu-1 antigen is expressed more commonly in breast tumors than some known tumor antigens. Sequences Y55320-629 represent predicted peptides from the plu-1 polypetide which may bind to the human class I alleles B27, A2, A3 and A11.
                                                                                                                                                                                                                        New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
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Pred. No. 2.1e+05;
2; Mismatches 1; Indels
                                                                                                                    (IMCR ) IMPERIAL CANCER RES TECHNOLOGY
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57.18;
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Best Local Similarity 57.1
Matches 4; Conservative
                                                                                                                                                       Taylor-papadimitriou J;
                                                                                                                                                                                      WPI; 1999-591090/50.
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3 flsgdsl 9
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                                                19-MAR-1999;
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              30-SEP-1999
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The invention relates to a human cancer-associated polypeptide plu-1. The polypeptide can be recombinantly expressed by standard recombinant methodology. Detection of the plu-1 nucleic acid or the polypeptide is cancer cancer; and diagnosis (including imaging) and prognosis used for the following: (i) diagnosis (including imaging) and prognosis of, and determination of susceptibility to, cancer, specifically ovarian or breast cancer; and i) treating cancer (by inducting an immune response against cancer cells, e.g. as a vaccine, or by antisense inhibition).

Controlly inhibitors of from the polypeptide are used to generate activated cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the patient for treatment of cancer. The polypeptide may also be used to identify inhibitors of plu-1 activity. Fragments of the polypeptide, and antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (to induce an anti-idiotype response or where commonly in breast tumors than some known tumor antigens. Sequences (%55320-629 represent predicted peptides from the plu-1 polypetide which may bind to the human class I alleles B27, A2, A3 and A11.
                                                                                                                                                                                                                                     New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine; breast cancer; immune response; cytotoxic T lymphocyte; imaging agent; therapeutic; plu-1 antigen; breast tumor; tumor antigen; epitope.
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(IMCR ) IMPERIAL CANCER RES TECHNOLOGY
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57.18;
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                                                                             Taylor-papadimitriou J;
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2 flsgdsl 8
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Claim 1; Page 75; 150pp; English.

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The invention relates to a human cancer-associated polypeptide plu-1. The plu-1 polypeptide can be recombinantly expressed by standard recombinant content of the plu-1 nucleic acid or the polypeptide is blu-1 polypeptide can be recombinantly expressed by standard recombinant content of betection of the plu-1 nucleic acid or the polypeptide is used for the following: (i) diagnosis (including imaging) and prognosis cof, and determination of susceptibility to, cancer, specifically ovariant or breast cancer: and ii) treating cancer (by inducing an immune response corntigent cancer cells, e.g. as a vaccine, or by antisense inhibition).

Antigens derived from the polypeptide are used to generate activated cancer the patient for treatment of cancer. The polypeptide may also be used to identify inhibitors of plu-1 activity. Fragments of the polypeptide, and antibodies raised against plu-1, are useful as assay and imaging agents, also therapeutically (to induce an anti-idiotype response or where conjugated to cytotoxic agents). The plu-1 antigen is expressed more commonly in breast tumors than some known tumor antigens. Sequences 755320-629 represent predicted peptides from the plu-1 polypetide which commonly the human class I alleles B27, A2, A3 and A11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide having a human leukocyte antigen binding motif #1144.
                  New nucleic acid encoding the cancer-associated polypeptide plu-1, for diagnosis, treatment and prevention of cancer, especially of breast and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
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Pred. No. 2.1e+
2; Mismatches
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                                                                                            Example 2; Fig 12; 173pp; English.
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Best Local Similarity 57.1%;
Matches 4; Conservative
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2 flsgdsl 8
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National to Y48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cesponse against the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound are particularly important in the mour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) corprevent viral infections and cancers in mammals (especially humans) they can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or served to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptide e.g. to produce CTLS a vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful chapturically and for immunisation as above.
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Pred. No. 2.1e+05;
0; Mismatches 3; Indels
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57.18;
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having a human major histocompatibility complex (MHC) Class I (also having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding metif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes capainst the antigen from which the peptide is derived.

HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T ceptides can bind to a specific HLA allele (i.e. HLA-A subtypes cyalists the antigen from which the peptide is derived.

Cytotoxic T lymphocytes (CTLS) which destroy antigen bearing cells are normally induced by an antigen in the form of a peptide fragment bound in a HLA molecule, rather than the intact foreign antigen itself, and care particularly important in tumour rejection and in fighting viral infections. The peptides are therefore useful therapeutically to treat or prevent viral infections and cancers in mammals (especially humans) corporate cancer, hepatitis B and C, ALDS, and renal carcinoma. They can be administered as vaccines to elicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell response, by contacting a cytotoxic T cell with the peptides are also useful perindes encoding the immunogenic peptides are also useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenic peptide having a human leukocyte antigen binding motif #2143.
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Best Local Similarity 50.0.
                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YLSGANLN 8
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| ylaeadls 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09945954-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y47532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 34
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va5390 to V48214 represent specifically claimed immunogenic peptides having a human major histocompatibility complex (MHC) Class I (also known as human leukocyte antigen (HLA) binding motif. The immunogenic peptides can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, Al, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against the antigen from which the peptide is derived. Cytotoxic T lymphocytes (CTLS) which destroy antigen-bearing cells are normally induced by an antigen in the form of a peptide fragment bound to marmally induced by an antigen in the form of a peptide fragment bound to man and in fighting viral infections. The peptides are therefore useful therapeutically to treat infections. The peptides are therefore useful therapeutically humans) or prevent viral infections and cancers in mammals (especially humans) or prevent viral infections as vaccines to calicit an immune response in individuals susceptible or otherwise at risk of viral infection or cancer, or used to treat chronic or acute conditions. They are also useful diagnostically, and can be used to induce a cytotoxic T cell with the peptide e.g. to produce CTLs ex vivo for infusion back into a patient. The polynucleotides encoding the immunogenic peptides are also useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pH 2.5; acid phosphatase; Trichoderma; host; Aspergillus; phytic acid; phytate degrading enzyme; PDE; removal; inositol hexaphosphoric acid; plant; feed composition; filtration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compsns. contg. phytate degrading enzymes - obtd. by expression of their genes in Trichoderma, used partic. for producing animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in R46793-824 are peptides derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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Piddington C, Rambosek JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20; DB 20; Length 9;
Pred. No. 2.1e+05;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page 43; 142pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R46809 standard; Protein; 7 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cantrell M, Fagerstroem RB,
Nevalainen HK, Paloheimo MT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.4%;
55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Phytase derived peptide 675.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93WO-FI00310.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nevalainen HK, Paloheimo
Torkkeli TK, Turunen MK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-065700/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ALKO-) ALKO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YLSGANLNL 9
                                                                                                                                                                                                                                                                                                                                                                                                                  9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|| |||
| flskqylnl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R46809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 35
R46809
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New immunogenic peptides with HLA binding motif, useful in treatment and diagnosis of cancers and viral diseases $\dot{}$

Claim 1; Page 113; 150pp; English.

Southwood

Grey HM,

Celis E,

Sidney J,

Kubo RT,

Sette A,

WPI; 1999-551214/46.

(EPIM-) EPIMMUNE INC.

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CC phytase protein. The phytase protein may be used in the composition of the invention. The DNA encoding the phytase protein may be controlled in the carrichderma host which then expresses it and the controlled is collected from the culture medium. By using Trichoderma as controlled is collected from the culture medium. By using Trichoderma as containing the form the culture medium. By using Trichoderma as containing the series of a host for Aspergillus results. The enzyme composition compared to that secreted from comparitions for phytic acid or inositol hexaphosphoric acid from raw material, compositions for animals. By using Trichoderma as a source of a composition containing phytate degrading enzymes some difficult downstream processing problems, eg. filtration, that occur with xx similar Aspergillus compositions are avoided and yields are improved.
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Query Match
Best Local Similarity 66.7%; Pred. No. 2.1e+05;
Matches 4; Conservative 1; Mismatches 1; Indels
Qy 3 SGANLN 8
| | | | | | | |
Db 1 saasIn 6
Search completed: December 16, 2000, 03:07:17
Job time: 8058 sec

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0; Gaps

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